(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) **World Intellectual Property Organization**
International Bureau

(43) **International Publication Date**
21 November 2019 (21.11.2019)

WIPO | PCT

(10) **International Publication Number**
WO 2019/222657 A1

(51) **International Patent Classification:**
G01N 33/50 (2006.01) *C12Q 1/6869* (2018.01)
A61P 35/00 (2006.01) *C12N 15/07* (2006.01)

(21) **International Application Number:**
PCT/US2019/032914

(22) **International Filing Date:**
17 May 2019 (17.05.2019)

(25) **Filing Language:** English

(26) **Publication Language:** English

(30) **Priority Data:**

62/673,516	18 May 2018 (18.05.2018)	US
62/795,900	23 January 2019 (23.01.2019)	US

(71) **Applicant: THE JOHNS HOPKINS UNIVERSITY** [US/US]; 3400 N. Charles Street, Baltimore, MD 21218 (US).

(72) **Inventors: VELCULESCU, Victor E.**; 14064 Big Branch Drive, Dayton, Maryland 21036 (US). **CRISTIANO, Stephen**; 3400 North Charles Street, Baltimore, Maryland 21218 (US). **LEAL, Alessandro**; 3400 North Charles Street, Baltimore, Maryland 21218 (US). **PHALLEN, Jillian A.**; 2123 Moyer St., Baltimore, Maryland 21231 (US). **FIKSEL, Jacob**; 3400 North Charles Street, Baltimore, Maryland 21218 (US). **ADLEFF, Vilmos**; 3400 North Charles Street, Baltimore, Maryland 21218 (US). **SCHARPF, Robert B.**; 3400 North Charles Street, Baltimore, Maryland 21218 (US).

(74) **Agent: WILLIS, Margaret S.** et al.; Fish & Richardson P.C., P.O. Box 1022, Minneapolis, Minnesota 55440-1022 (US).

(81) **Designated States** *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) **Designated States** *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report (Art. 21(3))*

(54) **Title:** CELL-FREE DNA FOR ASSESSING AND/OR TREATING CANCER

(57) **Abstract:** This document relates to methods and materials for assessed, monitored, and/or treated mammals (e.g., humans) having cancer. For example, methods and materials for identifying a mammal as having cancer (e.g., a localized cancer) are provided. For example, methods and materials for assessing, monitoring, and/or treating a mammal having cancer are provided.

WO 2019/222657 A1

CELL-FREE DNA FOR ASSESSING AND/OR TREATING CANCER

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Patent Application Serial No. 62/673,516, filed on May 18, 2018, and claims the benefit of U.S. Patent Application Serial No. 62/795,900, filed on January 23, 2019. The disclosure of the prior applications are considered part of (and are incorporated by reference in) the disclosure of this application.

STATEMENT REGARDING FEDERAL FUNDING

This invention was made with U.S. government support under grant No. CA121113 from the National Institutes of Health. The U.S. government has certain rights in the invention.

BACKGROUND

1. Technical Field

This document relates to methods and materials for assessing and/or treating mammals (e.g., humans) having cancer. For example, this document provides methods and materials for identifying a mammal as having cancer (e.g., a localized cancer). For example, this document provides methods and materials for monitoring and/or treating a mammal having cancer.

2. Background Information

Much of the morbidity and mortality of human cancers world-wide is a result of the late diagnosis of these diseases, where treatments are less effective (Torre et al., 2015 *CA Cancer J Clin* 65:87; and World Health Organization, 2017 *Guide to Cancer Early Diagnosis*). Unfortunately, clinically proven biomarkers that can be used to broadly diagnose and treat patients are not widely available (Mazzucchelli, 2000 *Advances in clinical pathology* 4:111; Ruibal Morell, 1992 *The International journal of biological mark*ers 7:160; Galli et al., 2013 *Clinical chemistry and laboratory medicine* 51:1369; Sikaris, 2011 *Heart, lung & circulation* 20:634; Lin et al., 2016 in *Screening for Colorectal Cancer: A Systematic*

Review for the U.S. Preventive Services Task Force. (Rockville, MD); Wanebo et al., 1978 N Engl J Med 299:448; and Zauber, 2015 *Dig Dis Sci* 60:681).

SUMMARY

Recent analyses of cell-free DNA suggests that such approaches may provide new avenues for early diagnosis (Phallen et al., 2017 *Sci Transl Med* 9; Cohen et al., 2018 *Science* 359:926; Alix-Panabieres et al., 2016 *Cancer discovery* 6:479; Siravegna et al., 2017 *Nature reviews. Clinical oncology* 14:531; Haber et al., 2014 *Cancer discovery* 4:650; Husain et al., 2017 *JAMA* 318:1272; and Wan et al., 2017 *Nat Rev Cancer* 17:223).

This document provides methods and materials for determining a cell free DNA (cfDNA) fragmentation profile in a mammal (e.g., in a sample obtained from a mammal). In some cases, determining a cfDNA fragmentation profile in a mammal can be used for identifying a mammal as having cancer. For example, cfDNA fragments obtained from a mammal (e.g., from a sample obtained from a mammal) can be subjected to low coverage whole-genome sequencing, and the sequenced fragments can be mapped to the genome (e.g., in non-overlapping windows) and assessed to determine a cfDNA fragmentation profile. This document also provides methods and materials for assessing and/or treating mammals (e.g., humans) having, or suspected of having, cancer. In some cases, this document provides methods and materials for identifying a mammal as having cancer. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine if the mammal has cancer based, at least in part, on the cfDNA fragmentation profile. In some cases, this document provides methods and materials for monitoring and/or treating a mammal having cancer. For example, one or more cancer treatments can be administered to a mammal identified as having cancer (e.g., based, at least in part, on a cfDNA fragmentation profile) to treat the mammal.

Described herein is a non-invasive method for the early detection and localization of cancer. cfDNA in the blood can provide a non-invasive diagnostic avenue for patients with cancer. As demonstrated herein, **D**NA **E**va**l**uation of **F**ragments for early **I**nterception (DELFI) was developed and used to evaluate genome-wide fragmentation patterns of cfDNA of 236 patients with breast, colorectal, lung, ovarian, pancreatic, gastric, or bile duct cancers as well as 245 healthy individuals. These analyses revealed that cfDNA profiles of healthy individuals reflected nucleosomal fragmentation patterns of white blood cells, while patients with cancer had altered fragmentation profiles. DELFI had sensitivities of detection ranging from 57% to >99% among the seven cancer types at 98% specificity and identified the tissue of origin of the cancers to a limited number of sites in 75% of cases. Assessing cfDNA (e.g., using DELFI) can provide a screening approach for early detection of cancer, which can increase the chance for successful treatment of a patient having cancer. Assessing cfDNA (e.g., using DELFI) can also provide an approach for monitoring cancer, which can increase the chance for successful treatment and improved outcome of a patient having cancer. In addition, a cfDNA fragmentation profile can be obtained from limited amounts of cfDNA and using inexpensive reagents and/or instruments.

In general, one aspect of this document features methods for determining a cfDNA fragmentation profile of a mammal. The methods can include, or consist essentially of, processing cfDNA fragments obtained from a sample obtained from the mammal into sequencing libraries, subjecting the sequencing libraries to whole genome sequencing (e.g., low-coverage whole genome sequencing) to obtain sequenced fragments, mapping the sequenced fragments to a genome to obtain windows of mapped sequences, and analyzing the windows of mapped sequences to determine cfDNA fragment lengths. The mapped sequences can include tens to thousands of windows. The windows of mapped sequences can be non-overlapping windows. The windows of mapped sequences can each include about 5 million base pairs. The cfDNA fragmentation profile can be determined within each window. The cfDNA fragmentation profile can include a median fragment size. The cfDNA fragmentation profile can include a fragment size distribution. The cfDNA fragmentation profile can include a ratio of small cfDNA fragments to large cfDNA fragments in the windows of mapped sequences. The cfDNA fragmentation profile can be over the whole genome. The cfDNA fragmentation profile can be over a subgenomic interval (e.g., an interval in a portion of a chromosome).

In another aspect, this document features methods for identifying a mammal as having cancer. The methods can include, or consist essentially of, determining a cfDNA fragmentation profile in a sample obtained from a mammal, comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile, and identifying the mammal as having cancer when the cfDNA fragmentation profile in the sample obtained from the mammal is different from the reference cfDNA fragmentation profile. The reference cfDNA fragmentation profile can be a cfDNA fragmentation profile of a healthy mammal. The reference cfDNA fragmentation profile can be generated by determining a cfDNA fragmentation profile in a sample obtained from the healthy mammal. The reference DNA fragmentation pattern can be a reference nucleosome cfDNA fragmentation profile. The cfDNA fragmentation profiles can include a median fragment size, and a median fragment size of the cfDNA fragmentation profile can be shorter than a median fragment size of the reference cfDNA fragmentation profile. The cfDNA fragmentation profiles can include a fragment size distribution, and a fragment size distribution of the cfDNA fragmentation profile can differ by at least 10 nucleotides as compared to a fragment size distribution of the reference cfDNA fragmentation profile. The cfDNA fragmentation profiles can include position dependent differences in fragmentation patterns, including a ratio of small cfDNA fragments to large cfDNA fragments, where a small cfDNA fragment can be 100 base pairs (bp) to 150 bp in length and a large cfDNA fragments can be 151 bp to 220 bp in length, and where a correlation of fragment ratios in the cfDNA fragmentation profile can be lower than a correlation of fragment ratios of the reference cfDNA fragmentation profile. The cfDNA fragmentation profiles can include sequence coverage of small cfDNA fragments, large cfDNA fragments, or of both small and large cfDNA fragments, across the genome. The cancer can be colorectal cancer, lung cancer, breast cancer, bile duct cancer, pancreatic cancer, gastric cancer, or ovarian cancer. The step of comparing can include comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile in windows across the whole genome. The step of comparing can include comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile over a subgenomic interval (e.g., an interval in a portion of a chromosome). The mammal can have been previously administered a cancer treatment to treat the cancer. The cancer treatment can be surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy, targeted therapy, or any combinations thereof. The method also can include administering to the mammal a cancer treatment (e.g., surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy, targeted therapy, or any combinations thereof). The mammal can be monitored for the presence of cancer after administration of the cancer treatment.

In another aspect, this document features methods for treating a mammal having cancer. The methods can include, or consist essentially of, identifying the mammal as having cancer, where the identifying includes determining a cfDNA fragmentation profile in a sample obtained from the mammal, comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile, and identifying the mammal as having cancer when the cfDNA fragmentation profile obtained from the mammal is different from the reference cfDNA fragmentation profile; and administering a cancer treatment to the mammal. The mammal can be a human. The cancer can be colorectal cancer, lung cancer, breast cancer, gastric cancers, pancreatic cancers, bile duct cancers, or ovarian cancer. The cancer treatment can be surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy, targeted therapy, or combinations thereof. The reference cfDNA fragmentation profile can be a cfDNA fragmentation profile of a healthy mammal. The reference cfDNA fragmentation profile can be generated by determining a cfDNA fragmentation profile in a sample obtained from a healthy mammal. The reference DNA fragmentation pattern can be a reference nucleosome cfDNA fragmentation profile. The cfDNA fragmentation profile can include a median fragment size, where a median fragment size of the cfDNA fragmentation profile is shorter than a median fragment size of the reference cfDNA fragmentation profile. The cfDNA fragmentation profile can include a fragment size distribution, where a fragment size distribution of the cfDNA fragmentation profile differs by at least 10 nucleotides as compared to a fragment size distribution of the reference cfDNA fragmentation profile. The cfDNA fragmentation profile can include a ratio of small cfDNA fragments to large cfDNA fragments in the windows of mapped sequences, where a small cfDNA fragment is 100 bp to 150 bp in length, where a large cfDNA fragments is 151 bp to 220 bp in length, and where a correlation of fragment ratios in the cfDNA fragmentation profile is lower than a correlation of fragment ratios of the reference cfDNA fragmentation profile. The cfDNA fragmentation profile can include the sequence coverage of small cfDNA fragments in windows across the genome. The cfDNA fragmentation profile can include the sequence coverage of large cfDNA fragments in windows across the genome. The cfDNA fragmentation profile can include the sequence coverage of small and large cfDNA fragments in windows across the genome. The step of comparing can include comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile over the whole genome. The step of comparing can include comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile over a subgenomic interval. The mammal can have previously been administered a cancer treatment to treat the cancer. The cancer treatment can be surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy, targeted therapy, or combinations thereof. The method also can include monitoring the mammal for the presence of cancer after administration of the cancer treatment.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Although methods and materials similar or equivalent to those described herein can be used to practice the invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

DESCRIPTION OF THE DRAWINGS

Figure 1. Schematic of an exemplary DELFI approach. Blood is collected from a cohort of healthy individuals and patients with cancer. Nucleosome protected cfDNA is extracted from the plasma fraction, processed into sequencing libraries, examined through whole genome sequencing, mapped to the genome, and analyzed to determine cfDNA fragment profiles in different windows across the genome. Machine learning approaches are used to categorize individuals as healthy or as having cancer and to identify the tumor tissue of origin using genome-wide cfDNA fragmentation patterns.

Figure 2. Simulations of non-invasive cancer detection based on number of alterations analyzed and tumor-derived cfDNA fragment distributions. Monte Carlo simulations were performed using different numbers of tumor-specific alterations to evaluate the probability of detecting cancer alterations in cfDNA at the indicated fraction of tumor-derived molecules. The simulations were performed assuming an average of 2000 genome equivalents of cfDNA and the requirement of five or more observations of any alteration. These analyses indicate that increasing the number of tumor-specific alterations improves the sensitivity of detection of circulating tumor DNA.

Figure 3. Tumor-derived cfDNA fragment distributions. Cumulative density functions of cfDNA fragment lengths of 42 loci containing tumor-specific alterations from 30 patients with breast, colorectal, lung, or ovarian cancer are shown with 95% confidence bands (blue). Lengths of mutant cfDNA fragments were significantly different in size compared to wild-type cfDNA fragments (red) at these loci.

Figures 4A and 4B. Tumor-derived cfDNA GC content and fragment length. A, GC content was similar for mutated and non-mutated fragments. B, GC content was not correlated to fragment length.

Figure 5. Germline cfDNA fragment distributions. Cumulative density functions of fragment lengths of 44 loci containing germline alterations (non-tumor derived) from 38 patients with breast, colorectal, lung, or ovarian cancer are shown with 95% confidence bands. Fragments with germline mutations (blue) were comparable in length to wild-type cfDNA fragment lengths (red).

Figure 6. Hematopoietic cfDNA fragment distributions. Cumulative density functions of fragment lengths of 41 loci containing hematopoietic alterations (non-tumor derived) from 28 patients with breast, colorectal, lung, or ovarian cancer are shown with 95% confidence bands. After correction for multiple testing, there were no significant differences ($\alpha=0.05$) in the size distributions of mutated hematopoietic cfDNA fragments (blue) and wild-type cfDNA fragments (red).

Figures 7A – 7F. cfDNA fragmentation profiles in healthy individuals and patients with cancer. A, Genome-wide cfDNA fragmentation profiles (defined as the ratio of short to long fragments) from ~9x whole genome sequencing are shown in 5 Mb bins for 30 healthy individuals (top) and 8 lung cancer patients (bottom). B, An analysis of healthy cfDNA (top), lung cancer cfDNA (middle), and healthy lymphocyte (bottom) fragmentation profiles and lymphocyte profiles from chromosome 1 at 1 Mb resolution. The healthy lymphocyte profiles were scaled with a standard deviation equal to that of the median healthy cfDNA profiles. Healthy cfDNA patterns closely mirrored those in healthy lymphocytes while lung cancer cfDNA profiles were more varied and differed from both healthy and lymphocyte profiles. C, Smoothed median distances between adjacent nucleosome centered at zero using 100 kb bins from healthy cfDNA (top) and nuclease-digested healthy lymphocytes (middle) are depicted together with the first eigenvector for the genome contact matrix obtained through previously reported Hi-C analyses of lymphoblastoid cells (bottom). Healthy cfDNA nucleosome distances closely mirrored those in nuclease-digested lymphocytes as well as those from lymphoblastoid Hi-C analyses. cfDNA fragmentation profiles from healthy individuals (n=30) had high correlations while patients with lung cancer had lower correlations to median fragmentation profiles of lymphocytes (D), healthy cfDNA (E), and lymphocyte nucleosome (F) distances.

Figure 8. Density of cfDNA fragment lengths in healthy individuals and patients with lung cancer. cfDNA fragments lengths are shown for healthy individuals (n=30, gray) and patients with lung cancer (n=8, blue).

Figures 9A and 9B. Subsampling of whole genome sequence data for analysis of cfDNA fragmentation profiles. A, High coverage (9x) whole-genome sequencing data were subsampled to 2x, 1x, 0.5x, 0.2x, and 0.1x fold coverage. Mean centered genome-wide fragmentation profiles in 5 Mb bins for 30 healthy individuals and 8 patients with lung cancer are depicted for each subsampled fold coverage with median profiles shown in blue. B, Pearson correlation of subsampled profiles to initial profile at 9x coverage for healthy individuals and patients with lung cancer.

Figure 10. cfDNA fragmentation profiles and sequence alterations during therapy. Detection and monitoring of cancer in serial blood draws from NSCLC patients (n=19) undergoing treatment with targeted tyrosine kinase inhibitors (black arrows) was performed using targeted sequencing (top) and genome-wide fragmentation profiles (bottom). For each case, the vertical axis of the lower panel displays -1 times the correlation of each sample to the median healthy cfDNA fragmentation profile. Error bars depict confidence intervals from binomial tests for mutant allele fractions and confidence intervals calculated using

Fisher transformation for genome-wide fragmentation profiles. Although the approaches analyze different aspects of cfDNA (whole genome compared to specific alterations) the targeted sequencing and fragmentation profiles were similar for patients responding to therapy as well as those with stable or progressive disease. As fragmentation profiles reflect both genomic and epigenomic alterations, while mutant allele fractions only reflect individual mutations, mutant allele fractions alone may not reflect the absolute level of correlation of fragmentation profiles to healthy individuals.

Figures 11A – 11C. cfDNA fragmentation profiles in healthy individuals and patients with cancer. A, Fragmentation profiles (bottom) in the context of tumor copy number changes (top) in a colorectal cancer patient where parallel analyses of tumor tissue were performed. The distribution of segment means and integer copy numbers are shown at top right in the indicated colors. Altered fragmentation profiles were present in regions of the genome that were copy neutral and were further affected in regions with copy number changes. B, GC adjusted fragmentation profiles from 1-2x whole genome sequencing for healthy individuals and patients with cancer are depicted per cancer type using 5 Mb windows. The median healthy profile is indicated in black and the 98% confidence band is shown in gray. For patients with cancer, individual profiles are colored based on their correlation to the healthy median. C, Windows are indicated in orange if more than 10% of the cancer samples had a fragment ratio more than three standard deviations from the median healthy fragment ratio. These analyses highlight the multitude of position dependent alterations across the genome in cfDNA of individuals with cancer.

Figures 12A and 12B. Profiles of cfDNA fragment lengths in copy neutral regions in healthy individuals and one patient with colorectal cancer. A, The fragmentation profile in 211 copy neutral windows in chromosomes 1-6 for 25 randomly selected healthy individuals (gray). For a patient with colorectal cancer (CGCRC291) with an estimated mutant allele fraction of 20%, the cancer fragment length profile was diluted to an approximate 10% tumor contribution (blue). A and B, While the marginal densities of the fragment profiles for the healthy samples and cancer patient show substantial overlap (A, right), the fragmentation profiles are different as can be seen visualization of the fragmentation profiles (A, left) and by the separation of the colorectal cancer patient from the healthy samples in a principal component analysis (B).

Figures 13A and 13B. Genome-wide GC correction of cfDNA fragments. To estimate and control for the effects of GC content on sequencing coverage, coverage in non-overlapping 100kb genomic windows was calculated across the autosomes. For each window, the average GC of the aligned fragments was calculated. A, Loess smoothing of raw coverage (top row) for two randomly selected healthy subjects (CGPLH189 and CGPLH380) and two cancer patients (CGPLLU161 and CGPLBR24) with undetectable aneuploidy (PA score < 2.35). After subtracting the average coverage predicted by the loess model, the residuals were rescaled to the median autosomal coverage (bottom row). As fragment length may also result in coverage biases, this GC correction procedure was performed separately for short (≤ 150 bp) and long (≥ 151 bp) fragments. While the 100 kb bins on chromosome 19 (blue points) consistently have less coverage than predicted by the loess model, we did not implement a chromosome-specific correction as such an approach would remove the effects of chromosomal copy number on coverage. B, Overall, a limited correlation was found between short or long fragment coverage and GC content after correction among healthy subjects and cancer patients with a PA score <3.

Figure 14. Schematic of machine learning model. Gradient tree boosting machine learning was used to examine whether cfDNA can be categorized as having characteristics of a cancer patient or healthy individual. The machine learning model included fragmentation size and coverage characteristics in windows throughout the genome, as well as chromosomal arm and mitochondrial DNA copy numbers. A 10-fold cross validation approach was employed in which each sample is randomly assigned to a fold and 9 of the folds (90% of the data) are used for training and one fold (10% of the data) is used for testing. The prediction accuracy from a single cross validation is an average over the 10 possible combinations of test and training sets. As this prediction accuracy can reflect bias from the initial randomization of patients, the entire procedure was repeat, including the randomization of patients to folds, 10 times. For all cases, feature selection and model estimation were performed on training data and were validated on test data and the test data were never used for feature selection. Ultimately, a DELFI score was obtained that could be used to classify individuals as likely healthy or having cancer.

Figure 15. Distribution of AUCs across the repeated 10-fold cross-validation. The 25th, 50th, and 75th percentiles of the 100 AUCs for the cohort of 215 healthy individuals and 208 patients with cancer are indicated by dashed lines.

Figures 16A and 16B. Whole-genome analyses of chromosomal arm copy number changes and mitochondrial genome representation. A, Z scores for each autosome arm are depicted for healthy individuals (n=215) and patients with cancer (n=208). The vertical axis depicts normal copy at zero with positive and negative values indicating arm gains and losses, respectively. Z scores greater than 50 or less than -50 are thresholded at the indicated values. B, The fraction of reads mapping to the mitochondrial genome is depicted for healthy individuals and patients with cancer.

Figures 17A and 17B. Detection of cancer using DELFI. A, Receiver operator characteristics for detection of cancer using cfDNA fragmentation profiles and other genome-wide features in a machine learning approach are depicted for a cohort of 215 healthy individuals and 208 patients with cancer (DELFI, AUC = 0.94), with $\geq$ 95% specificity shaded in blue. Machine learning analyses of chromosomal arm copy number (Chr copy number (ML)), and mitochondrial genome copy number (mtDNA), are shown in the indicated colors. B, Analyses of individual cancers types using the DELFI-combined approach had AUCs ranging from 0.86 to >0.99.

Figure 18. DELFI detection of cancer by stage. Receiver operator characteristics for detection of cancer using cfDNA fragmentation profiles and other genome-wide features in a machine learning approach are depicted for a cohort of 215 healthy individuals and each stage of 208 patients with cancer with $\geq$ 95% specificity shaded in blue.

Figure 19. DELFI tissue of origin prediction. Receiver operator characteristics for DELFI tissue prediction of bile duct, breast, colorectal, gastric, lung, ovarian, and pancreatic cancers are depicted. In order to increase sample sizes within cancer type classes, cases detected with a 90% specificity were included, and the lung cancer cohort was supplemented with the addition of baseline cfDNA data from 18 lung cancer patients with prior treatment (see, e.g., Shen *et al.*, 2018 *Nature*, 563:579–583).

Figure 20. Detection of cancer using DELFI and mutation-based cfDNA approaches. DELFI (green) and targeted sequencing for mutation identification (blue) were performed independently in a cohort of 126 patients with breast, bile duct, colorectal, gastric, lung, or

ovarian cancers. The number of individuals detected by each approach and in combination are indicated for DELFI detection with a specificity of 98%, targeted sequencing specificity at >99%, and a combined specificity of 98%. ND indicates not detected.

DETAILED DESCRIPTION

This document provides methods and materials for determining a cfDNA fragmentation profile in a mammal (e.g., in a sample obtained from a mammal). As used herein, the terms “fragmentation profile,” “position dependent differences in fragmentation patterns,” and “differences in fragment size and coverage in a position dependent manner across the genome” are equivalent and can be used interchangeably. In some cases, determining a cfDNA fragmentation profile in a mammal can be used for identifying a mammal as having cancer. For example, cfDNA fragments obtained from a mammal (e.g., from a sample obtained from a mammal) can be subjected to low coverage whole-genome sequencing, and the sequenced fragments can be mapped to the genome (e.g., in non-overlapping windows) and assessed to determine a cfDNA fragmentation profile. As described herein, a cfDNA fragmentation profile of a mammal having cancer is more heterogeneous (e.g., in fragment lengths) than a cfDNA fragmentation profile of a healthy mammal (e.g., a mammal not having cancer). As such, this document also provides methods and materials for assessing, monitoring, and/or treating mammals (e.g., humans) having, or suspected of having, cancer. In some cases, this document provides methods and materials for identifying a mammal as having cancer. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine the presence and, optionally, the tissue of origin of the cancer in the mammal based, at least in part, on the cfDNA fragmentation profile of the mammal. In some cases, this document provides methods and materials for monitoring a mammal as having cancer. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine the presence of the cancer in the mammal based, at least in part, on the cfDNA fragmentation profile of the mammal. In some cases, this document provides methods and materials for identifying a mammal as having cancer, and administering one or more cancer treatments to the mammal to treat the mammal. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine if the mammal has cancer based, at least in part, on the cfDNA fragmentation profile of the mammal, and one or more cancer treatments can be administered to the mammal.

A cfDNA fragmentation profile can include one or more cfDNA fragmentation patterns. A cfDNA fragmentation pattern can include any appropriate cfDNA fragmentation pattern. Examples of cfDNA fragmentation patterns include, without limitation, median fragment size, fragment size distribution, ratio of small cfDNA fragments to large cfDNA fragments, and the coverage of cfDNA fragments. In some cases, a cfDNA fragmentation pattern includes two or more (e.g., two, three, or four) of median fragment size, fragment size distribution, ratio of small cfDNA fragments to large cfDNA fragments, and the coverage of cfDNA fragments. In some cases, cfDNA fragmentation profile can be a genome-wide cfDNA profile (e.g., a genome-wide cfDNA profile in windows across the genome). In some cases, cfDNA fragmentation profile can be a targeted region profile. A targeted region can be any appropriate portion of the genome (e.g., a chromosomal region). Examples of chromosomal regions for which a cfDNA fragmentation profile can be determined as described herein include, without limitation, a portion of a chromosome (e.g., a portion of 2q, 4p, 5p, 6q, 7p, 8q, 9q, 10q, 11q, 12q, and/or 14q) and a chromosomal arm (e.g., a chromosomal arm of 8q,13q, 11q, and/or 3p). In some cases, a cfDNA fragmentation profile can include two or more targeted region profiles.

In some cases, a cfDNA fragmentation profile can be used to identify changes (e.g., alterations) in cfDNA fragment lengths. An alteration can be a genome-wide alteration or an alteration in one or more targeted regions/loci. A target region can be any region containing one or more cancer-specific alterations. Examples of cancer-specific alterations, and their chromosomal locations, include, without limitation, those shown in Table 3 (Appendix C) and those shown in Table 6 (Appendix F). In some cases, a cfDNA fragmentation profile can be used to identify (e.g., simultaneously identify) from about 10 alterations to about 500 alterations (e.g., from about 25 to about 500, from about 50 to about 500, from about 100 to about 500, from about 200 to about 500, from about 300 to about 500, from about 10 to about 400, from about 10 to about 300, from about 10 to about 200, from about 10 to about 100, from about 10 to about 50, from about 20 to about 400, from about 30 to about 300, from about 40 to about 200, from about 50 to about 100, from about 20 to about 100, from about 25 to about 75, from about 50 to about 250, or from about 100 to about 200, alterations).

In some cases, a cfDNA fragmentation profile can be used to detect tumor-derived DNA. For example, a cfDNA fragmentation profile can be used to detect tumor-derived DNA by comparing a cfDNA fragmentation profile of a mammal having, or suspected of having, cancer to a reference cfDNA fragmentation profile (e.g., a cfDNA fragmentation profile of a healthy mammal and/or a nucleosomal DNA fragmentation profile of healthy cells from the mammal having, or suspected of having, cancer). In some cases, a reference cfDNA fragmentation profile is a previously generated profile from a healthy mammal. For example, methods provided herein can be used to determine a reference cfDNA fragmentation profile in a healthy mammal, and that reference cfDNA fragmentation profile can be stored (e.g., in a computer or other electronic storage medium) for future comparison to a test cfDNA fragmentation profile in mammal having, or suspected of having, cancer. In some cases, a reference cfDNA fragmentation profile (e.g., a stored cfDNA fragmentation profile) of a healthy mammal is determined over the whole genome. In some cases, a reference cfDNA fragmentation profile (e.g., a stored cfDNA fragmentation profile) of a healthy mammal is determined over a subgenomic interval.

In some cases, a cfDNA fragmentation profile can be used to identify a mammal (e.g., a human) as having cancer (e.g., a colorectal cancer, a lung cancer, a breast cancer, a gastric cancer, a pancreatic cancer, a bile duct cancer, and/or an ovarian cancer).

A cfDNA fragmentation profile can include a cfDNA fragment size pattern. cfDNA fragments can be any appropriate size. For example, cfDNA fragment can be from about 50 base pairs (bp) to about 400 bp in length. As described herein, a mammal having cancer can have a cfDNA fragment size pattern that contains a shorter median cfDNA fragment size than the median cfDNA fragment size in a healthy mammal. A healthy mammal (e.g., a mammal not having cancer) can have cfDNA fragment sizes having a median cfDNA fragment size from about 166.6 bp to about 167.2 bp (e.g., about 166.9 bp). In some cases, a mammal having cancer can have cfDNA fragment sizes that are, on average, about 1.28 bp to about 2.49 bp (e.g., about 1.88 bp) shorter than cfDNA fragment sizes in a healthy mammal. For example, a mammal having cancer can have cfDNA fragment sizes having a median cfDNA fragment size of about 164.11 bp to about 165.92 bp (e.g., about 165.02 bp).

A cfDNA fragmentation profile can include a cfDNA fragment size distribution. As described herein, a mammal having cancer can have a cfDNA size distribution that is more variable than a cfDNA fragment size distribution in a healthy mammal. In some case, a size distribution can be within a targeted region. A healthy mammal (e.g., a mammal not having cancer) can have a targeted region cfDNA fragment size distribution of about 1 or less than about 1. In some cases, a mammal having cancer can have a targeted region cfDNA fragment size distribution that is longer (e.g., 10, 15, 20, 25, 30, 35, 40, 45, 50 or more bp longer, or any number of base pairs between these numbers) than a targeted region cfDNA fragment size distribution in a healthy mammal. In some cases, a mammal having cancer can have a targeted region cfDNA fragment size distribution that is shorter (e.g., 10, 15, 20, 25, 30, 35, 40, 45, 50 or more bp shorter, or any number of base pairs between these numbers) than a targeted region cfDNA fragment size distribution in a healthy mammal. In some cases, a mammal having cancer can have a targeted region cfDNA fragment size distribution that is about 47 bp smaller to about 30 bp longer than a targeted region cfDNA fragment size distribution in a healthy mammal. In some cases, a mammal having cancer can have a targeted region cfDNA fragment size distribution of, on average, a 10, 11, 12, 13, 14, 15, 15, 17, 18, 19, 20 or more bp difference in lengths of cfDNA fragments. For example, a mammal having cancer can have a targeted region cfDNA fragment size distribution of, on average, about a 13 bp difference in lengths of cfDNA fragments. In some case, a size distribution can be a genome-wide size distribution. A healthy mammal (e.g., a mammal not having cancer) can have very similar distributions of short and long cfDNA fragments genome-wide. In some cases, a mammal having cancer can have, genome-wide, one or more alterations (e.g., increases and decreases) in cfDNA fragment sizes. The one or more alterations can be any appropriate chromosomal region of the genome. For example, an alteration can be in a portion of a chromosome. Examples of portions of chromosomes that can contain one or more alterations in cfDNA fragment sizes include, without limitation, portions of 2q, 4p, 5p, 6q, 7p, 8q, 9q, 10q, 11q, 12q, and 14q. For example, an alteration can be across a chromosome arm (e.g., an entire chromosome arm).

A cfDNA fragmentation profile can include a ratio of small cfDNA fragments to large cfDNA fragments and a correlation of fragment ratios to reference fragment ratios. As used herein, with respect to ratios of small cfDNA fragments to large cfDNA fragments, a small cfDNA fragment can be from about 100 bp in length to about 150 bp in length. As used herein, with respect to ratios of small cfDNA fragments to large cfDNA fragments, a large cfDNA fragment can be from about 151 bp in length to 220 bp in length. As described herein, a mammal having cancer can have a correlation of fragment ratios (e.g., a correlation of cfDNA fragment ratios to reference DNA fragment ratios such as DNA fragment ratios from one or more healthy mammals) that is lower (e.g., 2-fold lower, 3-fold lower, 4-fold lower, 5-fold lower, 6-fold lower, 7-fold lower, 8-fold lower, 9-fold lower, 10-fold lower, or more) than in a healthy mammal. A healthy mammal (e.g., a mammal not having cancer) can have a correlation of fragment ratios (e.g., a correlation of cfDNA fragment ratios to reference DNA fragment ratios such as DNA fragment ratios from one or more healthy mammals) of about 1 (e.g., about 0.96). In some cases, a mammal having cancer can have a correlation of fragment ratios (e.g., a correlation of cfDNA fragment ratios to reference DNA fragment ratios such as DNA fragment ratios from one or more healthy mammals) that is, on average, about 0.19 to about 0.30 (e.g., about 0.25) lower than a correlation of fragment ratios (e.g., a correlation of cfDNA fragment ratios to reference DNA fragment ratios such as DNA fragment ratios from one or more healthy mammals) in a healthy mammal.

A cfDNA fragmentation profile can include coverage of all fragments. Coverage of all fragments can include windows (e.g., non-overlapping windows) of coverage. In some cases, coverage of all fragments can include windows of small fragments (e.g., fragments from about 100 bp to about 150 bp in length). In some cases, coverage of all fragments can include windows of large fragments (e.g., fragments from about 151 bp to about 220 bp in length).

In some cases, a cfDNA fragmentation profile can be used to identify the tissue of origin of a cancer (e.g., a colorectal cancer, a lung cancer, a breast cancer, a gastric cancer, a pancreatic cancer, a bile duct cancer, or an ovarian cancer). For example, a cfDNA fragmentation profile can be used to identify a localized cancer. When a cfDNA fragmentation profile includes a targeted region profile, one or more alterations described herein (e.g., in Table 3 (Appendix C) and/or in Table 6 (Appendix F)) can be used to identify the tissue of origin of a cancer. In some cases, one or more alterations in chromosomal regions can be used to identify the tissue of origin of a cancer.

A cfDNA fragmentation profile can be obtained using any appropriate method. In some cases, cfDNA from a mammal (e.g., a mammal having, or suspected of having, cancer) can be processed into sequencing libraries which can be subjected to whole genome sequencing (e.g., low-coverage whole genome sequencing), mapped to the genome, and analyzed to determine cfDNA fragment lengths. Mapped sequences can be analyzed in non-overlapping windows covering the genome. Windows can be any appropriate size. For example, windows can be from thousands to millions of bases in length. As one non-limiting example, a window can be about 5 megabases (Mb) long. Any appropriate number of windows can be mapped. For example, tens to thousands of windows can be mapped in the genome. For example, hundreds to thousands of windows can be mapped in the genome. A cfDNA fragmentation profile can be determined within each window. In some cases, a cfDNA fragmentation profile can be obtained as described in Example 1. In some cases, a cfDNA fragmentation profile can be obtained as shown in Figure 1.

In some cases, methods and materials described herein also can include machine learning. For example, machine learning can be used for identifying an altered fragmentation profile (e.g., using coverage of cfDNA fragments, fragment size of cfDNA fragments, coverage of chromosomes, and mtDNA).

In some cases, methods and materials described herein can be the sole method used to identify a mammal (e.g., a human) as having cancer (e.g., a colorectal cancer, a lung cancer, a breast cancer, a gastric cancer, a pancreatic cancer, a bile duct cancer, and/or an ovarian cancer). For example, determining a cfDNA fragmentation profile can be the sole method used to identify a mammal as having cancer.

In some cases, methods and materials described herein can be used together with one or more additional methods used to identify a mammal (e.g., a human) as having cancer (e.g., a colorectal cancer, a lung cancer, a breast cancer, a gastric cancer, a pancreatic cancer, a bile duct cancer, and/or an ovarian cancer). Examples of methods used to identify a mammal as having cancer include, without limitation, identifying one or more cancer-specific sequence alterations, identifying one or more chromosomal alterations (e.g., aneuploidies and rearrangements), and identifying other cfDNA alterations. For example, determining a cfDNA fragmentation profile can be used together with identifying one or more cancer-specific mutations in a mammal’s genome to identify a mammal as having cancer. For example, determining a cfDNA fragmentation profile can be used together with identifying one or more aneuploidies in a mammal’s genome to identify a mammal as having cancer.

In some aspects, this document also provides methods and materials for assessing, monitoring, and/or treating mammals (e.g., humans) having, or suspected of having, cancer. In some cases, this document provides methods and materials for identifying a mammal as having cancer. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine if the mammal has cancer based, at least in part, on the cfDNA fragmentation profile of the mammal. In some cases, this document provides methods and materials for identifying the location (e.g., the anatomic site or tissue of origin) of a cancer in a mammal. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine the tissue of origin of the cancer in the mammal based, at least in part, on the cfDNA fragmentation profile of the mammal. In some cases, this document provides methods and materials for identifying a mammal as having cancer, and administering one or more cancer treatments to the mammal to treat the mammal. For example, a sample (e.g., a blood sample) obtained from a mammal can be assessed to determine if the mammal has cancer based, at least in part, on the cfDNA fragmentation profile of the mammal, and administering one or more cancer treatments to the mammal. In some cases, this document provides methods and materials for treating a mammal having cancer. For example, one or more cancer treatments can be administered to a mammal identified as having cancer (e.g., based, at least in part, on the cfDNA fragmentation profile of the mammal) to treat the mammal. In some cases, during or after the course of a cancer treatment (e.g., any of the cancer treatments described herein), a mammal can undergo monitoring (or be selected for increased monitoring) and/or further diagnostic testing. In some cases, monitoring can include assessing mammals having, or suspected of having, cancer by, for example, assessing a sample (e.g., a blood sample) obtained from the mammal to determine the cfDNA fragmentation profile of the mammal as described herein, and changes in the cfDNA fragmentation profiles over time can be used to identify response to treatment and/or identify the mammal as having cancer (e.g., a residual cancer).

Any appropriate mammal can be assessed, monitored, and/or treated as described herein. A mammal can be a mammal having cancer. A mammal can be a mammal suspected of having cancer. Examples of mammals that can be assessed, monitored, and/or treated as described herein include, without limitation, humans, primates such as monkeys, dogs, cats, horses, cows, pigs, sheep, mice, and rats. For example, a human having, or suspected of having, cancer can be assessed to determine a cfDNA fragmentation profiled as described herein and, optionally, can be treated with one or more cancer treatments as described herein.

Any appropriate sample from a mammal can be assessed as described herein (e.g., assessed for a DNA fragmentation pattern). In some cases, a sample can include DNA (e.g., genomic DNA). In some cases, a sample can include cfDNA (e.g., circulating tumor DNA (ctDNA)). In some cases, a sample can be fluid sample (e.g., a liquid biopsy). Examples of samples that can contain DNA and/or polypeptides include, without limitation, blood (e.g., whole blood, serum, or plasma), amnion, tissue, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, pap smears, breast milk, and exhaled breath condensate. For example, a plasma sample can be assessed to determine a cfDNA fragmentation profiled as described herein.

A sample from a mammal to be assessed as described herein (e.g., assessed for a DNA fragmentation pattern) can include any appropriate amount of cfDNA. In some cases, a sample can include a limited amount of DNA. For example, a cfDNA fragmentation profile can be obtained from a sample that includes less DNA than is typically required for other cfDNA analysis methods, such as those described in, for example, Phallen et al., 2017 *Sci Transl Med* 9; Cohen et al., 2018 *Science* 359:926; Newman et al., 2014 *Nat Med* 20:548; and Newman et al., 2016 *Nat Biotechnol* 34:547).

In some cases, a sample can be processed (e.g., to isolate and/or purify DNA and/or polypeptides from the sample). For example, DNA isolation and/or purification can include cell lysis (e.g., using detergents and/or surfactants), protein removal (e.g., using a protease), and/or RNA removal (e.g., using an RNase). As another example, polypeptide isolation and/or purification can include cell lysis (e.g., using detergents and/or surfactants), DNA removal (e.g., using a DNase), and/or RNA removal (e.g., using an RNase).

A mammal having, or suspected of having, any appropriate type of cancer can be assessed (e.g., to determine a cfDNA fragmentation profile) and/or treated (e.g., by administering one or more cancer treatments to the mammal) using the methods and materials described herein. A cancer can be any stage cancer. In some cases, a cancer can be an early stage cancer. In some cases, a cancer can be an asymptomatic cancer. In some cases, a cancer can be a residual disease and/or a recurrence (e.g., after surgical resection and/or after cancer therapy). A cancer can be any type of cancer. Examples of types of cancers that can be assessed, monitored, and/or treated as described herein include, without limitation, colorectal cancers, lung cancers, breast cancers, gastric cancers, pancreatic cancers, bile duct cancers, and ovarian cancers.

When treating a mammal having, or suspected of having, cancer as described herein, the mammal can be administered one or more cancer treatments. A cancer treatment can be any appropriate cancer treatment. One or more cancer treatments described herein can be administered to a mammal at any appropriate frequency (e.g., once or multiple times over a period of time ranging from days to weeks). Examples of cancer treatments include, without limitation adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy (e.g., chimeric antigen receptors and/or T cells having wild-type or modified T cell receptors), targeted therapy such as administration of kinase inhibitors (e.g., kinase inhibitors that target a particular genetic lesion, such as a translocation or mutation), (e.g. a kinase inhibitor, an antibody, a bispecific antibody), signal transduction inhibitors, bispecific antibodies or antibody fragments (e.g., BiTEs), monoclonal antibodies, immune checkpoint inhibitors, surgery (e.g., surgical resection), or any combination of the above. In some cases, a cancer treatment can reduce the severity of the cancer, reduce a symptom of the cancer, and/or to reduce the number of cancer cells present within the mammal.

In some cases, a cancer treatment can include an immune checkpoint inhibitor. Non-limiting examples of immune checkpoint inhibitors include nivolumab (Opdivo), pembrolizumab (Keytruda), atezolizumab (tecentriq), avelumab (bavencio), durvalumab (imfinzi), ipilimumab (yervoy). See, e.g., Pardoll (2012) Nat. Rev Cancer 12: 252-264; Sun et al. (2017) Eur Rev Med Pharmacol Sci 21(6): 1198-1205; Hamanishi et al. (2015) J. Clin. Oncol. 33(34): 4015-22; Brahmer et al. (2012) N Engl J Med 366(26): 2455-65; Ricciuti et al. (2017) J. Thorac Oncol. 12(5): e51-e55; Ellis et al. (2017) Clin Lung Cancer pii: S1525-7304(17)30043-8; Zou and Awad (2017) Ann Oncol 28(4): 685-687; Sorscher (2017) N Engl J Med 376(10: 996-7; Hui et al. (2017) Ann Oncol 28(4): 874-881; Vansteenkiste et al. (2017) Expert Opin Biol Ther 17(6): 781-789; Hellmann et al. (2017) Lancet Oncol. 18(1): 31-41; Chen (2017) J. Chin Med Assoc 80(1): 7-14.

In some cases, a cancer treatment can be an adoptive T cell therapy (e.g., chimeric antigen receptors and/or T cells having wild-type or modified T cell receptors). See, e.g., Rosenberg and Restifo (2015) Science 348(6230): 62-68; Chang and Chen (2017) Trends Mol Med 23(5): 430-450; Yee and Lizee (2016) Cancer J. 23(2): 144-148; Chen et al. (2016) Oncoimmunology 6(2): e1273302; US 2016/0194404; US 2014/0050788; US 2014/0271635; US 9,233,125; incorporated by reference in their entirety herein.

In some cases, a cancer treatment can be a chemotherapeutic agent. Non-limiting examples of chemotherapeutic agents include: amsacrine, azacitidine, axathioprine, bevacizumab (or an antigen-binding fragment thereof), bleomycin, busulfan, carboplatin , capecitabine, chlorambucil, cisplatin, cyclophosphamide, cytarabine, dacarbazine, daunorubicin, docetaxel, doxifluridine, doxorubicin, epirubicin, erlotinib hydrochlorides, etoposide, fiudarabine, floxuridine, fludarabine, fluorouracil, gemcitabine, hydroxyurea, idarubicin, ifosfamide, irinotecan, lomustine, mechlorethamine, melphalan, mercaptopurine, methotrxate, mitomycin, mitoxantrone, oxaliplatin, paclitaxel, pemetrexed, procarbazine, all-trans retinoic acid, streptozocin, tafluposide, temozolomide, teniposide, tioguanine, topotecan, uramustine, valrubicin, vinblastine, vincristine, vindesine, vinorelbine, and combinations thereof. Additional examples of anti-cancer therapies are known in the art; see, e.g. the guidelines for therapy from the American Society of Clinical Oncology (ASCO), European Society for Medical Oncology (ESMO), or National Comprehensive Cancer Network (NCCN).

When monitoring a mammal having, or suspected of having, cancer as described herein (e.g., based, at least in part, on the cfDNA fragmentation profile of the mammal), the monitoring can be before, during, and/or after the course of a cancer treatment. Methods of monitoring provided herein can be used to determine the efficacy of one or more cancer treatments and/or to select a mammal for increased monitoring. In some cases, the monitoring can include identifying a cfDNA fragmentation profile as described herein. For example, a cfDNA fragmentation profile can be obtained before administering one or more cancer treatments to a mammal having, or suspected or having, cancer, one or more cancer treatments can be administered to the mammal, and one or more cfDNA fragmentation profiles can be obtained during the course of the cancer treatment. In some cases, a cfDNA fragmentation profile can change during the course of cancer treatment (e.g., any of the cancer treatments described herein). For example, a cfDNA fragmentation profile indicative that the mammal has cancer can change to a cfDNA fragmentation profile indicative that the mammal does not have cancer. Such a cfDNA fragmentation profile change can indicate that the cancer treatment is working. Conversely, a cfDNA fragmentation profile can remain static (e.g., the same or approximately the same) during the course of cancer treatment (e.g., any of the cancer treatments described herein). Such a static cfDNA fragmentation profile can indicate that the cancer treatment is not working. In some cases, the monitoring can include conventional techniques capable of monitoring one or more cancer treatments (e.g., the efficacy of one or more cancer treatments). In some cases, a mammal selected for increased monitoring can be administered a diagnostic test (e.g., any of the diagnostic tests disclosed herein) at an increased frequency compared to a mammal that has not been selected for increased monitoring. For example, a mammal selected for increased monitoring can be administered a diagnostic test at a frequency of twice daily, daily, bi-weekly, weekly, bi-monthly, monthly, quarterly, semi-annually, annually, or any at frequency therein. In some cases, a mammal selected for increased monitoring can be administered a one or more additional diagnostic tests compared to a mammal that has not been selected for increased monitoring. For example, a mammal selected for increased monitoring can be administered two diagnostic tests, whereas a mammal that has not been selected for increased monitoring is administered only a single diagnostic test (or no diagnostic tests). In some cases, a mammal that has been selected for increased monitoring can also be selected for further diagnostic testing. Once the presence of a tumor or a cancer (e.g., a cancer cell) has been identified (e.g., by any of the variety of methods disclosed herein), it may be beneficial for the mammal to undergo both increased monitoring (e.g., to assess the progression of the tumor or cancer in the mammal and/or to assess the development of one or more cancer biomarkers such as mutations), and further diagnostic testing (e.g., to determine the size and/or exact location (e.g., tissue of origin) of the tumor or the cancer). In some cases, one or more cancer treatments can be administered to the mammal that is selected for increased monitoring after a cancer biomarker is detected and/or after the cfDNA fragmentation profile of the mammal has not improved or deteriorated. Any of the cancer treatments disclosed herein or known in the art can be administered. For example, a mammal that has been selected for increased monitoring can be further monitored, and a cancer treatment can be administered if the presence of the cancer cell is maintained throughout the increased monitoring period. Additionally or alternatively, a mammal that has been selected for increased monitoring can be administered a cancer treatment, and further monitored as the cancer treatment progresses. In some cases, after a mammal that has been selected for increased monitoring has been administered a cancer treatment, the increased monitoring will reveal one or more cancer biomarkers (e.g., mutations). In some cases, such one or more cancer biomarkers will provide cause to administer a different cancer treatment (e.g., a resistance mutation may arise in a cancer cell during the cancer treatment, which cancer cell harboring the resistance mutation is resistant to the original cancer treatment).

When a mammal is identified as having cancer as described herein (e.g., based, at least in part, on the cfDNA fragmentation profile of the mammal), the identifying can be before and/or during the course of a cancer treatment. Methods of identifying a mammal as having cancer provided herein can be used as a first diagnosis to identify the mammal (e.g., as having cancer before any course of treatment) and/or to select the mammal for further diagnostic testing. In some cases, once a mammal has been determined to have cancer, the mammal may be administered further tests and/or selected for further diagnostic testing. In some cases, methods provided herein can be used to select a mammal for further diagnostic testing at a time period prior to the time period when conventional techniques are capable of diagnosing the mammal with an early-stage cancer. For example, methods provided herein for selecting a mammal for further diagnostic testing can be used when a mammal has not been diagnosed with cancer by conventional methods and/or when a mammal is not known to harbor a cancer. In some cases, a mammal selected for further diagnostic testing can be administered a diagnostic test (e.g., any of the diagnostic tests disclosed herein) at an increased frequency compared to a mammal that has not been selected for further diagnostic testing. For example, a mammal selected for further diagnostic testing can be administered a diagnostic test at a frequency of twice daily, daily, bi-weekly, weekly, bi-monthly, monthly, quarterly, semi-annually, annually, or any at frequency therein. In some cases, a mammal selected for further diagnostic testing can be administered a one or more additional diagnostic tests compared to a mammal that has not been selected for further diagnostic testing. For example, a mammal selected for further diagnostic testing can be administered two diagnostic tests, whereas a mammal that has not been selected for further diagnostic testing is administered only a single diagnostic test (or no diagnostic tests). In some cases, the diagnostic testing method can determine the presence of the same type of cancer (e.g., having the same tissue or origin) as the cancer that was originally detected (e.g., based, at least in part, on the cfDNA fragmentation profile of the mammal). Additionally or alternatively, the diagnostic testing method can determine the presence of a different type of cancer as the cancer that was original detected. In some cases, the diagnostic testing method is a scan. In some cases, the scan is a computed tomography (CT), a CT angiography (CTA), a esophagram (a Barium swallom), a Barium enema, a magnetic resonance imaging (MRI), a PET scan, an ultrasound (e.g., an endobronchial ultrasound, an endoscopic ultrasound), an X-ray, a DEXA scan. In some cases, the diagnostic testing method is a physical examination, such as an anoscopy, a bronchoscopy (e.g., an autofluorescence bronchoscopy, a white-light bronchoscopy, a navigational bronchoscopy), a colonoscopy, a digital breast tomosynthesis, an endoscopic retrograde cholangiopancreatography (ERCP), an ensophagogastroduodenoscopy, a mammography, a Pap smear, a pelvic exam, a positron emission tomography and computed tomography (PET-CT) scan. In some cases, a mammal that has been selected for further diagnostic testing can also be selected for increased monitoring. Once the presence of a tumor or a cancer (e.g., a cancer cell) has been identified (e.g., by any of the variety of methods disclosed herein), it may be beneficial for the mammal to undergo both increased monitoring (e.g., to assess the progression of the tumor or cancer in the mammal and/or to assess the development of one or more cancer biomarkers such as mutations), and further diagnostic testing (e.g., to determine the size and/or exact location of the tumor or the cancer). In some cases, a cancer treatment is administered to the mammal that is selected for further diagnostic testing after a cancer biomarker is detected and/or after the cfDNA fragmentation profile of the mammal has not improved or deteriorated. Any of the cancer treatments disclosed herein or known in the art can be administered. For example, a mammal that has been selected for further diagnostic testing can be administered a further diagnostic test, and a cancer treatment can be administered if the presence of the tumor or the cancer is confirmed. Additionally or alternatively, a mammal that has been selected for further diagnostic testing can be administered a cancer treatment, and can be further monitored as the cancer treatment progresses. In some cases, after a mammal that has been selected for further diagnostic testing has been administered a cancer treatment, the additional testing will reveal one or more cancer biomarkers (e.g., mutations). In some cases, such one or more cancer biomarkers (e.g., mutations) will provide cause to administer a different cancer treatment (e.g., a resistance mutation may arise in a cancer cell during the cancer treatment, which cancer cell harboring the resistance mutation is resistant to the original cancer treatment).

The invention will be further described in the following examples, which do not limit the scope of the invention described in the claims.

EXAMPLES

Example 1: Cell-free DNA fragmentation in patients with cancer

Analyses of cell free DNA have largely focused on targeted sequencing of specific genes. Such studies permit detection of a small number of tumor-specific alterations in patients with cancer and not all patients, especially those with early stage disease, have detectable changes. Whole genome sequencing of cell-free DNA can identify chromosomal abnormalities and rearrangements in cancer patients but detection of such alterations has been challenging in part due to the difficulty in distinguishing a small number of abnormal from normal chromosomal changes (Leary et al., 2010 *Sci Transl Med* 2:20ra14; and Leary et al., 2012 *Sci Transl Med* 4:162ra154). Other efforts have suggested nucleosome patterns and chromatin structure may be different between cancer and normal tissues, and that cfDNA in patients with cancer may result in abnormal cfDNA fragment size as well as position (Snyder et al., 2016 *Cell* 164:57; Jahr et al., 2001 *Cancer Res* 61:1659; Ivanov et al., 2015 *BMC Genomics* 16(Suppl 13):S1). However, the amount of sequencing needed for nucleosome footprint analyses of cfDNA is impractical for routine analyses.

The sensitivity of any cell-free DNA approach depends on the number of potential alterations examined as well as the technical and biological limitations of detecting such changes. As a typical blood sample contains ~2000 genome equivalents of cfDNA per milliliter of plasma (Phallen et al., 2017 *Sci Transl Med* 9), the theoretical limit of detection of a single alteration can be no better than one in a few thousand mutant to wild-type molecules. An approach that detects a larger number of alterations in the same number of genome equivalents would be more sensitive for detecting cancer in the circulation. Monte Carlo simulations show that increasing the number of potential abnormalities detected from only a few to tens or hundreds can potentially improve the limit of detection by orders of magnitude, similar to recent probability analyses of multiple methylation changes in cfDNA (Figure 2).

This study presents a novel method called DELFI for detection of cancer and further identification of tissue of origin using whole genome sequencing (Figure 1). The approach uses cfDNA fragmentation profiles and machine learning to distinguish patterns of healthy blood cell DNA from tumor-derived DNA and to identify the primary tumor tissue. DELFI was used for a retrospective analysis of cfDNA from 245 healthy individuals and 236 patients with breast, colorectal, lung, ovarian, pancreatic, gastric, or bile duct cancers, with most patients exhibiting localized disease. Assuming this approach had sensitivity ≥ 0.80 for discriminating cancer patients from healthy individuals while maintaining a specificity of 0.95, a study of at least 200 cancer patients would enable estimation of the true sensitivity with a margin of error of 0.06 at the desired specificity of 0.95 or greater.

Materials and Methods

Patient and sample characteristics

Plasma samples from healthy individuals and plasma and tissue samples from patients with breast, lung, ovarian, colorectal, bile duct, or gastric cancer were obtained from ILSBio/Bioreclamation, Aarhus University, Herlev Hospital of the University of Copenhagen, Hvidovre Hospital, the University Medical Center of the University of Utrecht, the Academic Medical Center of the University of Amsterdam, the Netherlands Cancer Institute, and the University of California, San Diego. All samples were obtained under Institutional Review Board approved protocols with informed consent for research use at participating institutions. Plasma samples from healthy individuals were obtained at the time of routine screening, including for colonoscopies or Pap smears. Individuals were considered healthy if they had no previous history of cancer and negative screening results.

Plasma samples from individuals with breast, colorectal, gastric, lung, ovarian, pancreatic, and bile duct cancer were obtained at the time of diagnosis, prior to tumor resection or therapy. Nineteen lung cancer patients analyzed for change in cfDNA fragmentation profiles across multiple time points were undergoing treatment with anti-EGFR or anti-ERBB2 therapy (see, e.g., Phallen *et al.*, 2019 *Cancer Research* 15, 1204-1213). Clinical data for all patients included in this study are listed in Table 1 (Appendix A).

Gender was confirmed through genomic analyses of X and Y chromosome representation. Pathologic staging of gastric cancer patients was performed after neoadjuvant therapy. Samples where the tumor stage was unknown were indicated as stage X or unknown.

Nucleosomal DNA purification

Viably frozen lymphocytes were elutriated from leukocytes obtained from a healthy male (C0618) and female (D0808-L) (Advanced Biotechnologies Inc., Eldersburg, MD). Aliquots of 1 x 10^6 cells were used for nucleosomal DNA purification using EZ Nucleosomal DNA Prep Kit (Zymo Research, Irvine, CA). Cells were initially treated with 100 µl of Nuclei Prep Buffer and incubated on ice for 5 minutes. After centrifugation at 200*g* for 5 minutes, supernatant was discarded and pelleted nuclei were treated twice with 100µl of Atlantis Digestion Buffer or with 100 µl of micrococcal nuclease (MN) Digestion Buffer. Finally, cellular nucleic DNA was fragmented with 0.5U of Atlantis dsDNase at 42°C for 20 minutes or 1.5U of MNase at 37°C for 20 minutes. Reactions were stopped using 5X MN Stop Buffer and DNA was purified using Zymo-Spin™ IIC Columns. Concentration and quality of eluted cellular nucleic DNA were analyzed using the Bioanalyzer 2100 (Agilent Technologies, Santa Clara, CA).

Sample preparation and sequencing of cfDNA

Whole blood was collected in EDTA tubes and processed immediately or within one day after storage at 4°C, or was collected in Streck tubes and processed within two days of collection for three cancer patients who were part of the monitoring analysis. Plasma and cellular components were separated by centrifugation at 800g for 10 min at 4°C. Plasma was centrifuged a second time at 18,000g at room temperature to remove any remaining cellular debris and stored at −80°C until the time of DNA extraction. DNA was isolated from plasma using the Qiagen Circulating Nucleic Acids Kit (Qiagen GmbH) and eluted in LoBind tubes (Eppendorf AG). Concentration and quality of cfDNA were assessed using the Bioanalyzer 2100 (Agilent Technologies).

NGS cfDNA libraries were prepared for whole genome sequencing and targeted sequencing using 5 to 250 ng of cfDNA as described elsewhere (see, e.g., Phallen *et al.*, 2017 *Sci Transl Med* 9:eaan2415). Briefly, genomic libraries were prepared using the NEBNext DNA Library Prep Kit for Illumina [New England Biolabs (NEB)] with four main modifications to the manufacturer's guidelines: (i) The library purification steps used the on-bead AMPure XP approach to minimize sample loss during elution and tube transfer steps (see, e.g., Fisher *et al.*, 2011 *Genome Biol* 12:R1); (ii) NEBNext End Repair, A-tailing, and adapter ligation enzyme and buffer volumes were adjusted as appropriate to accommodate the on-bead AMPure XP purification strategy; (iii) a pool of eight unique Illumina dual index adapters with 8–base pair (bp) barcodes was used in the ligation reaction instead of the standard Illumina single or dual index adapters with 6- or 8-bp barcodes, respectively; and (iv) cfDNA libraries were amplified with Phusion Hot Start Polymerase.

Whole genome libraries were sequenced directly. For targeted libraries, capture was performed using Agilent SureSelect reagents and a custom set of hybridization probes targeting 58 genes (see, e.g., Phallen *et al.*, 2017 *Sci Transl Med* 9:eaan2415) per the manufacturer's guidelines. The captured library was amplified with Phusion Hot Start Polymerase (NEB). Concentration and quality of captured cfDNA libraries were assessed on the Bioanalyzer 2100 using theDNA1000 Kit (Agilent Technologies). Targeted libraries were sequenced using 100-bp paired-end runs on the Illumina HiSeq 2000/2500 (Illumina).

Analyses of targeted sequencing data from cfDNA

Analyses of targeted NGS data for cfDNA samples was performed as described elsewhere (see, e.g., Phallen *et al.*, 2017 *Sci Transl Med* 9:eaan2415). Briefly, primary processing was completed using Illumina CASAVA (Consensus Assessment of Sequence and Variation) software (version 1.8), including demultiplexing and masking of dual-index adapter sequences. Sequence reads were aligned against the human reference genome (version hg18 or hg19) using NovoAlign with additional realignment of select regions using the Needleman-Wunsch method (see, e.g., Jones *et al.*, 2015 *Sci Transl Med* 7:283ra53). The positions of the sequence alterations have not been affected by the different genome builds. Candidate mutations, consisting of point mutations, small insertions, and deletions, were identified using VariantDx (see, e.g., Jones *et al.*, 2015 *Sci Transl Med* 7:283ra53) (Personal Genome Diagnostics, Baltimore, MD) across the targeted regions of interest.

To analyze the fragment lengths of cfDNA molecules, each read pair from a cfDNA molecule was required to have a Phred quality score ≥ 30. All duplicate ctDNA fragments, defined as having the same start, end, and index barcode were removed. For each mutation, only fragments for which one or both of the read pairs contained the mutated (or wild-type) base at the given position were included. This analysis was done using the R packages Rsamtools and GenomicAlignments.

For each genomic locus where a somatic mutation was identified, the lengths of fragments containing the mutant allele were compared to the lengths of fragments of the wild-type allele. If more than 100 mutant fragments were identified, Welch's two-sample t-test was used to compare the mean fragment lengths. For loci with fewer than 100 mutant fragments, a bootstrap procedure was implemented. Specifically, replacement N fragments containing the wild-type allele, where N denotes the number of fragments with the mutation, were sampled. For each bootstrap replicate of wild type fragments their median length was computed. The p-value was estimated as the fraction of bootstrap replicates with a median wild-type fragment length as or more extreme than the observed median mutant fragment length.

Analyses of whole genome sequencing data from cfDNA

Primary processing of whole genome NGS data for cfDNA samples was performed using Illumina CASAVA (Consensus Assessment of Sequence and Variation) software (version 1.8.2), including demultiplexing and masking of dual-index adapter sequences. Sequence reads were aligned against the human reference genome (version hg19) using ELAND.

Read pairs with a MAPQ score below 30 for either read and PCR duplicates were removed. hg19 autosomes were tiled into 26,236 adjacent, non-overlapping 100 kb bins. Regions of low mappability, indicated by the 10% of bins with the lowest coverage, were removed (see, e.g., Fortin *et al.*, 2015 *Genome Biol* 16:180), as were reads falling in the Duke blacklisted regions (see, e.g., hgdownload.cse.ucsc.edu/goldenpath/hg19/encodeDCC/wgEncodeMapability/). Using this approach, 361 Mb (13%) of the hg19 reference genome was excluded, including centromeric and telomeric regions. Short fragments were defined as having a length between 100 and 150 bp and long fragments were defined has having a length between 151 and 220 bp.

To account for biases in coverage attributable to GC content of the genome, the locally weighted smoother loess with span ¾ was applied to the scatterplot of average fragment GC versus coverage calculated for each 100kb bin. This loess regression was performed separately for short and long fragments to account for possible differences in GC effects on coverage in plasma by fragment length (see, e.g., Benjamini *et al.*, 2012 *Nucleic Acids Res* 40:e72). The predictions for short and long coverage explained by GC from the loess model were subtracted, obtaining residuals for short and long that were uncorrelated with GC. The residuals were returned to the original scale by adding back the genome-wide median short and long estimates of coverage. This procedure was repeated for each sample to account for possible differences in GC effects on coverage between samples. To further reduce the feature space and noise, the total GC-adjusted coverage in 5 Mb bins was calculated.

To compare the variability of fragment lengths from healthy subjects to fragments in patients with cancer, the standard deviation of the short to long fragmentation profiles for each individual was calculated. The standard deviations in the two groups were compared by a Wilcoxon rank sum test.

Analyses of chromosome arm copy number changes

To develop arm-level statistics for copy number changes, an approach for aneuploidy detection in plasma as described elsewhere (see, e.g., Leary *et al.*, 2012 *Sci Transl Med* 4:162ra154) was adopted. This approach divides the genome into non-overlapping 50KB bins for which GC-corrected log2 read depth was obtained after correction by loess with span 3/4. This loess-based correction is comparable to the approach outlined above, but is evaluated on a log2 scale to increase robustness to outliers in the smaller bins and does not stratify by fragment length. To obtain an arm-specific Z-score for copy number changes, the mean GC-adjusted read depth for each arm (GR) was centered and scaled by the average and standard deviation, respectively, of GR scores obtained from an independent set of 50 healthy samples.

Analyses of mitochondrial-aligned reads from cfDNA

Whole genome sequence reads that initially mapped to the mitochondrial genome were extracted from bam files and realigned to the hg19 reference genome in end-to-end mode with Bowtie2 as described elsewhere (see, e.g., Langmead *et al.*, 2012 *Nat Methods* 9:357-359). The resulting aligned reads were filtered such that both mates aligned to the mitochondrial genome with MAPQ >= 30. The number of fragments mapping to the mitochondrial genome was counted and converted to a percentage of the total number of fragments in the original bam files.

Prediction model for cancer classification

To distinguish healthy from cancer patients using fragmentation profiles, a stochastic gradient boosting model was used (gbm; see, e.g., Friedman *et al.*, 2001 *Ann Stat* 29:1189-1232; and Friedman *et al.*, 2002 *Comput Stat Data An* 38:367-378). GC-corrected total and short fragment coverage for all 504 bins were centered and scaled for each sample to have mean 0 and unit standard deviation. Additional features included Z-scores for each of the 39 autosomal arms and mitochondrial representation (log10-transformed proportion of reads mapped to the mitochondria). To estimate the prediction error of this approach, 10-fold cross-validation was used as described elsewhere (see, e.g., Efron et al., 1997 J Am Stat Assoc 92, 548-560). Feature selection, performed only on the training data in each cross-validation run, removed bins that were highly correlated (correlation > 0.9) or had near zero variance. Stochastic gradient boosted machine learning was implemented using the R package gbm package with parameters n.trees=150, interaction.depth=3, shrinkage=0.1, and n.minobsinside=10. To average over the prediction error from the randomization of patients to folds, the 10-fold cross validation procedure was repeated 10 times. Confidence intervals for sensitivity fixed at 98% and 95% specificity were obtained from 2000 bootstrap replicates.

Prediction model for tumor tissue of origin classification

For samples correctly classified as cancer patients at 90% specificity (n = 174), a separate stochastic gradient boosting model was trained to classify the tissue of origin. To account for the small number of lung samples used for prediction, 18 cfDNA baseline samples from late stage lung cancer patients were included from the monitoring analyses. Performance characteristics of the model were evaluated by 10-fold cross-validation repeated 10 times. This gbm model was trained using the same features as in the cancer classification model. As previously described, features that displayed correlation above 0.9 to each other or had near zero variance were removed within each training dataset during cross-validation.

The tissue class probabilities were averaged across the 10 replicates for each patient and the class with the highest probability was taken as the predicted tissue.

Analyses of nucleosomal DNA from human lymphocytes and cfDNA

From the nuclease treated lymphocytes, fragment sizes were analyzed in 5 Mb bins as described for whole genome cfDNA analyses. A genome-wide map of nucleosome positions was constructed from the nuclease treated lymphocyte cell-lines. This approach identified local biases in the coverage of circulating fragments, indicating a region protected from degradation. A “Window positioning score” (WPS) was used to score each base pair in the genome (see, e.g., Snyder et al., 2016 *Cell* 164:57). Using a sliding window of 60bp centered around each base, the WPS was calculated as the number of fragments completely spanning the window minus the number of fragments with only one end in the window. Since fragments arising from nucleosomes have a median length of 167 bp, a high WPS indicated a possible nucleosomic position. WPS scores were centered at zero using a running median and smoothed using a Kolmogorov-Zurbenko filter (see, e.g., Zurbenko, *The spectral analysis of time series*. North-Holland series in statistics and probability; Elsevier, New York, NY, 1986). For spans of positive WPS between 50 and 450 bp, a nucleosome peak was defined as the set of base pairs with a WPS above the median in that window. The calculation of nucleosome positions for cfDNA from 30 healthy individuals with sequence coverage of 9x was determined in the same manner as for lymphocyte DNA. To ensure that nucleosomes in healthy cfDNA were representative, a consensus track of nucleosomes was defined consisting only of nucleosomes identified in two or more individuals. Median distances between adjacent nucleosomes were calculated from the consensus track.

Monte Carlo simulation of detection sensitivity

A Monte Carlo simulation was used to estimate the probability of detecting a molecule with a tumor-derived alteration. Briefly, 1 million molecules were generated from a multinomial distribution. For a simulation with m alterations, wild-type molecules were simulated with probability p and each of the m tumor alterations were simulated with probability $(1-p)/m$. Next, $g * m$ molecules were sampled randomly with replacement, where g denotes the number of genome equivalents in 1 ml of plasma. If a tumor alteration was sampled s or more times, the sample was classified as cancer-derived. The simulation was repeated 1000 times, estimating the probability that the *in silico* sample would be correctly classified as cancer by the mean of the cancer indicator. Setting $g = 2000$ and $s = 5$, the number of tumor alterations was varied by powers of 2 from 1 to 256 and the fraction of tumor-derived molecules from 0.0001% to 1%.

Statistical analyses

All statistical analyses were performed using R version 3.4.3. The R packages caret (version 6.0-79) and gbm (version 2.1-4) were used to implement the classification of healthy versus cancer and tissue of origin. Confidence intervals from the model output were obtained with the pROC (version 1.13) R package (see, e.g., Robin *et al.*, 2011 *BMC bioinformatics* 12:77). Assuming the prevalence of undiagnosed cancer cases in this population is high (1 or 2 cases per 100 healthy), a genomic assay with a specificity of 0.95 and sensitivity of 0.8 would have useful operating characteristics (positive predictive value of 0.25 and negative predictive value near 1). Power calculations suggest that an analysis of more than 200 cancer patients and an approximately equal number of healthy controls, enable an estimation of the sensitivity with a margin of error of 0.06 at the desired specificity of 0.95 or greater.

Data and Code Availability

Sequence data utilized in this study have been deposited at the European Genome-phenome Archive under study accession nos. EGAS00001003611 and EGAS00001002577. Code for analyses is available at github.com/Cancer-Genomics/delfi_scripts.

Results

DELFI allows simultaneous analysis of a large number of abnormalities in cfDNA through genome-wide analysis of fragmentation patterns. The method is based on low coverage whole genome sequencing and analysis of isolated cfDNA. Mapped sequences are analyzed in non-overlapping windows covering the genome. Conceptually, windows may range in size from thousands to millions of bases, resulting in hundreds to thousands of windows in the genome. 5 Mb windows were used for evaluating cfDNA fragmentation patterns as these would provide over 20,000 reads per window even at a limited amount of 1-2x genome coverage. Within each window, the coverage and size distribution of cfDNA fragments was examined. This approach was used to evaluate the variation of genome-wide fragmentation profiles in healthy and cancer populations (Table 1; Appendix A). The genome-wide pattern from an individual can be compared to reference populations to determine if the pattern is likely healthy or cancer-derived. As genome-wide profiles reveal positional differences associated with specific tissues that may be missed in overall fragment size distributions, these patterns may also indicate the tissue source of cfDNA.

The fragmentation size of cfDNA was focused on as it was found that cancer-derived cfDNA molecules may be more variable in size than cfDNA derived from non-cancer cells. cfDNA fragments from targeted regions that were captured and sequenced at high coverage (43,706 total coverage, 8,044 distinct coverage) from patients with breast, colorectal, lung or ovarian cancer (Table 1 (Appendix A), Table 2 (Appendix B), and Table 3 (Appendix C)) were initially examined. Analyses of loci containing 165 tumor-specific alterations from 81 patients (range of 1-7 alterations per patient) revealed an average absolute difference of 6.5 bp (95% CI, 5.4-7.6 bp) between lengths of median mutant and wild-type cfDNA fragments (Fig. 3, Table 3 (Appendix C)). The median size of mutant cfDNA fragments ranged from 30 bases smaller at chromosome 3 position 41,266,124 to 47 bases larger at chromosome 11 position 108,117,753 than the wild-type sequences at these regions (Table 3; Appendix C). GC content was similar for mutated and non-mutated fragments (Fig. 4a), and there was no correlation between GC content and fragment length (Fig. 4b). Similar analyses of 44 germline alterations from 38 patients identified median cfDNA size differences of less than 1 bp between fragment lengths of different alleles (Fig. 5, Table 3 (Appendix C)). Additionally, 41 alterations related to clonal hematopoiesis were identified through a previous sequence comparison of DNA from plasma, buffy coat, and tumors of the same individuals. Unlike tumor-derived fragments, there were no significant differences between fragments with hematopoietic alterations and wild type fragments (Fig. 6, Table 3 (Appendix C)). Overall, cancer-derived cfDNA fragment lengths were significantly more variable compared to non-cancer cfDNA fragments at certain genomic regions ($p<0.001$, variance ratio test). It was hypothesized that these differences may be due to changes in higher-order chromatin structure as well as other genomic and epigenomic abnormalities in cancer and that cfDNA fragmentation in a position-specific mannercould therefore serve as a unique biomarker for cancer detection.

As targeted sequencing only analyzes a limited number of loci, larger-scale genome-wide analyses to detect additional abnormalities in cfDNA fragmentation were investigated. cfDNA was isolated from ~4 ml of plasma from 8 lung cancer patients with stage I-III disease , as well as from 30 healthy individuals (Table 1 (Appendix A), Table 4 (Appendix D), and Table 5 (Appendix E)). A high efficiency approach was used to convert cfDNA to next generation sequencing libraries and performed whole genome sequencing at ~9x coverage (Table 4; Appendix D). Overall cfDNA fragment lengths of healthy individuals were larger, with a median fragment size of 167.3 bp, while patients with cancer had median fragment sizes of 163.8 ($p<0.01$, Welch's t-test) (Table 5; Appendix E). To examine differences in fragment size and coverage in a position dependent manner across the genome, sequenced fragments were mapped to their genomic origin and fragment lengths were evaluated in 504 windows that were 5 Mb in size, covering ~2.6 Gb of the genome. For each window, the fraction of small cfDNA fragments (100 to 150 bp in length) to larger cfDNA fragments (151 to 220 bp) as well as overall coverage were determined and used to obtain genome-wide fragmentation profiles for each sample.

Healthy individuals had very similar fragmentation profiles throughout the genome (Fig. 7 and Fig. 8). To examine the origins of fragmentation patterns normally observed in cfDNA, nuclei were isolated from elutriated lymphocytes of two healthy individuals and treated with DNA nucleases to obtain nucleosomal DNA fragments. Analyses of cfDNA patterns in observed healthy individuals revealed a high correlation to lymphocyte nucleosomal DNA fragmentation profiles (Fig. 7b and 7d) and nucleosome distances (Fig. 7c and 7f). Median distances between nucleosomes in lymphocytes were correlated to open (A) and closed (B) compartments of lymphoblastoid cells as revealed using the Hi-C method (see, e.g., Lieberman-Aiden *et al.*, 2009 *Science* 326:289-293; and Fortin *et al.*, 2015 *Genome Biol* 16:180) for examining the three-dimensional architecture of genomes (Fig. 7c). These analyses suggest that the fragmentation patterns of normal cfDNA are the result of nucleosomal DNA patterns that largely reflect the chromatin structure of normal blood cells.

In contrast to healthy cfDNA, patients with cancer had multiple distinct genomic differences with increases and decreases in fragment sizes at different regions (Fig. 7a and 7b). Similar to our observations from targeted analyses, there was also greater variation in fragment lengths genome-wide for patients with cancer compared to healthy individuals.

To determine whether cfDNA fragment length patterns could be used to distinguish patients with cancer from healthy individuals, genome-wide correlation analyses were performed of the fraction of short to long cfDNA fragments for each sample compared to the median fragment length profile calculated from healthy individuals (Fig. 7a, 7b, and 7e). While the profiles of cfDNA fragments were remarkably consistent among healthy individuals (median correlation of 0.99), the median correlation of genome-wide fragment ratios among cancer patients was 0.84 (0.15 lower, 95% CI 0.07-0.50, $p<0.001$, Wilcoxon rank sum test; Table 5 (Appendix E)). Similar differences were observed when comparing fragmentation profiles of cancer patients to fragmentation profiles or nucleosome distances in healthy lymphocytes (Fig. 7c, 7d, and 7f). To account for potential biases in the fragmentation profiles attributable to GC content, a locally weighted smoother was applied independently to each sample and found that differences in fragmentation profiles between healthy individuals and cancer patients remained after this adjustment (median correlation of cancer patientsto healthy = 0.83) (Table 5; Appendix E).

Subsampling analyses of whole genome sequence data was performed at 9x coverage from cfDNA of patients with cancer at ~2x, ~1x, ~0.5x, ~0.2x, and ~0.1x genome coverage, and it was determined that altered fragmentation profiles were readily identified even at 0.5x genome coverage (Fig. 9). Based on these observations, whole genome sequencing was performed with coverage of 1-2x to evaluate whether fragmentation profiles may change during the course of targeted therapy in a manner similar to monitoring of sequence alterations. cfDNA from 19 non-small cell lung cancer patients including 5 with partial radiographic response, 8 with stable disease, 4 with progressive disease, and 2 with unmeasurable disease, during the course of anti-EGFR or anti-ERBB2 therapy was evaluated (Table 6; Appendix F). As shown in Fig. 10, the degree of abnormality in the fragmentation profiles during therapy closely matched levels of EGFR or ERBB2 mutant allele fractions as determined using targeted sequencing (Spearman correlation of mutant allele fractions to fragmentation profiles = 0.74). This correlation is remarkable as genome-wide and mutation-based methods are orthogonal and examine different cfDNA alterations that may be suppressed in these patients due to prior therapy. Notably all cases that had progression free survival of six or more months displayed a drop of or had extremely low levels of ctDNA after initiation of therapy as determined by fragmentation profiles, while cases with poor clinical outcome had increases in ctDNA. These results demonstrate the feasibility of fragmentation analyses for detecting the presence of tumor-derived cfDNA, and suggests that such analyses may also be useful for quantitative monitoring of cancer patients during treatment.

The fragmentation profiles were examined in the context of known copy number changes in a patient where parallel analyses of tumor tissue were obtained. These analyses demonstrated that altered fragmentation profiles were present in regions of the genome that were copy neutral and that these may be further affected in regions with copy number changes (Fig. 11a and Fig. 12a). Position dependent differences in fragmentation patterns could be used to distinguish cancer-derived cfDNA from healthy cfDNA in these regions (Fig. 12a, b), while overall cfDNA fragment size measurements would have missed such differences (Fig. 12a).

These analyses were extended to an independent cohort of cancer patients and healthy individuals. Whole genome sequencing of cfDNA at 1-2x coverage from a total of 208 patients with cancer, including breast (n=54), colorectal (n=27), lung (n=12), ovarian (n=28), pancreatic (n=34), gastric (n=27), or bile duct cancers (n=26), as well as 215 individuals without cancer was performed (Table 1 (Appendix A) and Table 4 (Appendix D)). All cancer patients were treatment naïve and the majority had resectable disease (n=183). After GC adjustment of short and long cfDNA fragment coverage (Fig. 13a), coverage and size characteristics of fragments in windows throughout the genome were examined (Fig. 11b, Table 4 (Appendix D) and Table 7 (Appendix G)). Genome-wide correlations of coverage to GC content were limited and no differences in these correlations between cancer patients and healthy individuals were observed (Fig. 13b). Healthy individuals had highly concordant fragmentation profiles, while patients with cancer had high variability with decreased correlation to the median healthy profile (Table 7; Appendix G). An analysis of the most commonly altered fragmentation windows in the genome among cancer patients revealed a median of 60 affected windows across the cancer types analyzed, highlighting the multitude of position dependent alterations in fragmentation of cfDNA in individuals with cancer (Fig. 11c).

To determine if position dependent fragmentation changes can be used to detect individuals with cancer, a gradient tree boosting machine learning model was implemented to examine whether cfDNA can be categorized as having characteristics of a cancer patient or healthy individual and estimated performance characteristics of this approach by ten-fold cross validation repeated ten times (Figs. 14 and 15). The machine learning model included GC-adjusted short and long fragment coverage characteristics in windows throughout the genome. A machine learning classifier for copy number changes from chromosomal arm dependent features rather than a single score was also developed (Fig. 16a and Table 8 (Appendix H)) and mitochondrial copy number changes were also included (Fig. 16b) as these could also help distinguish cancer from healthy individuals. Using this implementation of DELFI, a score was obtained that could be used to classify patients as healthy or having cancer. 152 of the 208 cancer patients were detected (73% sensitivity, 95% CI 67%-79%) while four of the 215 healthy individuals were misclassified (98% specificity) (Table 9). At a threshold of 95% specificity, 80% of patients with cancer were detected (95% CI, 74%-85%), including 79% of resectable (stage I – III) patients (145 of 183) and 82% of metastatic (stage IV) patients (18 out of 22) (Table 9). Receiver operator characteristic analyses for detection of patients with cancer had an AUC of 0.94 (95% CI 0.92 – 0.96), ranged among cancer types from 0.86 for pancreatic cancer to ≥0.99 for lung and ovarian cancers (Figs. 17a and 17b), and had AUCs ≥0.92 across all stages (Fig. 18). The DELFI classifier score did not differ with age among either cancer patients or healthy individuals (Table 1; Appendix A).

Table 9. DELFI performance for cancer detection.

		Individuals analyzed	95% specificity			98% specificity		
			Individuals detected	Sensitivity	95% CI	Individuals detected	Sensitivity	95% CI
Healthy		215	10	-	-	4	-	-
Cancer		208	166	80%	74%-85%	152	73%	67%-79%
Type	Breast	54	38	70%	56%-82%	31	57%	43%-71%
	Bile duct	26	23	88%	70%-98%	21	81%	61%-93%
	Colorectal	27	22	81%	62%-94%	19	70%	50%-86%
	Gastric	27	22	81%	62%-94%	22	81%	62%-94%
	Lung	12	12	100%	74%-100%	12	100%	74%-100%
	Ovarian	28	25	89%	72%-98%	25	89%	72%-98%
	Pancreatic	34	24	71%	53%-85%	22	65%	46%-80%
Stage	I	41	30	73%	53%-86%	28	68%	52%-82%
	II	109	85	78%	69%-85%	78	72%	62%-80%
	III	33	30	91%	76%-98%	26	79%	61%-91%
	IV	22	18	82%	60%-95%	17	77%	55%-92%
	0, X	3	3	100%	29%-100%	3	100%	29%-100%

To assess the contribution of fragment size and coverage, chromosome arm copy number, or mitochondrial mapping to the predictive accuracy of the model, the repeated 10-fold cross-validation procedure was implemented to assess performance characteristics of these features in isolation. It was observed that fragment coverage features alone (AUC = 0.94) were nearly identical to the classifier that combined all features (AUC = 0.94) (Fig. 17a). In contrast, analyses of chromosomal copy number changes had lower performance (AUC = 0.88) but were still more predictive than copy number changes based on individual scores (AUC=0.78) or mitochondrial mapping (AUC = 0.72) (Fig. 17a). These results suggest that fragment coverage is the major contributor to our classifier. Including all features in the prediction model may contribute in a complementary fashion for detection of patients with cancer as they can be obtained from the same genome sequence data.

As fragmentation profiles reveal regional differences in fragmentation that may differ between tissues, a similar machine learning approach was used to examine whether cfDNA patterns could identify the tissue of origin of these tumors. It was found that this approach had a 61% accuracy (95% CI 53%-67%), including 76% for breast, 44% for bile duct, 71% for colorectal, 67% for gastric, 53% for lung, 48% for ovarian, and 50% for pancreatic cancers (Fig. 19, Table 10). The accuracy increased to 75% (95% CI 69%-81%) when considering assigning patients with abnormal cfDNA to one of two sites of origin (Table 10). For all tumor types, the classification of the tissue of origin by DELFI was significantly higher than determined by random assignment ($p<0.01$, binomial test, Table 10).

Table 10. DELFI tissue of origin prediction

Cancer Type	Patients Detected*	Top Prediction		Top Two Predictions		Random Assignment	
		Patients	Accuracy (95% CI)	Patients	Accuracy (95% CI)	Patients	Accuracy
Breast	42	32	76% (61%-88%)	38	91% (77%-97%)	9	22%
Bile Duct	23	10	44% (23%-66%)	15	65% (43%-84%)	3	12%
Colorectal	24	17	71% (49%-87%)	19	79% (58%-93%)	3	12%
Gastric	24	16	67% (45%-84%)	19	79% (58%-93%)	3	12%
Lung	30	16	53% (34%-72%)	23	77% (58%-90%)	2	6%
Ovarian	27	13	48% (29%-68%)	16	59% (38%-78%)	4	14%
Pancreatic	24	12	50% (29%-71%)	16	67% (45%-84%)	3	12%
Total	194	116	61% (53%-67%)	146	75% (69%-81%)	26	13%

*Patients detected are based on DELFI detection at 90% specificity. Lung cohort includes additional lung cancer patients with prior therapy.

As cancer-specific sequence alterations can be used to identify patients with cancer, it was evaluated whether combining DELFI with this approach could increase the sensitivity of cancer detection (Fig. 20). An analysis of cfDNA from a subset of the treatment naïve cancer patients using both DELFI and targeted sequencing revealed that 82% (103 of 126) of patients had fragmentation profile alterations, while 66% (83 of 126) had sequence alterations. Over 89% of cases with mutant allele fractions >1% were detected by DELFI while for cases with mutant allele fractions <1% the fraction detected by DELFI was 80%, including for cases that were undetectable using targeted sequencing (Table 7; Appendix G). When these approaches were used together, the combined sensitivity of detection increased to 91% (115 of 126 patients) with a specificity of 98% (Fig. 20).

Overall, genome-wide cfDNA fragmentation profiles are different between cancer patients and healthy individuals. The variability in fragment lengths and coverage in a position dependent manner throughout the genome may explain the apparently contradictory observations of previous analyses of cfDNA at specific loci or of overall fragment sizes. In patients with cancer, heterogeneous fragmentation patterns in cfDNA appear to be a result of mixtures of nucleosomal DNA from both blood and neoplastic cells. These studies provide a method for simultaneous analysis of tens to potentially hundreds of tumor-specific abnormalities from minute amounts of cfDNA, overcoming a limitation that has precluded the possibility of more sensitive analyses of cfDNA. DELFI analyses detected a higher fraction of cancer patients than previous cfDNA analysis methods that have focused on sequence or overall fragmentation sizes (see, e.g., Phallen *et al.*, 2017 *Sci Transl Med* 9:eaan2415; Cohen *et al.*, 2018 *Science* 359:926; Newman *et al.*, 2014 *Nat Med* 20:548; Bettegowda *et al.*, 2014 *Sci Transl Med* 6:224ra24; Newman *et al.*, 2016 *Nat Biotechnol* 34:547). As demonstrated in this Example, combining DELFI with analyses of other cfDNA alterations may further increase the sensitivity of detection. As fragmentation profiles appear related to nucleosomal DNA patterns, DELFI may be used for determining the primary source of tumor-derived cfDNA. The identification of the source of circulating tumor DNA in over half of patients analyzed may be further improved by including clinical characteristics, other biomarkers, including methylation changes, and additional diagnostic approaches (Ruibal Morell, 1992 *The International journal of biological markers* 7:160;

Galli et al., 2013 *Clinical chemistry and laboratory medicine* 51:1369; Sikaris, 2011 *Heart, lung & circulation* 20:634; Cohen *et al.*, 2018 *Science* 359:926). Finally, this approach requires only a small amount of whole genome sequencing, without the need for deep sequencing typical of approaches that focus on specific alterations. The performance characteristics and limited amount of sequencing needed for DELFI suggests that our approach could be broadly applied for screening and management of patients with cancer.

These results demonstrate that genome-wide cfDNA fragmentation profiles are different between cancer patients and healthy individuals. As such, cfDNA fragmentation profiles can have important implications for future research and applications of non-invasive approaches for detection of human cancer.

Other Embodiments

It is to be understood that while the invention has been described in conjunction with the detailed description thereof, the foregoing description is intended to illustrate and not limit the scope of the invention, which is defined by the scope of the appended claims. Other aspects, advantages, and modifications are within the scope of the following claims.

APPENDIX A: Table 1. Summary of patients and samples analyzed

Patient	Patient Type	Sample Type	Timepoint	Age at Diagnosis	Gender	Stage	TNM Staging	Site of Primary Tumor	Histopathological Diagnosis	Degree of Differentiation	Location of Metastases at Diagnosis	Volume of Plasma (ml)	cfDNA Extracted (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGCRC291	Colorectal Cancer	cfDNA	Preoperative treatment naive	69	F	IV	T3N2M1	Coecum	Adenocarcinoma	Moderate	Synchronous Liver	7.9	7.80	7.80	Y	Y	Y
CGCRC292	Colorectal Cancer	cfDNA	Preoperative treatment naive	51	M	IV	T3N2M1	Sigmoid Colon	Adenocarcinoma	Moderate	Synchronous Liver, Lung	7.9	6.73	6.73	Y	Y	Y
CGCRC293	Colorectal Cancer	cfDNA	Preoperative treatment naive	55	M	IV	T3N2M1	Rectum	Adenocarcinoma	Moderate	Synchronous Liver	7.2	3.83	3.83	Y	Y	Y
CGCRC294	Colorectal Cancer	cfDNA	Preoperative treatment naive	67	F	II	T3N0M0	Sigmoid Colon	Adenocarcinoma	Moderate	None	8.4	18.87	18.87	Y	Y	Y
CGCRC296	Colorectal Cancer	cfDNA	Preoperative treatment naive	76	F	II	T4N0M0	Coecum	Adenocarcinoma	Poor	None	4.3	31.24	31.24	Y	Y	Y
CGCRC299	Colorectal Cancer	cfDNA	Preoperative treatment naive	71	M	I	T1N0M0	Rectum	Adenocarcinoma	Moderate	None	8.8	10.18	10.18	Y	Y	Y
CGCRC300	Colorectal Cancer	cfDNA	Preoperative treatment naive	65	M	I	T2N0M0	Rectum	Adenocarcinoma	Moderate	None	4.3	10.48	10.48	Y	Y	Y
CGCRC301	Colorectal Cancer	cfDNA	Preoperative treatment naive	76	F	I	T2N0M0	Rectum	Adenocarcinoma	Moderate	None	4.1	6.51	6.51	Y	Y	Y
CGCRC302	Colorectal Cancer	cfDNA	Preoperative treatment naive	73	M	II	T3N0M0	Transverse Colon	Adenocarcinoma	Moderate	None	4.3	52.13	52.13	Y	Y	Y
CGCRC304	Colorectal Cancer	cfDNA	Preoperative treatment naive	86	F	II	T3N0M0	Rectum	Adenocarcinoma	Moderate	None	4.1	30.19	30.19	Y	Y	Y
CGCRC305	Colorectal Cancer	cfDNA	Preoperative treatment naive	83	F	II	T3N0M0	Transverse Colon	Adenocarcinoma	Moderate	None	8.6	9.10	9.10	Y	Y	Y
CGCRC306	Colorectal Cancer	cfDNA	Preoperative treatment naive	80	F	II	T4N0M0	Ascending Colon	Adenocarcinoma	Moderate	None	4.5	24.31	24.31	Y	Y	Y
CGCRC307	Colorectal Cancer	cfDNA	Preoperative treatment naive	78	F	II	T3N0M0	Ascending Colon	Adenocarcinoma	Moderate	None	8.5	14.26	14.26	Y	Y	Y
CGCRC308	Colorectal Cancer	cfDNA	Preoperative treatment naive	72	F	III	T4N2M0	Ascending Colon	Adenocarcinoma	Moderate	None	4.3	46.87	46.87	Y	Y	Y
CGCRC311	Colorectal Cancer	cfDNA	Preoperative treatment naive	59	M	I	T2N0M0	Sigmoid Colon	Adenocarcinoma	Moderate	None	8.5	3.91	3.91	Y	Y	Y
CGCRC315	Colorectal Cancer	cfDNA	Preoperative treatment naive	74	M	III	T3N1M0	Sigmoid Colon	Adenocarcinoma	Moderate	None	8.6	9.67	9.67	Y	Y	Y
CGCRC316	Colorectal Cancer	cfDNA	Preoperative treatment naive	80	M	III	T3N2M0	Transverse Colon	Adenocarcinoma	Moderate	None	4.9	52.16	52.16	Y	Y	Y
CGCRC317	Colorectal Cancer	cfDNA	Preoperative treatment naive	74	M	III	T3N2M0	Descending Colon	Adenocarcinoma	Moderate	None	8.8	16.08	16.08	Y	Y	Y
CGCRC318	Colorectal Cancer	cfDNA	Preoperative treatment naive	81	M	I	T2N0M0	Coecum	Adenocarcinoma	Moderate	None	9.8	18.24	18.24	Y	Y	Y
CGCRC319	Colorectal Cancer	cfDNA	Preoperative treatment naive	80	F	III	T2N1M0	Descending Colon	Adenocarcinoma	Moderate	None	4.2	53.54	53.54	Y	N	Y
CGCRC320	Colorectal Cancer	cfDNA	Preoperative treatment naive	73	F	I	T2N0M0	Ascending Colon	Adenocarcinoma	Moderate	None	4.5	30.37	30.37	Y	Y	Y
CGCRC321	Colorectal Cancer	cfDNA	Preoperative treatment naive	68	M	I	T2N0M0	Rectum	Adenocarcinoma	Moderate	None	9.3	4.25	4.25	Y	Y	Y
CGCRC333	Colorectal Cancer	cfDNA	Preoperative treatment naive	NA	F	IV	NA	Colon/Rectum	Adenocarcinoma	NA	Liver	4.0	113.88	113.88	Y	Y	Y
CGCRC336	Colorectal Cancer	cfDNA	Preoperative treatment naive	NA	M	IV	NA	Colon/Rectum	Adenocarcinoma	NA	Liver	4.4	211.74	211.74	Y	Y	Y
CGCRC338	Colorectal Cancer	cfDNA	Preoperative treatment naive	NA	F	IV	NA	Colon/Rectum	Adenocarcinoma	NA	Liver	2.3	109.76	109.76	Y	Y	Y
CGCRC341	Colorectal Cancer	cfDNA	Preoperative treatment naive	NA	F	IV	NA	Colon/Rectum	Adenocarcinoma	NA	Liver	4.6	156.62	156.62	Y	N	Y
CGCRC342	Colorectal Cancer	cfDNA	Preoperative treatment naive	NA	M	IV	NA	Colon/Rectum	Adenocarcinoma	NA	Liver	3.9	56.09	56.09	Y	N	Y
CGLU316	Lung Cancer	cfDNA	Pre-treatment, Day -53	50	F	IV	T3N2M0	Left Upper Lobe of Lung	Adeno, Squamous, Small Cell Carcinoma	Poor	Lung	5.0	2.38	2.38	Y	N	Y
CGLU316	Lung Cancer	cfDNA	Pre-treatment, Day -4	50	F	IV	T3N2M0	Left Upper Lobe of Lung	Adeno, Squamous, Small Cell Carcinoma	Poor	Lung	5.0	2.11	2.11	Y	N	Y
CGLU316	Lung Cancer	cfDNA	Post-treatment, Day 18	50	F	IV	T3N2M0	Left Upper Lobe of Lung	Adeno, Squamous, Small Cell Carcinoma	Poor	Lung	5.0	0.87	1.07	Y	N	Y
CGLU316	Lung Cancer	cfDNA	Post-treatment, Day 87	50	F	IV	T3N2M0	Left Upper Lobe of Lung	Adeno, Squamous, Small Cell Carcinoma	Poor	Lung	2.0	8.74	8.75	Y	N	Y
CGLU344	Lung Cancer	cfDNA	Pre-treatment, Day -21	65	F	IV	T2N2M1	Right Upper Lobe of Lung	Adenocarcinoma	NA	Pleura, Liver, Peritoneum	5.0	34.77	25.00	Y	N	Y
CGLU344	Lung Cancer	cfDNA	Pre-treatment, Day 0	65	F	IV	T2N2M1	Right Upper Lobe of Lung	Adenocarcinoma	NA	Pleura, Liver, Peritoneum	5.0	15.63	15.64	Y	N	Y
CGLU344	Lung Cancer	cfDNA	Post-treatment, Day 0.1875	65	F	IV	T2N2M1	Right Upper Lobe of Lung	Adenocarcinoma	NA	Pleura, Liver, Peritoneum	5.0	9.22	9.22	Y	N	Y
CGLU344	Lung Cancer	cfDNA	Post-treatment, Day 59	65	F	IV	T2N2M1	Right Upper Lobe of Lung	Adenocarcinoma	NA	Pleura, Liver, Peritoneum	5.0	5.31	5.32	Y	N	Y
CGLU369	Lung Cancer	cfDNA	Pre-treatment, Day -2	48	F	IV	T2NxM1	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain	2.0	11.28	11.28	Y	N	Y
CGLU369	Lung Cancer	cfDNA	Post-treatment, Day 12	48	F	IV	T2NxM1	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain	5.0	10.09	10.09	Y	N	Y
CGLU369	Lung Cancer	cfDNA	Post-treatment, Day 68	48	F	IV	T2NxM1	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain	5.0	6.69	6.70	Y	N	Y
CGLU369	Lung Cancer	cfDNA	Post-treatment, Day 110	48	F	IV	T2NxM1	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain	5.0	8.41	8.42	Y	N	Y
CGLU373	Lung Cancer	cfDNA	Pre-treatment, Day -2	56	F	IV	T3N1M0	Right Upper Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	6.35	6.35	Y	N	Y
CGLU373	Lung Cancer	cfDNA	Post-treatment, Day 0.125	56	F	IV	T3N1M0	Right Upper Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	6.28	6.28	Y	N	Y
CGLU373	Lung Cancer	cfDNA	Post-treatment, Day 7	56	F	IV	T3N1M0	Right Upper Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	3.82	3.82	Y	N	Y
CGLU373	Lung Cancer	cfDNA	Post-treatment, Day 47	56	F	IV	T3N1M0	Right Upper Lobe of Lung	Adenocarcinoma	Moderate	None	3.5	5.55	5.55	Y	N	Y
CGPLBR100	Breast Cancer	cfDNA	Preoperative treatment naive	44	F	III	T2N2M0	Left Breast	Infiltrating Ductal Carcinoma	NA	None	4.0	4.25	4.25	Y	N	Y
CGPLBR101	Breast Cancer	cfDNA	Preoperative treatment naive	46	F	II	T2N1M0	Left Breast	Infiltrating Lobular Carcinoma	Moderate	None	4.0	37.88	37.88	Y	N	Y
CGPLBR102	Breast Cancer	cfDNA	Preoperative treatment naive	47	F	II	T2N1M0	Right Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.6	13.67	13.67	Y	N	Y
CGPLBR103	Breast Cancer	cfDNA	Preoperative treatment naive	48	F	II	T2N1M0	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.6	7.11	7.11	Y	N	Y
CGPLBR104	Breast Cancer	cfDNA	Preoperative treatment naive	68	F	II	T2N0M0	Right Breast	Infiltrating Lobular Carcinoma	Moderate	None	4.7	19.89	19.89	Y	N	Y
CGPLBR12	Breast Cancer	cfDNA	Preoperative treatment naive	NA	F	III	NA	Breast	Ductal Carcinoma insitu with Microinvasion	NA	NA	4.3	4.21	4.21	Y	N	N
CGPLBR18	Breast Cancer	cfDNA	Preoperative treatment naive	NA	F	III	NA	Breast	Infiltrating Lobular Carcinoma	NA	NA	4.1	40.39	30.49	Y	N	N
CGPLBR23	Breast Cancer	cfDNA	Preoperative treatment naive	53	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.7	20.09	20.09	Y	N	N
CGPLBR24	Breast Cancer	cfDNA	Preoperative treatment naive	53	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	3.6	58.33	34.72	Y	N	N
CGPLBR28	Breast Cancer	cfDNA	Preoperative treatment naive	59	F	III	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.2	12.86	12.86	Y	N	N
CGPLBR30	Breast Cancer	cfDNA	Preoperative treatment naive	61	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.1	59.73	30.49	Y	N	N
CGPLBR31	Breast Cancer	cfDNA	Preoperative treatment naive	54	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	3.4	23.94	23.94	Y	N	N
CGPLBR32	Breast Cancer	cfDNA	Preoperative treatment naive	NA	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.4	71.23	28.41	Y	N	N
CGPLBR33	Breast Cancer	cfDNA	Preoperative treatment naive	47	F	II	NA	Breast	Infiltrating Lobular Carcinoma	NA	None	4.4	11.00	11.00	Y	N	N
CGPLBR34	Breast Cancer	cfDNA	Preoperative treatment naive	60	F	II	NA	Breast	Infiltrating Lobular Carcinoma	NA	None	4.4	23.61	23.61	Y	N	N
CGPLBR35	Breast Cancer	cfDNA	Preoperative treatment naive	43	F	II	NA	Breast	Ductal Carcinoma insitu with Microinvasion	NA	None	4.5	22.58	22.58	Y	N	N
CGPLBR36	Breast Cancer	cfDNA	Preoperative treatment naive	36	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.4	17.73	17.73	Y	N	N
CGPLBR37	Breast Cancer	cfDNA	Preoperative treatment naive	58	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.4	9.39	9.39	Y	N	N
CGPLBR38	Breast Cancer	cfDNA	Preoperative treatment naive	54	F	I	T1N0M0	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.0	5.77	5.77	Y	Y	Y
CGPLBR40	Breast Cancer	cfDNA	Preoperative treatment naive	66	F	III	T2N2M0	Left Breast	Infiltrating Ductal Carcinoma	Poor	None	4.6	15.69	15.69	Y	Y	Y
CGPLBR41	Breast Cancer	cfDNA	Preoperative treatment naive	51	F	III	T3N1M0	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.5	11.56	11.56	Y	N	Y
CGPLBR45	Breast Cancer	cfDNA	Preoperative treatment naive	57	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	20.36	20.36	Y	N	N
CGPLBR46	Breast Cancer	cfDNA	Preoperative treatment naive	54	F	III	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	3.5	20.17	20.17	Y	N	N
CGPLBR47	Breast Cancer	cfDNA	Preoperative treatment naive	54	F	I	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	13.89	13.89	Y	N	N
CGPLBR48	Breast Cancer	cfDNA	Preoperative treatment naive	47	F	II	T2N1M0	Left Breast	Infiltrating Ductal Carcinoma	Poor	None	3.9	7.07	7.07	Y	Y	Y
CGPLBR49	Breast Cancer	cfDNA	Preoperative treatment naive	37	F	II	T2N1M0	Left Breast	Infiltrating Ductal Carcinoma	Poor	None	4.0	5.74	5.74	Y	N	Y
CGPLBR50	Breast Cancer	cfDNA	Preoperative treatment naive	51	F	I	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	45.58	27.78	Y	N	N
CGPLBR51	Breast Cancer	cfDNA	Preoperative treatment naive	53	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.0	8.83	8.83	Y	N	N
CGPLBR52	Breast Cancer	cfDNA	Preoperative treatment naive	68	F	III	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	80.71	27.78	Y	N	N
CGPLBR55	Breast Cancer	cfDNA	Preoperative treatment naive	53	F	III	T3N1M0	Right Breast	Infiltrating Ductal Carcinoma	Poor	None	4.3	4.57	4.57	Y	Y	Y
CGPLBR56	Breast Cancer	cfDNA	Preoperative treatment naive	56	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	22.16	22.16	Y	N	N
CGPLBR57	Breast Cancer	cfDNA	Preoperative treatment naive	54	F	III	T2N2M0	Left Breast	Infiltrating Ductal Carcinoma	NA	None	4.3	4.02	4.02	Y	N	Y
CGPLBR59	Breast Cancer	cfDNA	Preoperative treatment naive	42	F	I	T1N0M0	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.1	8.24	8.24	Y	N	Y
CGPLBR60	Breast Cancer	cfDNA	Preoperative treatment naive	61	F	II	NA	Left Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	11.09	11.09	Y	N	N
CGPLBR61	Breast Cancer	cfDNA	Preoperative treatment naive	67	F	II	T2N1M0	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.1	13.25	13.25	Y	N	Y
CGPLBR63	Breast Cancer	cfDNA	Preoperative treatment naive	48	F	II	T2N1M0	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.0	6.19	6.19	Y	Y	Y
CGPLBR65	Breast Cancer	cfDNA	Preoperative treatment naive	50	F	II	NA	Left Breast	Infiltrating Ductal Carcinoma	NA	None	3.5	41.75	35.71	Y	N	N
CGPLBR68	Breast Cancer	cfDNA	Preoperative treatment naive	64	F	III	T4N1M0	Breast	Infiltrating Ductal Carcinoma	Poor	None	3.4	10.41	10.41	Y	N	Y
CGPLBR69	Breast Cancer	cfDNA	Preoperative treatment naive	43	F	II	T2N0M0	Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.4	4.07	4.07	Y	Y	Y
CGPLBR70	Breast Cancer	cfDNA	Preoperative treatment naive	60	F	II	T2N1M0	Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.4	11.94	11.94	Y	Y	Y
CGPLBR71	Breast Cancer	cfDNA	Preoperative treatment naive	65	F	II	T2N0M0	Breast	Infiltrating Ductal Carcinoma	Poor	None	3.1	7.64	7.64	Y	Y	Y
CGPLBR72	Breast Cancer	cfDNA	Preoperative treatment naive	67	F	II	T2N0M0	Breast	Infiltrating Ductal Carcinoma	Well	None	3.9	4.43	4.43	Y	Y	Y
CGPLBR73	Breast Cancer	cfDNA	Preoperative treatment naive	60	F	II	T2N1M0	Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.3	14.69	14.69	Y	Y	Y
CGPLBR76	Breast Cancer	cfDNA	Preoperative treatment naive	53	F	II	T2N0M0	Right Breast	Infiltrating Ductal Carcinoma	Well	None	4.9	8.71	8.71	Y	Y	Y
CGPLBR81	Breast Cancer	cfDNA	Preoperative treatment naive	54	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	2.5	83.14	50.00	Y	N	N
CGPLBR82	Breast Cancer	cfDNA	Preoperative treatment naive	70	F	I	T1N0M0	Right Breast	Infiltrating Lobular Carcinoma	Moderate	None	4.8	23.39	23.39	Y	N	Y
CGPLBR83	Breast Cancer	cfDNA	Preoperative treatment naive	53	F	II	T2N1M0	Right Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.7	100.17	100.17	Y	Y	Y
CGPLBR84	Breast Cancer	cfDNA	Preoperative treatment naive	NA	F	III	NA	Breast	Infiltrating Ductal Carcinoma	NA	NA	3.6	16.95	16.95	Y	N	N
CGPLBR87	Breast Cancer	cfDNA	Preoperative treatment naive	80	F	II	T2N1M0	Right Breast	Papillary Carcinoma	Well	None	3.6	277.39	69.44	Y	Y	Y
CGPLBR88	Breast Cancer	cfDNA	Preoperative treatment naive	48	F	II	T1N1M0	Left Breast	Infiltrating Ductal Carcinoma	Poor	None	3.6	49.75	49.75	Y	Y	Y

Patient	Patient Type	Sample Type	Timepoint	Age at Diagnosis	Gender	Stage	TNM Staging	Site of Primary Tumor	Histopathological Diagnosis	Degree of Differentiation	Location of Metastases at Diagnosis	Volume of Plasma (ml)	cfDNA Extracted (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLBR90	Breast Cancer	cfDNA	Preoperative treatment naive	51	F	II	NA	Right Breast	Infiltrating Ductal Carcinoma	NA	None	3.0	14.24	14.24	Y	N	N
CGPLBR91	Breast Cancer	cfDNA	Preoperative treatment naive	62	F	III	T2N2M0	Breast	Infiltrating Lobular Carcinoma	Poor	None	3.2	22.41	22.41	Y	N	Y
CGPLBR92	Breast Cancer	cfDNA	Preoperative treatment naive	58	F	II	T2N1M0	Breast	Infiltrating Medullary Carcinoma	Poor	None	3.1	81.00	81.00	Y	Y	Y
CGPLBR93	Breast Cancer	cfDNA	Preoperative treatment naive	59	F	II	T1N0M0	Breast	Infiltrating Ductal Carcinoma	Moderate	None	3.3	27.94	27.94	Y	N	Y
CGPLH189	Healthy	cfDNA	Preoperative treatment naive	74	M	NA	NA	NA	NA	NA	NA	5.0	5.84	5.84	Y	N	N
CGPLH190	Healthy	cfDNA	Preoperative treatment naive	67	M	NA	NA	NA	NA	NA	NA	4.7	18.07	18.07	Y	N	N
CGPLH192	Healthy	cfDNA	Preoperative treatment naive	74	M	NA	NA	NA	NA	NA	NA	4.7	12.19	12.19	Y	N	N
CGPLH193	Healthy	cfDNA	Preoperative treatment naive	72	F	NA	NA	NA	NA	NA	NA	5.0	5.47	5.47	Y	N	N
CGPLH194	Healthy	cfDNA	Preoperative treatment naive	75	F	NA	NA	NA	NA	NA	NA	5.0	9.98	9.98	Y	N	N
CGPLH196	Healthy	cfDNA	Preoperative treatment naive	64	M	NA	NA	NA	NA	NA	NA	5.0	11.69	11.69	Y	N	N
CGPLH197	Healthy	cfDNA	Preoperative treatment naive	74	M	NA	NA	NA	NA	NA	NA	5.0	5.69	5.69	Y	N	N
CGPLH198	Healthy	cfDNA	Preoperative treatment naive	66	M	NA	NA	NA	NA	NA	NA	5.0	4.36	4.36	Y	N	N
CGPLH199	Healthy	cfDNA	Preoperative treatment naive	75	F	NA	NA	NA	NA	NA	NA	5.0	9.77	9.77	Y	N	N
CGPLH200	Healthy	cfDNA	Preoperative treatment naive	51	M	NA	NA	NA	NA	NA	NA	5.0	5.60	5.60	Y	N	N
CGPLH201	Healthy	cfDNA	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	5.0	8.82	8.82	Y	N	N
CGPLH202	Healthy	cfDNA	Preoperative treatment naive	73	M	NA	NA	NA	NA	NA	NA	5.0	5.54	5.54	Y	N	N
CGPLH203	Healthy	cfDNA	Preoperative treatment naive	59	M	NA	NA	NA	NA	NA	NA	5.0	9.03	9.03	Y	N	N
CGPLH205	Healthy	cfDNA	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	5.0	4.74	4.74	Y	N	N
CGPLH208	Healthy	cfDNA	Preoperative treatment naive	75	F	NA	NA	NA	NA	NA	NA	5.0	4.67	4.67	Y	N	N
CGPLH209	Healthy	cfDNA	Preoperative treatment naive	74	M	NA	NA	NA	NA	NA	NA	5.0	5.15	5.15	Y	N	N
CGPLH210	Healthy	cfDNA	Preoperative treatment naive	75	M	NA	NA	NA	NA	NA	NA	5.0	5.41	5.41	Y	N	N
CGPLH211	Healthy	cfDNA	Preoperative treatment naive	75	F	NA	NA	NA	NA	NA	NA	5.0	6.24	6.24	Y	N	N
CGPLH300	Healthy	cfDNA	Preoperative treatment naive	72	F	NA	NA	NA	NA	NA	NA	4.4	6.75	6.75	Y	N	N
CGPLH307	Healthy	cfDNA	Preoperative treatment naive	53	M	NA	NA	NA	NA	NA	NA	4.5	3.50	3.50	Y	N	N
CGPLH308	Healthy	cfDNA	Preoperative treatment naive	60	M	NA	NA	NA	NA	NA	NA	4.5	6.01	6.01	Y	N	N
CGPLH309	Healthy	cfDNA	Preoperative treatment naive	61	F	NA	NA	NA	NA	NA	NA	4.5	5.21	5.21	Y	N	N
CGPLH310	Healthy	cfDNA	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.5	15.25	15.25	Y	N	N
CGPLH311	Healthy	cfDNA	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.5	4.47	4.47	Y	N	N
CGPLH314	Healthy	cfDNA	Preoperative treatment naive	59	M	NA	NA	NA	NA	NA	NA	4.5	9.62	9.62	Y	N	N
CGPLH314	Healthy	cfDNA, technical replicate	Preoperative treatment naive	59	M	NA	NA	NA	NA	NA	NA	4.4	16.24	16.24	Y	N	N
CGPLH315	Healthy	cfDNA	Preoperative treatment naive	59	F	NA	NA	NA	NA	NA	NA	4.2	11.55	11.55	Y	N	N
CGPLH316	Healthy	cfDNA	Preoperative treatment naive	64	M	NA	NA	NA	NA	NA	NA	4.5	28.92	27.78	Y	N	N
CGPLH317	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.5	7.62	7.62	Y	N	N
CGPLH319	Healthy	cfDNA	Preoperative treatment naive	60	F	NA	NA	NA	NA	NA	NA	4.2	4.41	4.41	Y	N	N
CGPLH320	Healthy	cfDNA	Preoperative treatment naive	75	F	NA	NA	NA	NA	NA	NA	4.5	6.93	6.93	Y	N	N
CGPLH322	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.2	8.17	8.17	Y	N	N
CGPLH324	Healthy	cfDNA	Preoperative treatment naive	59	F	NA	NA	NA	NA	NA	NA	5.0	6.63	6.63	Y	N	N
CGPLH325	Healthy	cfDNA	Preoperative treatment naive	54	M	NA	NA	NA	NA	NA	NA	4.6	4.15	4.15	Y	N	N
CGPLH326	Healthy	cfDNA	Preoperative treatment naive	67	F	NA	NA	NA	NA	NA	NA	4.5	6.06	6.06	Y	N	N
CGPLH327	Healthy	cfDNA	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.8	1.24	1.24	Y	N	N
CGPLH328	Healthy	cfDNA	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.4	3.42	3.42	Y	N	N
CGPLH328	Healthy	cfDNA, technical replicate	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.9	5.47	5.47	Y	N	N
CGPLH329	Healthy	cfDNA	Preoperative treatment naive	59	M	NA	NA	NA	NA	NA	NA	4.5	5.27	5.27	Y	N	N
CGPLH330	Healthy	cfDNA	Preoperative treatment naive	75	M	NA	NA	NA	NA	NA	NA	4.3	10.21	10.21	Y	N	N
CGPLH331	Healthy	cfDNA	Preoperative treatment naive	55	M	NA	NA	NA	NA	NA	NA	4.6	2.63	2.63	Y	N	N
CGPLH331	Healthy	cfDNA, technical replicate	Preoperative treatment naive	55	M	NA	NA	NA	NA	NA	NA	4.3	4.15	4.15	Y	N	N
CGPLH333	Healthy	cfDNA	Preoperative treatment naive	60	M	NA	NA	NA	NA	NA	NA	4.7	4.06	4.06	Y	N	N
CGPLH335	Healthy	cfDNA	Preoperative treatment naive	74	M	NA	NA	NA	NA	NA	NA	4.4	9.39	9.39	Y	N	N
CGPLH336	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.6	6.64	6.64	Y	N	N
CGPLH337	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.2	4.48	4.48	Y	N	N
CGPLH338	Healthy	cfDNA	Preoperative treatment naive	75	M	NA	NA	NA	NA	NA	NA	4.5	59.44	27.78	Y	N	N
CGPLH339	Healthy	cfDNA	Preoperative treatment naive	70	M	NA	NA	NA	NA	NA	NA	4.5	12.27	12.27	Y	N	N
CGPLH340	Healthy	cfDNA	Preoperative treatment naive	62	M	NA	NA	NA	NA	NA	NA	4.5	4.86	4.86	Y	N	N
CGPLH341	Healthy	cfDNA	Preoperative treatment naive	61	F	NA	NA	NA	NA	NA	NA	4.1	7.62	7.62	Y	N	N
CGPLH342	Healthy	cfDNA	Preoperative treatment naive	49	F	NA	NA	NA	NA	NA	NA	4.2	18.29	18.29	Y	N	N
CGPLH343	Healthy	cfDNA	Preoperative treatment naive	58	M	NA	NA	NA	NA	NA	NA	4.5	3.49	3.49	Y	N	N
CGPLH344	Healthy	cfDNA	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.2	8.41	8.41	Y	N	N
CGPLH345	Healthy	cfDNA	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.5	9.73	9.73	Y	N	N
CGPLH346	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	7.86	7.86	Y	N	N
CGPLH35	Healthy	cfDNA	Preoperative treatment naive	48	F	NA	NA	NA	NA	NA	NA	4.0	13.15	13.15	Y	N	Y
CGPLH350	Healthy	cfDNA	Preoperative treatment naive	65	M	NA	NA	NA	NA	NA	NA	3.5	6.09	6.09	Y	N	N
CGPLH351	Healthy	cfDNA	Preoperative treatment naive	71	M	NA	NA	NA	NA	NA	NA	4.0	15.91	15.91	Y	N	N
CGPLH352	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.2	6.47	6.47	Y	N	N
CGPLH353	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.2	4.47	4.47	Y	N	N
CGPLH354	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.2	17.49	17.49	Y	N	N
CGPLH355	Healthy	cfDNA	Preoperative treatment naive	70	M	NA	NA	NA	NA	NA	NA	4.2	11.58	11.58	Y	N	N
CGPLH356	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	3.94	3.94	Y	N	N
CGPLH357	Healthy	cfDNA	Preoperative treatment naive	52	F	NA	NA	NA	NA	NA	NA	4.2	11.79	11.79	Y	N	N
CGPLH358	Healthy	cfDNA	Preoperative treatment naive	55	M	NA	NA	NA	NA	NA	NA	4.2	21.06	21.06	Y	N	N
CGPLH36	Healthy	cfDNA	Preoperative treatment naive	36	F	NA	NA	NA	NA	NA	NA	4.0	13.00	13.00	Y	N	Y
CGPLH360	Healthy	cfDNA	Preoperative treatment naive	60	M	NA	NA	NA	NA	NA	NA	4.2	3.48	3.48	Y	N	N
CGPLH361	Healthy	cfDNA	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.3	6.98	6.98	Y	N	N
CGPLH362	Healthy	cfDNA	Preoperative treatment naive	72	F	NA	NA	NA	NA	NA	NA	4.4	8.49	8.49	Y	N	N
CGPLH363	Healthy	cfDNA	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.5	4.44	4.44	Y	N	N
CGPLH364	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	17.31	17.31	Y	N	N
CGPLH365	Healthy	cfDNA	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.5	0.55	0.55	Y	N	N
CGPLH366	Healthy	cfDNA	Preoperative treatment naive	61	M	NA	NA	NA	NA	NA	NA	4.5	4.88	4.88	Y	N	N
CGPLH367	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.4	6.48	6.48	Y	N	N
CGPLH368	Healthy	cfDNA	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.3	2.63	2.63	Y	N	N
CGPLH369	Healthy	cfDNA	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.3	10.18	10.18	Y	N	N
CGPLH369	Healthy	cfDNA, technical replicate	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.4	10.71	10.71	Y	N	N
CGPLH37	Healthy	cfDNA	Preoperative treatment naive	39	F	NA	NA	NA	NA	NA	NA	4.0	9.73	9.73	Y	N	Y
CGPLH370	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	7.22	7.22	Y	N	N
CGPLH371	Healthy	cfDNA	Preoperative treatment naive	57	F	NA	NA	NA	NA	NA	NA	4.6	5.62	5.62	Y	N	N
CGPLH380	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.2	6.61	6.61	Y	N	N
CGPLH381	Healthy	cfDNA	Preoperative treatment naive	56	F	NA	NA	NA	NA	NA	NA	4.2	27.38	27.38	Y	N	N
CGPLH382	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.5	11.58	11.58	Y	N	N
CGPLH383	Healthy	cfDNA	Preoperative treatment naive	62	F	NA	NA	NA	NA	NA	NA	4.5	25.50	25.50	Y	N	N
CGPLH384	Healthy	cfDNA	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.5	15.66	15.66	Y	N	N
CGPLH385	Healthy	cfDNA	Preoperative treatment naive	69	M	NA	NA	NA	NA	NA	NA	4.5	19.35	19.35	Y	N	N
CGPLH386	Healthy	cfDNA	Preoperative treatment naive	62	M	NA	NA	NA	NA	NA	NA	4.5	6.46	6.46	Y	N	N
CGPLH386	Healthy	cfDNA, technical replicate	Preoperative treatment naive	62	M	NA	NA	NA	NA	NA	NA	4.6	6.54	6.54	Y	N	N
CGPLH387	Healthy	cfDNA	Preoperative treatment naive	71	F	NA	NA	NA	NA	NA	NA	4.5	6.19	6.19	Y	N	N
CGPLH388	Healthy	cfDNA	Preoperative treatment naive	57	F	NA	NA	NA	NA	NA	NA	4.5	6.62	6.62	Y	N	N

Patient	Patient Type	Sample Type	Timepoint	Age at Diagnosis	Gender	Stage	TNM Staging	Site of Primary Tumor	Histopathological Diagnosis	Degree of Differentiation	Location of Metastases at Diagnosis	Volume of Plasma (ml)	cfDNA Extracted (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLH389	Healthy	cfDNA	Preoperative treatment naïve	73	F	NA	NA	NA	NA	NA	NA	4.6	14.78	14.78	Y	N	N
CGPLH390	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.5	12.14	12.14	Y	N	N
CGPLH391	Healthy	cfDNA	Preoperative treatment naïve	58	M	NA	NA	NA	NA	NA	NA	4.5	8.88	8.88	Y	N	N
CGPLH391	Healthy	cfDNA, technical replicate	Preoperative treatment naïve	58	M	NA	NA	NA	NA	NA	NA	4.5	8.37	8.37	Y	N	N
CGPLH392	Healthy	cfDNA	Preoperative treatment naïve	57	F	NA	NA	NA	NA	NA	NA	4.5	8.39	8.39	Y	N	N
CGPLH393	Healthy	cfDNA	Preoperative treatment naïve	54	M	NA	NA	NA	NA	NA	NA	4.5	5.27	5.27	Y	N	N
CGPLH394	Healthy	cfDNA	Preoperative treatment naïve	55	F	NA	NA	NA	NA	NA	NA	4.4	3.79	3.79	Y	N	N
CGPLH395	Healthy	cfDNA	Preoperative treatment naïve	56	F	NA	NA	NA	NA	NA	NA	4.4	9.56	9.56	Y	N	N
CGPLH395	Healthy	cfDNA, technical replicate	Preoperative treatment naïve	56	F	NA	NA	NA	NA	NA	NA	4.4	5.40	5.40	Y	N	N
CGPLH396	Healthy	cfDNA	Preoperative treatment naïve	50	M	NA	NA	NA	NA	NA	NA	4.4	20.31	20.31	Y	N	N
CGPLH398	Healthy	cfDNA	Preoperative treatment naïve	68	M	NA	NA	NA	NA	NA	NA	4.3	13.01	13.01	Y	N	N
CGPLH399	Healthy	cfDNA	Preoperative treatment naïve	62	F	NA	NA	NA	NA	NA	NA	4.4	4.79	4.79	Y	N	N
CGPLH400	Healthy	cfDNA	Preoperative treatment naïve	64	M	NA	NA	NA	NA	NA	NA	4.4	7.70	7.70	Y	N	N
CGPLH400	Healthy	cfDNA, technical replicate	Preoperative treatment naïve	64	M	NA	NA	NA	NA	NA	NA	4.4	6.26	6.26	Y	N	N
CGPLH401	Healthy	cfDNA	Preoperative treatment naïve	50	M	NA	NA	NA	NA	NA	NA	4.3	13.01	13.01	Y	N	N
CGPLH401	Healthy	cfDNA, technical replicate	Preoperative treatment naïve	50	M	NA	NA	NA	NA	NA	NA	4.4	11.13	11.13	Y	N	N
CGPLH402	Healthy	cfDNA	Preoperative treatment naïve	57	F	NA	NA	NA	NA	NA	NA	4.5	2.89	2.89	Y	N	N
CGPLH403	Healthy	cfDNA	Preoperative treatment naïve	64	M	NA	NA	NA	NA	NA	NA	4.3	4.41	4.41	Y	N	N
CGPLH404	Healthy	cfDNA	Preoperative treatment naïve	50	M	NA	NA	NA	NA	NA	NA	4.2	6.38	6.38	Y	N	N
CGPLH405	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.4	7.28	7.28	Y	N	N
CGPLH406	Healthy	cfDNA	Preoperative treatment naïve	57	M	NA	NA	NA	NA	NA	NA	4.2	5.40	5.40	Y	N	N
CGPLH407	Healthy	cfDNA	Preoperative treatment naïve	75	F	NA	NA	NA	NA	NA	NA	4.0	13.30	13.30	Y	N	N
CGPLH408	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.2	5.18	5.18	Y	N	N
CGPLH409	Healthy	cfDNA	Preoperative treatment naïve	53	M	NA	NA	NA	NA	NA	NA	3.7	3.98	3.98	Y	N	N
CGPLH410	Healthy	cfDNA	Preoperative treatment naïve	52	M	NA	NA	NA	NA	NA	NA	4.1	6.91	6.91	Y	N	N
CGPLH411	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.1	3.30	3.30	Y	N	N
CGPLH412	Healthy	cfDNA	Preoperative treatment naïve	53	F	NA	NA	NA	NA	NA	NA	4.1	5.55	5.55	Y	N	N
CGPLH413	Healthy	cfDNA	Preoperative treatment naïve	54	F	NA	NA	NA	NA	NA	NA	4.5	8.18	8.18	Y	N	N
CGPLH414	Healthy	cfDNA	Preoperative treatment naïve	56	M	NA	NA	NA	NA	NA	NA	3.8	5.85	5.85	Y	N	N
CGPLH415	Healthy	cfDNA	Preoperative treatment naïve	59	M	NA	NA	NA	NA	NA	NA	4.7	10.20	10.20	Y	N	N
CGPLH416	Healthy	cfDNA	Preoperative treatment naïve	58	F	NA	NA	NA	NA	NA	NA	4.5	11.73	11.73	Y	N	N
CGPLH417	Healthy	cfDNA	Preoperative treatment naïve	70	M	NA	NA	NA	NA	NA	NA	4.2	10.98	10.98	Y	N	N
CGPLH418	Healthy	cfDNA	Preoperative treatment naïve	70	F	NA	NA	NA	NA	NA	NA	4.5	10.96	10.96	Y	N	N
CGPLH419	Healthy	cfDNA	Preoperative treatment naïve	65	F	NA	NA	NA	NA	NA	NA	4.5	10.17	10.17	Y	N	N
CGPLH42	Healthy	cfDNA	Preoperative treatment naïve	54	F	NA	NA	NA	NA	NA	NA	4.0	14.30	14.30	Y	N	Y
CGPLH420	Healthy	cfDNA	Preoperative treatment naïve	51	M	NA	NA	NA	NA	NA	NA	4.2	12.32	12.32	Y	N	N
CGPLH422	Healthy	cfDNA	Preoperative treatment naïve	68	F	NA	NA	NA	NA	NA	NA	4.6	5.42	5.42	Y	N	N
CGPLH423	Healthy	cfDNA	Preoperative treatment naïve	54	M	NA	NA	NA	NA	NA	NA	4.2	2.85	2.85	Y	N	N
CGPLH424	Healthy	cfDNA	Preoperative treatment naïve	53	F	NA	NA	NA	NA	NA	NA	4.7	1.66	1.66	Y	N	N
CGPLH425	Healthy	cfDNA	Preoperative treatment naïve	53	F	NA	NA	NA	NA	NA	NA	4.4	5.98	5.98	Y	N	N
CGPLH426	Healthy	cfDNA	Preoperative treatment naïve	68	M	NA	NA	NA	NA	NA	NA	4.4	2.84	2.84	Y	N	N
CGPLH427	Healthy	cfDNA	Preoperative treatment naïve	68	M	NA	NA	NA	NA	NA	NA	4.4	10.86	10.86	Y	N	N
CGPLH428	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.5	6.27	6.27	Y	N	N
CGPLH429	Healthy	cfDNA	Preoperative treatment naïve	63	F	NA	NA	NA	NA	NA	NA	4.5	3.89	3.89	Y	N	N
CGPLH43	Healthy	cfDNA	Preoperative treatment naïve	49	F	NA	NA	NA	NA	NA	NA	4.0	8.50	8.50	Y	N	Y
CGPLH430	Healthy	cfDNA	Preoperative treatment naïve	69	F	NA	NA	NA	NA	NA	NA	4.2	10.33	10.33	Y	N	N
CGPLH431	Healthy	cfDNA	Preoperative treatment naïve	59	F	NA	NA	NA	NA	NA	NA	4.8	12.81	12.81	Y	N	N
CGPLH432	Healthy	cfDNA	Preoperative treatment naïve	59	F	NA	NA	NA	NA	NA	NA	4.8	2.42	2.42	Y	N	N
CGPLH434	Healthy	cfDNA	Preoperative treatment naïve	59	M	NA	NA	NA	NA	NA	NA	4.6	8.83	8.83	Y	N	N
CGPLH435	Healthy	cfDNA	Preoperative treatment naïve	50	M	NA	NA	NA	NA	NA	NA	4.5	8.95	8.95	Y	N	N
CGPLH436	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.5	4.29	4.29	Y	N	N
CGPLH437	Healthy	cfDNA	Preoperative treatment naïve	56	M	NA	NA	NA	NA	NA	NA	4.6	18.07	18.07	Y	N	N
CGPLH438	Healthy	cfDNA	Preoperative treatment naïve	69	M	NA	NA	NA	NA	NA	NA	4.8	16.62	16.62	Y	N	N
CGPLH439	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.7	4.38	4.38	Y	N	N
CGPLH440	Healthy	cfDNA	Preoperative treatment naïve	72	M	NA	NA	NA	NA	NA	NA	4.7	4.32	4.32	Y	N	N
CGPLH441	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.7	7.80	7.80	Y	N	N
CGPLH442	Healthy	cfDNA	Preoperative treatment naïve	59	F	NA	NA	NA	NA	NA	NA	4.5	6.15	6.15	Y	N	N
CGPLH443	Healthy	cfDNA	Preoperative treatment naïve	52	F	NA	NA	NA	NA	NA	NA	4.4	3.44	3.44	Y	N	N
CGPLH444	Healthy	cfDNA	Preoperative treatment naïve	60	F	NA	NA	NA	NA	NA	NA	4.4	4.12	4.12	Y	N	N
CGPLH445	Healthy	cfDNA	Preoperative treatment naïve	53	F	NA	NA	NA	NA	NA	NA	4.4	4.38	4.38	Y	N	N
CGPLH446	Healthy	cfDNA	Preoperative treatment naïve	51	F	NA	NA	NA	NA	NA	NA	4.4	2.92	2.92	Y	N	N
CGPLH447	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.6	3.87	3.87	Y	N	N
CGPLH448	Healthy	cfDNA	Preoperative treatment naïve	51	F	NA	NA	NA	NA	NA	NA	4.4	5.29	5.29	Y	N	N
CGPLH449	Healthy	cfDNA	Preoperative treatment naïve	51	F	NA	NA	NA	NA	NA	NA	4.5	3.77	3.77	Y	N	N
CGPLH45	Healthy	cfDNA	Preoperative treatment naïve	58	F	NA	NA	NA	NA	NA	NA	4.0	10.85	10.85	Y	N	Y
CGPLH450	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.5	5.62	5.62	Y	N	N
CGPLH451	Healthy	cfDNA	Preoperative treatment naïve	54	F	NA	NA	NA	NA	NA	NA	4.6	7.24	7.24	Y	N	N
CGPLH452	Healthy	cfDNA	Preoperative treatment naïve	69	M	NA	NA	NA	NA	NA	NA	4.4	2.54	2.54	Y	N	N
CGPLH453	Healthy	cfDNA	Preoperative treatment naïve	53	F	NA	NA	NA	NA	NA	NA	4.6	9.11	9.11	Y	N	N
CGPLH455	Healthy	cfDNA	Preoperative treatment naïve	55	F	NA	NA	NA	NA	NA	NA	4.4	2.64	2.64	Y	N	N
CGPLH455	Healthy	cfDNA, technical replicate	Preoperative treatment naïve	55	F	NA	NA	NA	NA	NA	NA	4.5	2.42	2.42	Y	N	N
CGPLH456	Healthy	cfDNA	Preoperative treatment naïve	54	F	NA	NA	NA	NA	NA	NA	4.5	3.11	3.11	Y	N	N
CGPLH457	Healthy	cfDNA	Preoperative treatment naïve	54	F	NA	NA	NA	NA	NA	NA	4.4	5.92	5.92	Y	N	N
CGPLH458	Healthy	cfDNA	Preoperative treatment naïve	52	F	NA	NA	NA	NA	NA	NA	4.5	16.04	16.04	Y	N	N
CGPLH459	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.4	6.52	6.52	Y	N	N
CGPLH46	Healthy	cfDNA	Preoperative treatment naïve	35	F	NA	NA	NA	NA	NA	NA	4.0	8.25	8.25	Y	N	Y
CGPLH460	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.6	5.24	5.24	Y	N	N
CGPLH463	Healthy	cfDNA	Preoperative treatment naïve	53	F	NA	NA	NA	NA	NA	NA	4.5	22.77	22.77	Y	N	N
CGPLH464	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.4	2.90	2.90	Y	N	N
CGPLH465	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.5	4.76	4.76	Y	N	N
CGPLH466	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.6	5.68	5.68	Y	N	N
CGPLH466	Healthy	cfDNA, technical replicate	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.5	6.75	6.75	Y	N	N
CGPLH467	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.5	4.59	4.59	Y	N	N
CGPLH468	Healthy	cfDNA	Preoperative treatment naïve	53	M	NA	NA	NA	NA	NA	NA	4.5	11.19	11.19	Y	N	N
CGPLH469	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.5	3.25	3.25	Y	N	N
CGPLH47	Healthy	cfDNA	Preoperative treatment naïve	50	F	NA	NA	NA	NA	NA	NA	4.0	7.43	7.43	Y	N	Y
CGPLH470	Healthy	cfDNA	Preoperative treatment naïve	68	F	NA	NA	NA	NA	NA	NA	4.5	13.64	13.64	Y	N	N
CGPLH471	Healthy	cfDNA	Preoperative treatment naïve	70	F	NA	NA	NA	NA	NA	NA	4.3	13.00	13.00	Y	N	N
CGPLH472	Healthy	cfDNA	Preoperative treatment naïve	69	F	NA	NA	NA	NA	NA	NA	4.2	10.17	10.17	Y	N	N
CGPLH473	Healthy	cfDNA	Preoperative treatment naïve	62	M	NA	NA	NA	NA	NA	NA	4.3	2.98	2.98	Y	N	N
CGPLH474	Healthy	cfDNA	Preoperative treatment naïve	63	M	NA	NA	NA	NA	NA	NA	4.3	29.15	29.15	Y	N	N
CGPLH475	Healthy	cfDNA	Preoperative treatment naïve	67	F	NA	NA	NA	NA	NA	NA	4.0	7.26	7.26	Y	N	N
CGPLH476	Healthy	cfDNA	Preoperative treatment naïve	65	F	NA	NA	NA	NA	NA	NA	4.3	6.16	6.16	Y	N	N
CGPLH477	Healthy	cfDNA	Preoperative treatment naïve	61	F	NA	NA	NA	NA	NA	NA	4.3	15.21	15.21	Y	N	N

Patient	Patient Type	Sample Type	Timepoint	Age at Diagnosis	Gender	Stage	TNM Staging	Site of Primary Tumor	Histopathological Diagnosis	Degree of Differentiation	Location of Metastases at Diagnosis	Volume of Plasma (ml)	cfDNA Extracted (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLH478	Healthy	cfDNA	Preoperative treatment naive	51	F	NA	NA	NA	NA	NA	NA	4.4	7.29	7.29	Y	N	N
CGPLH479	Healthy	cfDNA	Preoperative treatment naive	52	M	NA	NA	NA	NA	NA	NA	4.5	8.73	8.73	Y	N	N
CGPLH48	Healthy	cfDNA	Preoperative treatment naive	38	F	NA	NA	NA	NA	NA	NA	4.0	6.38	6.38	Y	N	Y
CGPLH480	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.4	10.62	10.62	Y	N	N
CGPLH481	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.3	6.75	6.75	Y	N	N
CGPLH482	Healthy	cfDNA	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.3	23.58	23.58	Y	N	N
CGPLH483	Healthy	cfDNA	Preoperative treatment naive	66	M	NA	NA	NA	NA	NA	NA	4.4	14.44	14.44	Y	N	N
CGPLH484	Healthy	cfDNA	Preoperative treatment naive	72	M	NA	NA	NA	NA	NA	NA	4.2	14.32	14.32	Y	N	N
CGPLH485	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.3	9.64	9.64	Y	N	N
CGPLH486	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.3	10.16	10.16	Y	N	N
CGPLH487	Healthy	cfDNA	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.4	6.11	6.11	Y	N	N
CGPLH488	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	7.88	7.88	Y	N	N
CGPLH49	Healthy	cfDNA	Preoperative treatment naive	39	F	NA	NA	NA	NA	NA	NA	4.0	6.60	6.60	Y	N	Y
CGPLH490	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	4.18	4.18	Y	N	N
CGPLH491	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	13.16	13.16	Y	N	N
CGPLH492	Healthy	cfDNA	Preoperative treatment naive	51	F	NA	NA	NA	NA	NA	NA	4.5	3.83	3.83	Y	N	N
CGPLH493	Healthy	cfDNA	Preoperative treatment naive	64	M	NA	NA	NA	NA	NA	NA	4.5	25.06	25.06	Y	N	N
CGPLH494	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.4	5.24	5.24	Y	N	N
CGPLH495	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.4	5.03	5.03	Y	N	N
CGPLH496	Healthy	cfDNA	Preoperative treatment naive	74	M	NA	NA	NA	NA	NA	NA	4.5	34.01	27.78	Y	N	N
CGPLH497	Healthy	cfDNA	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.5	8.24	8.24	Y	N	N
CGPLH497	Healthy	cfDNA, technical replicate	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.4	5.88	5.88	Y	N	N
CGPLH498	Healthy	cfDNA	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.4	5.33	5.33	Y	N	N
CGPLH499	Healthy	cfDNA	Preoperative treatment naive	52	F	NA	NA	NA	NA	NA	NA	4.5	7.85	7.85	Y	N	N
CGPLH50	Healthy	cfDNA	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.0	7.05	7.05	Y	N	Y
CGPLH500	Healthy	cfDNA	Preoperative treatment naive	51	F	NA	NA	NA	NA	NA	NA	4.5	3.49	3.49	Y	N	N
CGPLH501	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.3	6.29	6.29	Y	N	N
CGPLH502	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.5	2.24	2.24	Y	N	N
CGPLH503	Healthy	cfDNA	Preoperative treatment naive	67	M	NA	NA	NA	NA	NA	NA	4.5	11.01	11.01	Y	N	N
CGPLH504	Healthy	cfDNA	Preoperative treatment naive	57	F	NA	NA	NA	NA	NA	NA	4.3	6.60	6.60	Y	N	N
CGPLH504	Healthy	cfDNA, technical replicate	Preoperative treatment naive	57	F	NA	NA	NA	NA	NA	NA	4.2	10.02	10.02	Y	N	N
CGPLH505	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.1	5.23	5.23	Y	N	N
CGPLH506	Healthy	cfDNA	Preoperative treatment naive	51	F	NA	NA	NA	NA	NA	NA	4.5	12.23	12.23	Y	N	N
CGPLH507	Healthy	cfDNA	Preoperative treatment naive	56	M	NA	NA	NA	NA	NA	NA	4.1	9.89	9.89	Y	N	N
CGPLH508	Healthy	cfDNA	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.5	8.68	8.68	Y	N	N
CGPLH508	Healthy	cfDNA, technical replicate	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.4	9.55	9.55	Y	N	N
CGPLH509	Healthy	cfDNA	Preoperative treatment naive	60	M	NA	NA	NA	NA	NA	NA	4.0	9.79	9.79	Y	N	N
CGPLH51	Healthy	cfDNA	Preoperative treatment naive	48	F	NA	NA	NA	NA	NA	NA	4.0	7.85	7.85	Y	N	Y
CGPLH510	Healthy	cfDNA	Preoperative treatment naive	67	M	NA	NA	NA	NA	NA	NA	4.2	14.20	14.20	Y	N	N
CGPLH511	Healthy	cfDNA	Preoperative treatment naive	75	M	NA	NA	NA	NA	NA	NA	4.5	12.94	12.94	Y	N	N
CGPLH512	Healthy	cfDNA	Preoperative treatment naive	52	M	NA	NA	NA	NA	NA	NA	4.3	8.60	8.60	Y	N	N
CGPLH513	Healthy	cfDNA	Preoperative treatment naive	57	M	NA	NA	NA	NA	NA	NA	4.3	6.54	6.54	Y	N	N
CGPLH514	Healthy	cfDNA	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.4	10.94	10.94	Y	N	N
CGPLH515	Healthy	cfDNA	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.5	8.71	8.71	Y	N	N
CGPLH516	Healthy	cfDNA	Preoperative treatment naive	65	F	NA	NA	NA	NA	NA	NA	4.5	7.32	7.32	Y	N	N
CGPLH517	Healthy	cfDNA	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.6	5.16	5.16	Y	N	N
CGPLH517	Healthy	cfDNA, technical replicate	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.5	9.74	9.74	Y	N	N
CGPLH518	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.4	5.92	5.92	Y	N	N
CGPLH519	Healthy	cfDNA	Preoperative treatment naive	54	M	NA	NA	NA	NA	NA	NA	4.4	6.96	6.96	Y	N	N
CGPLH52	Healthy	cfDNA	Preoperative treatment naive	40	F	NA	NA	NA	NA	NA	NA	4.0	9.90	9.90	Y	N	Y
CGPLH520	Healthy	cfDNA	Preoperative treatment naive	51	F	NA	NA	NA	NA	NA	NA	4.3	8.27	8.27	Y	N	N
CGPLH54	Healthy	cfDNA	Preoperative treatment naive	47	F	NA	NA	NA	NA	NA	NA	4.0	14.18	14.18	Y	N	Y
CGPLH55	Healthy	cfDNA	Preoperative treatment naive	46	F	NA	NA	NA	NA	NA	NA	4.0	7.35	7.35	Y	N	Y
CGPLH56	Healthy	cfDNA	Preoperative treatment naive	42	F	NA	NA	NA	NA	NA	NA	4.0	5.20	5.20	Y	N	Y
CGPLH57	Healthy	cfDNA	Preoperative treatment naive	39	F	NA	NA	NA	NA	NA	NA	4.0	7.15	7.15	Y	N	Y
CGPLH59	Healthy	cfDNA	Preoperative treatment naive	34	F	NA	NA	NA	NA	NA	NA	4.0	6.03	6.03	Y	N	Y
CGPLH625	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.5	2.64	2.64	Y	N	N
CGPLH625	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.5	2.69	2.69	Y	N	N
CGPLH626	Healthy	cfDNA, technical replicate	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.0	11.12	11.12	Y	N	N
CGPLH63	Healthy	cfDNA	Preoperative treatment naive	47	F	NA	NA	NA	NA	NA	NA	4.0	10.10	10.10	Y	N	Y
CGPLH639	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	2.00	2.00	Y	N	N
CGPLH64	Healthy	cfDNA	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.0	8.03	8.03	Y	N	Y
CGPLH640	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	9.36	9.36	Y	N	N
CGPLH642	Healthy	cfDNA	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.5	4.99	4.99	Y	N	N
CGPLH643	Healthy	cfDNA	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.4	7.12	7.12	Y	N	N
CGPLH644	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.4	5.06	5.06	Y	N	N
CGPLH646	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.4	6.75	6.75	Y	N	N
CGPLH75	Healthy	cfDNA	Preoperative treatment naive	46	F	NA	NA	NA	NA	NA	NA	4.0	3.87	3.87	Y	N	Y
CGPLH76	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.0	4.03	4.03	Y	N	Y
CGPLH77	Healthy	cfDNA	Preoperative treatment naive	46	F	NA	NA	NA	NA	NA	NA	4.0	5.89	5.89	Y	N	Y
CGPLH78	Healthy	cfDNA	Preoperative treatment naive	34	F	NA	NA	NA	NA	NA	NA	4.0	2.51	2.51	Y	N	Y
CGPLH79	Healthy	cfDNA	Preoperative treatment naive	37	F	NA	NA	NA	NA	NA	NA	4.0	3.68	3.68	Y	N	Y
CGPLH80	Healthy	cfDNA	Preoperative treatment naive	37	F	NA	NA	NA	NA	NA	NA	4.0	1.94	1.94	Y	N	Y
CGPLH81	Healthy	cfDNA	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.0	5.16	5.16	Y	N	Y
CGPLH82	Healthy	cfDNA	Preoperative treatment naive	38	F	NA	NA	NA	NA	NA	NA	4.0	3.30	3.30	Y	N	Y
CGPLH83	Healthy	cfDNA	Preoperative treatment naive	60	F	NA	NA	NA	NA	NA	NA	4.0	5.04	5.04	Y	N	Y
CGPLH84	Healthy	cfDNA	Preoperative treatment naive	45	F	NA	NA	NA	NA	NA	NA	4.0	3.33	3.33	Y	N	Y
CGPLLU13	Lung Cancer	cfDNA	Pre-treatment, Day -2	72	F	IV	T1BN2bM1a	Right Lung	Adenocarcinoma	NA	Bone	5.0	7.67	7.67	Y	N	Y
CGPLLU13	Lung Cancer	cfDNA	Post-treatment, Day 5	72	F	IV	T1BN2bM1a	Right Lung	Adenocarcinoma	NA	Bone	4.5	8.39	8.39	Y	N	Y
CGPLLU13	Lung Cancer	cfDNA	Post-treatment, Day 28	72	F	IV	T1BN2bM1a	Right Lung	Adenocarcinoma	NA	Bone	3.2	8.66	8.66	Y	N	Y
CGPLLU13	Lung Cancer	cfDNA	Post-treatment, Day 91	72	F	IV	T1BN2bM1a	Right Lung	Adenocarcinoma	NA	Bone	5.0	5.97	5.97	Y	N	Y
CGPLLU14	Lung Cancer	cfDNA	Pre-treatment, Day -38	55	F	IV	T1N1M0	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55	Y	N	Y
CGPLLU14	Lung Cancer	cfDNA	Pre-treatment, Day -16	55	F	IV	T1N1M0	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55	Y	N	Y
CGPLLU14	Lung Cancer	cfDNA	Pre-treatment, Day -3	55	F	IV	T1N1M0	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55	Y	N	Y
CGPLLU14	Lung Cancer	cfDNA	Pre-treatment, Day 0	55	F	IV	T1N1M0	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55	Y	N	Y
CGPLLU14	Lung Cancer	cfDNA	Post-treatment, Day 0.33	55	F	IV	T1N1M0	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55	Y	N	Y
CGPLLU14	Lung Cancer	cfDNA	Post-treatment, Day 7	55	F	IV	T1N1M0	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55	Y	N	Y
CGPLLU144	Lung Cancer	cfDNA	Preoperative treatment naive	52	M	II	T2aN1M0	Lung	Adenocarcinoma	Poor	None	3.5	31.51	31.51	Y	Y	Y
CGPLLU147	Lung Cancer	cfDNA	Preoperative treatment naive	60	M	III	T3N2M0	Lung	Adenosquamous Carcinoma	Poor	None	3.8	6.72	6.72	Y	Y	Y
CGPLLU161	Lung Cancer	cfDNA	Preoperative treatment naive	41	F	II	T3N0M0	Lung	Adenocarcinoma	Well	None	4.0	83.04	83.04	Y	N	Y
CGPLLU162	Lung Cancer	cfDNA	Preoperative treatment naive	38	M	II	T1N1M0	Right Lung	Adenocarcinoma	Moderate	None	3.1	40.32	40.32	Y	Y	Y
CGPLLU163	Lung Cancer	cfDNA	Preoperative treatment naive	66	M	II	T1N1M0	Left Lung	Adenocarcinoma	Poor	None	5.0	54.03	54.03	Y	Y	Y
CGPLLU165	Lung Cancer	cfDNA	Preoperative treatment naive	68	F	II	T1N1M0	Right Lung	Adenocarcinoma	Well	None	4.5	20.13	20.13	Y	Y	Y
CGPLLU168	Lung Cancer	cfDNA	Preoperative treatment naive	70	F	I	T2aN0M0	Lung	Adenocarcinoma	Poor	None	4.3	19.38	19.38	Y	Y	Y

Patient	Patient Type	Sample Type	Timepoint	Age at Diagnosis	Gender	Stage	TNM Staging	Site of Primary Tumor	Histopathological Diagnosis	Degree of Differentiation	Location of Metastases at Diagnosis	Volume of Plasma (ml)	cfDNA Extracted (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLLU169	Lung Cancer	cfDNA	Preoperative treatment naive	64	M	I	T1bN0M0	Lung	Squamous Cell Carcinoma	Moderate	None	4.2	13.70	13.70	Y	N	Y
CGPLLU175	Lung Cancer	cfDNA	Preoperative treatment naive	47	M	I	T2N0M0	Lung	Squamous Cell Carcinoma	Moderate	None	4.4	16.84	16.84	Y	Y	Y
CGPLLU176	Lung Cancer	cfDNA	Preoperative treatment naive	58	M	I	T2N0M0	Lung	Adenosquamous Carcinoma	Moderate	None	3.2	7.86	7.86	Y	Y	Y
CGPLLU177	Lung Cancer	cfDNA	Preoperative treatment naive	45	M	II	T3N0M0	Right Lung	Adenocarcinoma	NA	None	3.9	19.07	19.07	Y	Y	Y
CGPLLU180	Lung Cancer	cfDNA	Preoperative treatment naive	57	M	I	T2N0M0	Right Lung	Large Cell Carcinoma	Poor	None	3.2	19.31	19.31	Y	Y	Y
CGPLLU198	Lung Cancer	cfDNA	Preoperative treatment naive	49	F	I	T2N0M0	Left Lung	Adenocarcinoma	Moderate	None	4.2	14.09	14.09	Y	Y	Y
CGPLLU202	Lung Cancer	cfDNA	Preoperative treatment naive	68	M	I	T2aN0M0	Right Lung	Adenocarcinoma	NA	None	4.4	24.72	24.72	Y	Y	Y
CGPLLU203	Lung Cancer	cfDNA	Preoperative treatment naive	66	M	II	T3N0M0	Right Lung	Squamous Cell Carcinoma	Well	None	4.2	26.24	26.24	Y	N	Y
CGPLLU205	Lung Cancer	cfDNA	Preoperative treatment naive	65	M	II	T3N0M0	Left Lung	Adenocarcinoma	Poor	None	4.0	18.56	18.56	Y	Y	Y
CGPLLU206	Lung Cancer	cfDNA	Preoperative treatment naive	55	M	III	T3N1M0	Right Lung	Squamous Cell Carcinoma	Poor	None	3.5	18.24	18.24	Y	Y	Y
CGPLLU207	Lung Cancer	cfDNA	Preoperative treatment naive	60	F	II	T2N1M0	Lung	Adenocarcinoma	Well	None	4.0	17.29	17.29	Y	Y	Y
CGPLLU208	Lung Cancer	cfDNA	Preoperative treatment naive	56	F	II	T2N1M0	Lung	Adenocarcinoma	Moderate	None	3.0	24.34	24.34	Y	Y	Y
CGPLLU209	Lung Cancer	cfDNA	Preoperative treatment naive	65	M	II	T2aN0M0	Lung	Large Cell Carcinoma	Poor	None	5.5	53.95	53.95	Y	Y	Y
CGPLLU244	Lung Cancer	cfDNA	Pre-treatment, Day -7	66	F	IV	NA	Right Upper Lobe of Lung	Adenocarcinoma	Moderate/Poor	Liver, Rib, Brain, Pleura	4.5	17.84	17.84	Y	N	Y
CGPLLU244	Lung Cancer	cfDNA	Pre-treatment, Day -1	66	F	IV	NA	Right Upper Lobe of Lung	Adenocarcinoma	Moderate/Poor	Liver, Rib, Brain, Pleura	4.5	17.84	17.84	Y	N	Y
CGPLLU244	Lung Cancer	cfDNA	Post-treatment, Day 6	66	F	IV	NA	Right Upper Lobe of Lung	Adenocarcinoma	Moderate/Poor	Liver, Rib, Brain, Pleura	4.5	17.84	17.84	Y	N	Y
CGPLLU244	Lung Cancer	cfDNA	Post-treatment, Day 62	66	F	IV	NA	Right Upper Lobe of Lung	Adenocarcinoma	Moderate/Poor	Liver, Rib, Brain, Pleura	4.5	17.84	17.84	Y	N	Y
CGPLLU245	Lung Cancer	cfDNA	Pre-treatment, Day -32	49	M	IV	T2aN2M1B	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42	Y	N	Y
CGPLLU245	Lung Cancer	cfDNA	Pre-treatment, Day 0	49	M	IV	T2aN2M1B	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42	Y	N	Y
CGPLLU245	Lung Cancer	cfDNA	Post-treatment, Day 7	49	M	IV	T2aN2M1B	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42	Y	N	Y
CGPLLU245	Lung Cancer	cfDNA	Post-treatment, Day 21	49	M	IV	T2aN2M1B	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42	Y	N	Y
CGPLLU246	Lung Cancer	cfDNA	Pre-treatment, Day -21	65	F	IV	NA	Right Lower Lobe of Lung	Adenocarcinoma	Poor	Pleura	5.5	18.51	18.51	Y	N	Y
CGPLLU246	Lung Cancer	cfDNA	Pre-treatment, Day 0	65	F	IV	NA	Right Lower Lobe of Lung	Adenocarcinoma	Poor	Pleura	5.5	18.51	18.51	Y	N	Y
CGPLLU246	Lung Cancer	cfDNA	Post-treatment, Day 9	65	F	IV	NA	Right Lower Lobe of Lung	Adenocarcinoma	Poor	Pleura	5.5	18.51	18.51	Y	N	Y
CGPLLU246	Lung Cancer	cfDNA	Post-treatment, Day 42	65	F	IV	NA	Right Lower Lobe of Lung	Adenocarcinoma	Poor	Pleura	5.5	18.51	18.51	Y	N	Y
CGPLLU264	Lung Cancer	cfDNA	Pre-treatment, Day -1	84	M	IV	T4N2BM1	Left Middle Lung	Adenocarcinoma	NA	Lung	4.0	22.97	22.97	Y	N	Y
CGPLLU264	Lung Cancer	cfDNA	Post-treatment, Day 6	84	M	IV	T4N2BM1	Left Middle Lung	Adenocarcinoma	NA	Lung	4.5	10.53	10.53	Y	N	Y
CGPLLU264	Lung Cancer	cfDNA	Post-treatment, Day 27	84	M	IV	T4N2BM1	Left Middle Lung	Adenocarcinoma	NA	Lung	3.0	7.15	7.15	Y	N	Y
CGPLLU264	Lung Cancer	cfDNA	Post-treatment, Day 69	84	M	IV	T4N2BM1	Left Middle Lung	Adenocarcinoma	NA	Lung	4.0	9.60	9.60	Y	N	Y
CGPLLU265	Lung Cancer	cfDNA	Pre-treatment, Day 0	71	F	IV	T1N0Mx	Left Lower Lobe of Lung	Adenocarcinoma	NA	None	4.2	7.16	7.16	Y	N	Y
CGPLLU265	Lung Cancer	cfDNA	Post-treatment, Day 3	71	F	IV	T1N0Mx	Left Lower Lobe of Lung	Adenocarcinoma	NA	None	4.0	8.11	8.11	Y	N	Y
CGPLLU265	Lung Cancer	cfDNA	Post-treatment, Day 7	71	F	IV	T1N0Mx	Left Lower Lobe of Lung	Adenocarcinoma	NA	None	4.2	7.53	7.53	Y	N	Y
CGPLLU265	Lung Cancer	cfDNA	Post-treatment, Day 84	71	F	IV	T1N0Mx	Left Lower Lobe of Lung	Adenocarcinoma	NA	None	5.0	16.17	16.17	Y	N	Y
CGPLLU266	Lung Cancer	cfDNA	Pre-treatment, Day 0	78	M	IV	T2aN1	Left Lower Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	5.32	5.32	Y	N	Y
CGPLLU266	Lung Cancer	cfDNA	Post-treatment, Day 16	78	M	IV	T2aN1	Left Lower Lobe of Lung	Adenocarcinoma	Moderate	None	3.5	6.31	6.31	Y	N	Y
CGPLLU266	Lung Cancer	cfDNA	Post-treatment, Day 83	78	M	IV	T2aN1	Left Lower Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	7.64	7.64	Y	N	Y
CGPLLU266	Lung Cancer	cfDNA	Post-treatment, Day 328	78	M	IV	T2aN1	Left Lower Lobe of Lung	Adenocarcinoma	Moderate	None	5.0	14.39	14.39	Y	N	Y
CGPLLU267	Lung Cancer	cfDNA	Pre-treatment, Day -1	55	F	IV	T3NxM1a	Right Upper Lobe of Lung	Squamous Cell Carcinoma	Poor	Lung	4.5	2.87	2.87	Y	N	Y
CGPLLU267	Lung Cancer	cfDNA	Post-treatment, Day 34	55	F	IV	T3NxM1a	Right Upper Lobe of Lung	Squamous Cell Carcinoma	Poor	Lung	4.5	3.34	3.34	Y	N	Y
CGPLLU267	Lung Cancer	cfDNA	Post-treatment, Day 90	55	F	IV	T3NxM1a	Right Upper Lobe of Lung	Squamous Cell Carcinoma	Poor	Lung	3.5	3.00	3.00	Y	N	Y
CGPLLU269	Lung Cancer	cfDNA	Pre-treatment, Day 0	52	F	IV	T1CNxM1C	Right Paratracheal Lesion	Adenocarcinoma	NA	Brain, Liver, Bone, Pleura	5.0	11.40	11.40	Y	N	Y
CGPLLU269	Lung Cancer	cfDNA	Post-treatment, Day 9	52	F	IV	T1CNxM1C	Right Paratracheal Lesion	Adenocarcinoma	NA	Brain, Liver, Bone, Pleura	5.0	8.35	8.35	Y	N	Y
CGPLLU269	Lung Cancer	cfDNA	Post-treatment, Day 28	52	F	IV	T1CNxM1C	Right Paratracheal Lesion	Adenocarcinoma	NA	Brain, Liver, Bone, Pleura	3.5	17.79	17.79	Y	N	Y
CGPLLU271	Lung Cancer	cfDNA	Post-treatment, Day 259	73	M	IV	T1aNxM1	Left Upper Lobe of Lung	Adenocarcinoma	NA	Pleura	4.0	4.70	4.70	Y	N	Y
CGPLLU271	Lung Cancer	cfDNA	Pre-treatment, Day 0	73	M	IV	T1aNxM1	Left Upper Lobe of Lung	Adenocarcinoma	NA	Pleura	5.0	18.86	18.86	Y	N	Y
CGPLLU271	Lung Cancer	cfDNA	Post-treatment, Day 6	73	M	IV	T1aNxM1	Left Upper Lobe of Lung	Adenocarcinoma	NA	Pleura	4.5	13.84	13.84	Y	N	Y
CGPLLU271	Lung Cancer	cfDNA	Post-treatment, Day 20	73	M	IV	T1aNxM1	Left Upper Lobe of Lung	Adenocarcinoma	NA	Pleura	3.5	13.46	13.46	Y	N	Y
CGPLLU271	Lung Cancer	cfDNA	Post-treatment, Day 104	73	M	IV	T1aNxM1	Left Upper Lobe of Lung	Adenocarcinoma	NA	Pleura	4.0	13.77	13.77	Y	N	Y
CGPLLU43	Lung Cancer	cfDNA	Pre-treatment, Day -1	57	F	IV	T1BN0M0	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	None	4.9	2.17	2.17	Y	N	Y
CGPLLU43	Lung Cancer	cfDNA	Post-treatment, Day 6	57	F	IV	T1BN0M0	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	None	3.7	3.26	3.26	Y	N	Y
CGPLLU43	Lung Cancer	cfDNA	Post-treatment, Day 27	57	F	IV	T1BN0M0	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	None	4.0	4.12	4.12	Y	N	Y
CGPLLU43	Lung Cancer	cfDNA	Post-treatment, Day 83	57	F	IV	T1BN0M0	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	None	3.7	8.20	8.20	Y	N	Y
CGPLLU86	Lung Cancer	cfDNA	Pre-treatment, Day 0	55	M	IV	NA	Left Upper Lobe of Lung	Adenocarcinoma	NA	Lung	4.0	7.90	7.90	Y	N	Y
CGPLLU86	Lung Cancer	cfDNA	Post-treatment, Day 0.5	55	M	IV	NA	Left Upper Lobe of Lung	Adenocarcinoma	NA	Lung	4.0	7.90	7.90	Y	N	Y
CGPLLU86	Lung Cancer	cfDNA	Post-treatment, Day 7	55	M	IV	NA	Left Upper Lobe of Lung	Adenocarcinoma	NA	Lung	4.0	7.90	7.90	Y	N	Y
CGPLLU86	Lung Cancer	cfDNA	Post-treatment, Day 17	55	M	IV	NA	Left Upper Lobe of Lung	Adenocarcinoma	NA	Lung	4.0	7.90	7.90	Y	N	Y
CGPLLU88	Lung Cancer	cfDNA	Pre-treatment, Day 0	59	M	IV	NA	Right Middle Lobe of Lung	Adenocarcinoma	NA	None	5.0	27.66	27.66	Y	N	Y
CGPLLU88	Lung Cancer	cfDNA	Post-treatment, Day 7	59	M	IV	NA	Right Middle Lobe of Lung	Adenocarcinoma	NA	None	5.0	6.49	6.49	Y	N	Y
CGPLLU88	Lung Cancer	cfDNA	Post-treatment, Day 297	59	M	IV	NA	Right Middle Lobe of Lung	Adenocarcinoma	NA	None	4.0	3.04	3.04	Y	N	Y
CGPLLU89	Lung Cancer	cfDNA	Pre-treatment, Day 0	54	F	IV	NA	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain, Bone, Lung	8.0	8.43	8.43	Y	N	Y
CGPLLU89	Lung Cancer	cfDNA	Post-treatment, Day 7	54	F	IV	NA	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain, Bone, Lung	8.0	8.43	8.43	Y	N	Y
CGPLLU89	Lung Cancer	cfDNA	Post-treatment, Day 22	54	F	IV	NA	Right Upper Lobe of Lung	Adenocarcinoma	NA	Brain, Bone, Lung	8.0	8.43	8.43	Y	N	Y
CGPLOV11	Ovarian Cancer	cfDNA	Preoperative treatment naïve	51	F	IV	T3cN0M1	Right Ovary	Endometrioid Adenoarcinoma	Moderate	Omentum	3.4	17.35	17.35	Y	Y	Y
CGPLOV12	Ovarian Cancer	cfDNA	Preoperative treatment naïve	45	F	I	T1aN0MX	Ovary	Endometrioid Adenoarcinoma	NA	None	3.2	12.44	12.44	Y	N	Y
CGPLOV13	Ovarian Cancer	cfDNA	Preoperative treatment naïve	62	F	IV	T1bN0M1	Right Ovary	Endometrioid Adenoarcinoma	Poor	Omentum	3.8	27.00	27.00	Y	Y	Y
CGPLOV15	Ovarian Cancer	cfDNA	Preoperative treatment naïve	54	F	III	T3N1M0	Ovary	Adenocarcinoma	Poor	None	5.0	4.77	4.77	Y	Y	Y
CGPLOV16	Ovarian Cancer	cfDNA	Preoperative treatment naïve	40	F	III	T3aN0M0	Ovary	Serous Adenocarcinoma	Moderate	None	4.5	27.28	27.28	Y	N	Y
CGPLOV19	Ovarian Cancer	cfDNA	Preoperative treatment naïve	52	F	II	T2aN0M0	Ovary	Endometrioid Adenoarcinoma	Moderate	None	5.0	23.46	23.46	Y	Y	Y
CGPLOV20	Ovarian Cancer	cfDNA	Preoperative treatment naïve	52	F	II	T2aN0M0	Left Ovary	Endometrioid Adenoarcinoma	Poor	None	4.2	5.67	5.67	Y	Y	Y
CGPLOV21	Ovarian Cancer	cfDNA	Preoperative treatment naïve	51	M	IV	TanyN1M1	Ovary	Serous Adenocarcinoma	Poor	Omentum, Appendix	4.3	56.32	56.32	Y	Y	Y
CGPLOV22	Ovarian Cancer	cfDNA	Preoperative treatment naïve	64	F	III	T1cNXMX	Left Ovary	Serous Adenocarcinoma	Well	None	4.6	17.42	17.42	Y	Y	Y
CGPLOV23	Ovarian Cancer	cfDNA	Preoperative treatment naïve	47	F	I	T1aN0M0	Ovary	Serous Adenocarcinoma	Poor	None	5.0	26.73	26.73	Y	N	Y
CGPLOV24	Ovarian Cancer	cfDNA	Preoperative treatment naïve	14	F	I	T1aN0M0	Ovary	Germ Cell Tumor	Poor	None	4.2	10.71	10.71	Y	N	Y
CGPLOV25	Ovarian Cancer	cfDNA	Preoperative treatment naïve	18	F	I	T1aN0M0	Ovary	Germ Cell Tumor	Poor	None	4.8	6.78	6.78	Y	N	Y
CGPLOV26	Ovarian Cancer	cfDNA	Preoperative treatment naïve	35	F	I	T1aN0M0	Ovary	Germ Cell Tumor	Poor	None	4.5	27.90	27.90	Y	N	Y
CGPLOV28	Ovarian Cancer	cfDNA	Preoperative treatment naïve	63	F	I	T1aNxM0	Right Ovary	Serous Carcinoma	NA	None	3.2	10.74	10.74	Y	N	Y
CGPLOV31	Ovarian Cancer	cfDNA	Preoperative treatment naïve	45	F	III	T3aNxM0	Right Ovary	Clear Cell adenocarcinoma	NA	None	4.0	14.45	14.45	Y	N	Y
CGPLOV32	Ovarian Cancer	cfDNA	Preoperative treatment naïve	53	F	I	T1aNxM0	Left Ovary	Mucinous Cystadenoma	NA	None	3.2	27.36	27.36	Y	N	Y
CGPLOV37	Ovarian Cancer	cfDNA	Preoperative treatment naïve	40	F	I	T1cN0M0	Ovary	Serous Carcinoma	NA	None	3.2	46.88	46.88	Y	N	Y
CGPLOV38	Ovarian Cancer	cfDNA	Preoperative treatment naïve	46	F	I	T1cN0M0	Ovary	Serous Carcinoma	NA	None	2.4	34.29	34.29	Y	N	Y
CGPLOV40	Ovarian Cancer	cfDNA	Preoperative treatment naïve	53	F	IV	T3N0M1	Ovary	Serous Carcinoma	NA	Omentum, Uterus, Appendix	1.6	193.60	156.25	Y	N	Y
CGPLOV41	Ovarian Cancer	cfDNA	Preoperative treatment naïve	57	F	IV	T3N0M1	Ovary	Serous Carcinoma	NA	Omentum, Uterus, Cervix	4.4	10.03	10.03	Y	N	Y
CGPLOV42	Ovarian Cancer	cfDNA	Preoperative treatment naïve	52	F	I	T3aN0M0	Ovary	Serous Carcinoma	NA	None	4.2	49.51	49.51	Y	N	Y
CGPLOV43	Ovarian Cancer	cfDNA	Preoperative treatment naïve	30	F	I	T1aN0M0	Ovary	Mucinous Cystadenocarcinoma	NA	None	4.4	9.09	9.09	Y	N	Y
CGPLOV44	Ovarian Cancer	cfDNA	Preoperative treatment naïve	69	F	I	T1aN0M0	Ovary	Mucinous Adenocarcinoma	NA	None	4.5	8.79	8.79	Y	N	Y
CGPLOV46	Ovarian Cancer	cfDNA	Preoperative treatment naïve	58	F	I	T1bN0M0	Ovary	Serous Carcinoma	NA	None	4.1	8.97	8.97	Y	N	Y
CGPLOV47	Ovarian Cancer	cfDNA	Preoperative treatment naïve	41	F	I	T1aN0M0	Ovary	Serous Cystadenoma	NA	None	4.5	19.35	19.35	Y	N	Y
CGPLOV48	Ovarian Cancer	cfDNA	Preoperative treatment naïve	52	F	I	T1bN0M0	Ovary	Serous Carcinoma	NA	None	3.5	22.80	22.80	Y	N	Y
CGPLOV49	Ovarian Cancer	cfDNA	Preoperative treatment naïve	68	F	III	T3bN0M0	Ovary	Serous Carcinoma	NA	None	4.2	16.48	16.48	Y	N	Y
CGPLOV50	Ovarian Cancer	cfDNA	Preoperative treatment naïve	30	F	III	T3cN0M0	Ovary	Serous Carcinoma	NA	None	4.5	8.89	8.89	Y	N	Y
CGPLPA112	Pancreatic Cancer	cfDNA	Preoperative treatment naïve	58	M	II	NA	Intra Pancreatic Bile Duct	NA	NA	None	3.5	18.52	18.52	Y	N	N
CGPLPA113	Duodenal Cancer	cfDNA	Preoperative treatment naïve	71	M	I	NA	Intra Pancreatic Bile Duct	NA	NA	None	4.8	8.24	8.24	Y	N	N
CGPLPA114	Bile Duct Cancer	cfDNA	Preoperative treatment naïve	NA	F	II	NA	Intra Pancreatic Bile Duct	NA	NA	None	4.8	26.43	26.43	Y	N	N
CGPLPA115	Bile Duct Cancer	cfDNA	Preoperative treatment naïve	NA	M	IV	NA	Intra Hepatic Bile Duct	NA	NA	NA	5.0	31.41	31.41	Y	N	N

Patient	Patient Type	Sample Type	Timepoint	Age at Diagnosis	Gender	Stage	TNM Staging	Site of Primary Tumor	Histopathological Diagnosis	Degree of Differentiation	Location of Metastases at Diagnosis	Volume of Plasma (ml)	cfDNA Extracted (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLPA117	Bile Duct Cancer	cfDNA	Preoperative treatment naive	NA	M	II	NA	Intra Pancreatic Bile Duct	NA	NA	None	3.4	2.29	2.29	Y	N	N
CGPLPA118	Bile Duct Cancer	cfDNA	Preoperative treatment naive	68	F	I	NA	Bile Duct	Intra-Ampullary Bile Duct	NA	None	3.8	9.93	9.93	Y	N	Y
CGPLPA122	Bile Duct Cancer	cfDNA	Preoperative treatment naive	62	F	II	NA	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	3.8	66.54	32.89	Y	N	Y
CGPLPA124	Bile Duct Cancer	cfDNA	Preoperative treatment naive	83	F	II	NA	Bile Duct	Intra-Ampullary Bile Duct	moderate	None	4.6	29.24	27.17	Y	N	Y
CGPLPA125	Bile Duct Cancer	cfDNA	Preoperative treatment naive	58	M	II	NA	Bile Duct	Intra-Pancreatic Bile Duct	poor	None	2.7	8.31	8.31	Y	N	N
CGPLPA126	Bile Duct Cancer	cfDNA	Preoperative treatment naive	60	M	II	NA	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	4.3	80.56	29.07	Y	N	Y
CGPLPA127	Bile Duct Cancer	cfDNA	Preoperative treatment naive	71	F	IV	NA	Bile Duct	Extra-Pancreatic Bile Duct	NA	NA	3.0	20.60	20.60	Y	N	N
CGPLPA128	Bile Duct Cancer	cfDNA	Preoperative treatment naive	67	M	II	NA	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	3.9	5.91	5.91	Y	N	Y
CGPLPA129	Bile Duct Cancer	cfDNA	Preoperative treatment naive	56	F	II	NA	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	4.6	27.07	27.07	Y	N	Y
CGPLPA130	Bile Duct Cancer	cfDNA	Preoperative treatment naive	82	F	II	NA	Bile Duct	Intra-Ampullary Bile Duct	well	None	4.0	4.34	4.34	Y	N	Y
CGPLPA131	Bile Duct Cancer	cfDNA	Preoperative treatment naive	71	M	II	NA	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	3.9	68.95	32.05	Y	N	Y
CGPLPA134	Bile Duct Cancer	cfDNA	Preoperative treatment naive	68	M	II	NA	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	4.1	58.08	30.49	Y	N	Y
CGPLPA135	Bile Duct Cancer	cfDNA	Preoperative treatment naive	67	F	I	NA	Bile Duct	Intra-Pancreatic Bile Duct	NA	NA	3.9	4.22	4.22	Y	N	N
CGPLPA136	Bile Duct Cancer	cfDNA	Preoperative treatment naive	69	F	II	NA	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	4.1	20.23	20.23	Y	N	Y
CGPLPA137	Bile Duct Cancer	cfDNA	Preoperative treatment naive	NA	M	II	NA	Bile Duct	NA	NA	NA	4.0	5.75	5.75	Y	N	N
CGPLPA139	Bile Duct Cancer	cfDNA	Preoperative treatment naive	NA	M	IV	NA	Bile Duct	NA	NA	NA	4.0	14.89	14.89	Y	N	N
CGPLPA14	Pancreatic Cancer	cfDNA	Preoperative treatment naive	68	M	II	NA	Pancreas	Ductal Adenocarcinoma	Poor	None	4.0	1.30	1.30	Y	N	N
CGPLPA140	Bile Duct Cancer	cfDNA	Preoperative treatment naive	52	M	II	NA	Extra Hepatic Bile Duct	Intra-Pancreatic Bile Duct	Poor	None	4.7	29.34	26.60	Y	N	Y
CGPLPA141	Bile Duct Cancer	cfDNA	Preoperative treatment naive	68	F	II	NA	Extra Hepatic Bile Duct	Intra-Pancreatic Bile Duct	Moderate	None	2.8	53.67	44.64	Y	N	N
CGPLPA15	Pancreatic Cancer	cfDNA	Preoperative treatment naive	70	F	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	1.92	1.92	Y	N	N
CGPLPA155	Bile Duct Cancer	cfDNA	Preoperative treatment naive	NA	F	II	NA	NA	NA	NA	NA	4.0	25.72	25.72	Y	N	N
CGPLPA156	Pancreatic Cancer	cfDNA	Preoperative treatment naive	73	F	II	NA	Pancreas	Ductal Adenocarcinoma	Poor	Lymph Node	4.5	7.54	7.54	Y	N	N
CGPLPA165	Bile Duct Cancer	cfDNA	Preoperative treatment naive	42	M	I	NA	Bile Duct	Intra-Pancreatic Bile Duct with Medullary Features	well	None	3.9	10.48	10.48	Y	N	N
CGPLPA168	Bile Duct Cancer	cfDNA	Preoperative treatment naive	58	M	II	NA	Bile Duct	Extra-Pancreatic Bile Duct	NA	NA	3.6	139.12	34.72	Y	N	N
CGPLPA17	Pancreatic Cancer	cfDNA	Preoperative treatment naive	65	M	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	13.08	13.08	Y	N	N
CGPLPA184	Bile Duct Cancer	cfDNA	Preoperative treatment naive	75	F	II	NA	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	NA	NA	NA	Y	N	N
CGPLPA187	Bile Duct Cancer	cfDNA	Preoperative treatment naive	67	F	II	NA	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	NA	NA	NA	Y	N	N
CGPLPA23	Pancreatic Cancer	cfDNA	Preoperative treatment naive	58	F	II	NA	Pancreas	Ductal Adenocarcinoma	Moderate	Lymph Node	4.0	16.62	16.62	Y	N	N
CGPLPA25	Pancreatic Cancer	cfDNA	Preoperative treatment naive	69	F	II	NA	Pancreas	Ductal Adenocarcinoma	Poor	Lymph Node	4.0	8.71	8.71	Y	N	N
CGPLPA26	Pancreatic Cancer	cfDNA	Preoperative treatment naive	64	M	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	6.97	6.97	Y	N	N
CGPLPA28	Pancreatic Cancer	cfDNA	Preoperative treatment naive	79	F	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	18.13	18.13	Y	N	N
CGPLPA33	Pancreatic Cancer	cfDNA	Preoperative treatment naive	67	F	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	1.80	1.80	Y	N	N
CGPLPA34	Pancreatic Cancer	cfDNA	Preoperative treatment naive	73	M	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	3.36	3.36	Y	N	N
CGPLPA37	Pancreatic Cancer	cfDNA	Preoperative treatment naive	67	F	II	NA	Pancreas	Ductal Adenocarcinoma	NA	Lymph Node	4.0	21.83	21.83	Y	N	N
CGPLPA38	Pancreatic Cancer	cfDNA	Preoperative treatment naive	65	M	II	NA	Pancreas	Ductal Adenocarcinoma	Moderate	None	4.0	5.29	5.29	Y	N	N
CGPLPA39	Pancreatic Cancer	cfDNA	Preoperative treatment naive	67	F	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	11.73	11.73	Y	N	N
CGPLPA40	Pancreatic Cancer	cfDNA	Preoperative treatment naive	64	M	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	4.78	4.78	Y	N	N
CGPLPA42	Pancreatic Cancer	cfDNA	Preoperative treatment naive	73	M	II	NA	Pancreas	Ductal Adenocarcinoma	Moderate	Lymph Node	4.0	3.41	3.41	Y	N	N
CGPLPA46	Pancreatic Cancer	cfDNA	Preoperative treatment naive	59	F	II	NA	Pancreas	Ductal Adenocarcinoma	Poor	Lymph Node	4.0	0.74	0.74	Y	N	N
CGPLPA47	Pancreatic Cancer	cfDNA	Preoperative treatment naive	67	M	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	4.0	6.01	6.01	Y	N	N
CGPLPA48	Pancreatic Cancer	cfDNA	Preoperative treatment naive	72	F	I	NA	Pancreas	Ductal Adenocarcinoma	Well	None	NA	NA	NA	Y	N	N
CGPLPA52	Pancreatic Cancer	cfDNA	Preoperative treatment naive	63	M	II	NA	Pancreas	Ductal Adenocarcinoma	Moderate	None	2.5	9.86	9.86	Y	N	N
CGPLPA53	Pancreatic Cancer	cfDNA	Preoperative treatment naive	46	M	I	NA	Pancreas	Ductal Adenocarcinoma	Poor	Lymph Node	3.0	14.48	14.48	Y	N	N
CGPLPA58	Pancreatic Cancer	cfDNA	Preoperative treatment naive	74	F	II	NA	Pancreas	Ductal Adenocarcinoma	NA	None	3.0	6.87	6.87	Y	N	N
CGPLPA59	Pancreatic Cancer	cfDNA	Preoperative treatment naive	59	F	II	NA	Pancreas	Ductal Adenocarcinoma or Adenoma	Well	Lymph Node	NA	NA	NA	Y	N	N
CGPLPA67	Pancreatic Cancer	cfDNA	Preoperative treatment naive	55	M	III	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	3.2	9.72	9.72	Y	N	N
CGPLPA69	Pancreatic Cancer	cfDNA	Preoperative treatment naive	70	M	I	NA	Pancreas	Ductal Adenocarcinoma	Well	None	2.0	1.72	1.72	Y	N	N
CGPLPA71	Pancreatic Cancer	cfDNA	Preoperative treatment naive	64	M	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	2.2	39.07	39.07	Y	N	N
CGPLPA74	Pancreatic Cancer	cfDNA	Preoperative treatment naive	71	F	II	NA	Pancreas	Ductal Adenocarcinoma	Moderate	Lymph Node	2.5	4.99	4.99	Y	N	N
CGPLPA76	Pancreatic Cancer	cfDNA	Preoperative treatment naive	69	M	II	NA	Pancreas	Ductal Adenocarcinoma	Poor	None	2.5	23.19	23.19	Y	N	N
CGPLPA85	Pancreatic Cancer	cfDNA	Preoperative treatment naive	77	F	II	NA	Pancreas	Ductal Adenocarcinoma	Poor	Lymph Node	3.0	152.46	41.67	Y	N	N
CGPLPA86	Pancreatic Cancer	cfDNA	Preoperative treatment naive	66	M	II	NA	Pancreas	Ductal Adenocarcinoma	Moderate	Lymph Node	2.5	11.02	11.02	Y	N	N
CGPLPA92	Pancreatic Cancer	cfDNA	Preoperative treatment naive	72	M	II	NA	Pancreas	Ductal Adenocarcinoma	NA	Lymph Node	2.0	5.34	5.34	Y	N	N
CGPLPA93	Pancreatic Cancer	cfDNA	Preoperative treatment naive	48	M	II	NA	Pancreas	Ductal Adenocarcinoma	Poor	None	3.0	96.28	41.67	Y	N	N
CGPLPA94	Pancreatic Cancer	cfDNA	Preoperative treatment naive	72	F	II	NA	Pancreas	Ductal Adenocarcinoma	NA	Lymph Node	3.0	29.66	29.66	Y	N	N
CGPLPA95	Pancreatic Cancer	cfDNA	Preoperative treatment naive	64	F	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	NA	NA	NA	Y	N	N
CGST102	Gastric cancer	cfDNA	Preoperative treatment naive	76	F	II	T3N0M0	Stomach	Tubular Adenocarcinoma	Moderate	None	4.1	8.03	8.03	Y	N	Y
CGST11	Gastric cancer	cfDNA	Preoperative treatment naive	49	M	IV	TXNXM1	Stomach	Mixed Carcinoma	Moderate	None	3.8	3.57	3.57	Y	N	N
CGST110	Gastric cancer	cfDNA	Preoperative treatment naive	77	M	III	T4AN3aM0	Stomach	Tubular Adenocarcinoma	Moderate	None	3.8	5.00	5.00	Y	N	Y
CGST114	Gastric cancer	cfDNA	Preoperative treatment naive	65	M	III	T4AN1M0	Stomach	Tubular Adenocarcinoma	Poor	None	4.4	10.35	10.35	Y	N	Y
CGST13	Gastric cancer	cfDNA	Preoperative treatment naive	72	F	II	T1AN2M0	Stomach	Signet Ring Cell Carcinoma	Poor	None	4.4	24.33	24.33	Y	N	Y
CGST131	Gastric cancer	cfDNA	Preoperative treatment naive	63	M	III	T2N3aM0	Stomach	Signet ring cell carcinoma	Poor	None	4.0	4.28	4.28	Y	N	N
CGST141	Gastric cancer	cfDNA	Preoperative treatment naive	33	F	III	T3N2M0	Stomach	Signet Ring Cell Carcinoma	Poor	None	4.4	10.84	10.84	Y	N	Y
CGST16	Gastric cancer	cfDNA	Preoperative treatment naive	78	M	III	T4AN3aM0	Stomach	Tubular Adenocarcinoma	Poor	None	4.0	40.69	40.69	Y	N	Y
CGST18	Gastric cancer	cfDNA	Preoperative treatment naive	56	M	II	T3N0M0	Stomach	Mucinous Adenocarcinoma	Well	None	4.3	9.78	9.78	Y	N	Y
CGST21	Gastric cancer	cfDNA	Preoperative treatment naive	39	M	II	T2N1 (mi)M0	Stomach	Papillary Adenocarcinoma	Moderate	None	4.0	0.83	0.83	Y	N	N
CGST26	Gastric cancer	cfDNA	Preoperative treatment naive	51	M	IV	TXNXM1	Stomach	Signet ring cell carcinoma	Poor	None	3.5	5.56	5.56	Y	N	N
CGST28	Gastric cancer	cfDNA	Preoperative treatment naive	55	M	X	TXNXMx	Stomach	Undifferentiated Carcinoma	Poor	None	4.0	5.86	5.86	Y	N	Y
CGST30	Gastric cancer	cfDNA	Preoperative treatment naive	64	F	III	T3N2M0	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.0	4.22	4.22	Y	N	Y
CGST32	Gastric cancer	cfDNA	Preoperative treatment naive	67	M	II	T3N1M0	Stomach	Tubular Adenocarcinoma	Moderate	None	4.0	11.49	11.49	Y	N	Y
CGST33	Gastric cancer	cfDNA	Preoperative treatment naive	61	M	I	T2N0M0	Stomach	Tubular Adenocarcinoma	Moderate	None	3.5	5.71	5.71	Y	N	Y
CGST38	Gastric cancer	cfDNA	Preoperative treatment naive	71	F	0	T0N0M0	Stomach	Mucinous adenocarcinoma	NA	None	4.0	NA	NA	Y	N	N
CGST39	Gastric cancer	cfDNA	Preoperative treatment naive	51	M	IV	TXNXM1	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.5	20.69	20.69	Y	N	Y
CGST41	Gastric cancer	cfDNA	Preoperative treatment naive	66	F	IV	TXNXM1	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.5	7.83	7.83	Y	N	Y
CGST45	Gastric cancer	cfDNA	Preoperative treatment naive	41	F	II	T3N0M0	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.8	7.14	7.14	Y	N	Y
CGST47	Gastric cancer	cfDNA	Preoperative treatment naive	74	F	I	T1AN0M0	Stomach	Tubular Adenocarcinoma	Moderate	None	4.0	4.55	4.55	Y	N	Y
CGST48	Gastric cancer	cfDNA	Preoperative treatment naive	62	M	IV	TXNXM1	Stomach	Tubular Adenocarcinoma	Poor	None	4.5	8.79	8.79	Y	N	Y
CGST53	Gastric cancer	cfDNA	Preoperative treatment naive	70	M	0	T0N0M0	Stomach	NA	NA	None	3.8	15.82	15.82	Y	N	N
CGST58	Gastric cancer	cfDNA	Preoperative treatment naive	58	M	III	T4AN3bM0	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.8	19.81	19.81	Y	N	Y
CGST67	Gastric cancer	cfDNA	Preoperative treatment naive	69	M	I	T1BN0M0	Stomach	Tubular adenocarcinoma	Moderate	None	3.0	23.01	23.01	Y	N	N
CGST77	Gastric cancer	cfDNA	Preoperative treatment naive	70	M	IV	TXNXM1	Stomach	Tubular adenocarcinoma	Moderate	None	4.5	15.09	15.09	Y	N	N
CGST80	Gastric cancer	cfDNA	Preoperative treatment naive	58	M	III	T3N3aM0	Stomach	Mucinous Adenocarcinoma	Poor	None	4.5	8.56	8.56	Y	N	Y
CGST81	Gastric cancer	cfDNA	Preoperative treatment naive	64	F	I	T2N0Mx	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.5	37.32	37.32	Y	N	Y
CGH14	Healthy	ian adult elutriated lymphoc	NA	NA	M	NA	NA	NA	NA	NA	NA	NA	NA	NA	Y	N	N
CGH15	Healthy	ian adult elutriated lymphoc	NA	NA	F	NA	NA	NA	NA	NA	NA	NA	NA	NA	Y	N	N

*NA denotes data not available or not applicable for healthy individuals.

APPENDIX B: Table 2. Summary of targeted cfDNA analyses

Patient	Patient Type	Timepoint	Fragment Profile Analysis	Mutation Analysis	Read Length	Bases in Target Region	Bases Mapped to Genome	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage	Distinct Coverage
CGCRC291	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7501485600	3771359756	50%	44345	10359
CGCRC292	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	6736035200	3098886973	46%	36448	8603
CGCRC293	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	6300244000	2818734206	45%	33117	5953
CGCRC294	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7786872600	3911796709	50%	46016	12071
CGCRC295	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	8240660200	3478059753	42%	40787	5826
CGCRC296	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	5718556500	2898549356	51%	33912	10180
CGCRC297	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	7550826100	3717222432	49%	43545	5870
CGCRC298	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	12501036400	6096393764	49%	71196	9617
CGCRC299	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7812602900	4121569690	53%	48098	10338
CGCRC300	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	8648090300	3962285136	46%	46364	5756
CGCRC301	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7538758100	3695480348	49%	43024	6618
CGCRC302	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	8573658300	4349420574	51%	51006	13799
CGCRC303	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	5224046400	2505714343	48%	29365	8372
CGCRC304	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	5762112600	2942170530	51%	34462	10208
CGCRC305	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7213384100	3726953480	52%	43516	8589
CGCRC306	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7075579700	3552441899	50%	41507	7372
CGCRC307	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7572687100	3492191519	46%	40793	9680
CGCRC308	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7945738000	3895908986	49%	45224	11809
CGCRC309	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	8487455800	3921079811	46%	45736	10739
CGCRC310	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	9003580500	4678812441	52%	54713	11139
CGCRC311	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	6528162700	3276653864	50%	38324	6044
CGCRC312	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	7683294300	3316719187	43%	38652	4622
CGCRC313	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	5874099200	2896148722	49%	33821	6506
CGCRC314	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	6883148500	3382767492	49%	39414	6664
CGCRC315	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7497252500	3775556051	50%	44034	8666
CGCRC316	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	10684720400	5533857153	52%	64693	14289
CGCRC317	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7086877600	3669434216	52%	43538	10944
CGCRC318	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	6880041100	3326357413	48%	39077	11571
CGCRC319	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	7485342900	3982677483	53%	47327	10502
CGCRC320	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7058703200	3450648135	49%	40888	10198
CGCRC321	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	7203625900	3633396892	50%	43065	6499
CGCRC332	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	7202969100	3758323705	52%	44580	3243
CGCRC333	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	8767144700	4199126827	48%	49781	8336
CGCRC334	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	7771869100	3944578280	51%	46518	5014
CGCRC335	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	7972524600	4064901201	51%	48308	6151
CGCRC336	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	8597346400	4333410573	50%	51390	7551
CGCRC337	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	7399611700	3800666199	51%	45083	8092
CGCRC338	Colorectal Cancer	Preoperative, Treatment naive	Y	Y	100	80930	8029493700	4179383804	52%	49380	5831
CGCRC339	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	7938963600	4095555110	52%	48397	3808
CGCRC340	Colorectal Cancer	Preoperative, Treatment naive	Y	N	100	80930	7214889500	3706643098	51%	43805	3014
CGCRC341	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	8803159200	3668208527	42%	43106	11957
CGCRC342	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	8478811500	3425540889	40%	40328	9592
CGCRC344	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	6942167800	3098232737	45%	36823	2300
CGCRC345	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	8182868200	2383173431	29%	28233	7973
CGCRC346	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	7448272300	3925056341	53%	46679	5582
CGCRC347	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	5804744500	2986809912	51%	35490	4141
CGCRC349	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	6943451600	3533145275	51%	41908	5762
CGCRC350	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	7434818400	3848923016	52%	45678	4652
CGCRC351	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	7306546400	3636910409	50%	43162	5205
CGCRC352	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	7864655000	3336939252	42%	39587	4502
CGCRC353	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	7501674800	3642919375	49%	43379	4666
CGCRC354	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	7938270200	2379068977	30%	28256	4858
CGCRC356	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	6013175900	3046754994	51%	36127	3425
CGCRC357	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	6013454600	3022035300	50%	35813	4259
CGCRC358	Colorectal Cancer	Preoperative, Treatment naive	N	Y	100	80930	7227212400	3188723303	44%	37992	5286

Patient	Patient Type	Timepoint	Fragment Profile Analysis	Mutation Analysis	Read Length	Bases in Target Region	Bases Mapped to Genome	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage	Distinct Coverage
CGCRC359	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7818567700	425110101	5%	5040	2566
CGCRC367	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6582043200	3363063597	51%	39844	5839
CGCRC368	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8042242400	4101646000	51%	48636	11471
CGCRC370	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6940330100	3198954121	46%	38153	4826
CGCRC373	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6587201700	3120088035	47%	37234	5190
CGCRC376	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6727983100	3162416807	47%	37735	3445
CGCRC377	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6716339200	3131415570	47%	37160	4524
CGCRC378	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6523969900	2411096720	37%	28728	3239
CGCRC379	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6996252100	3371081103	48%	39999	2891
CGCRC380	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7097496300	2710244446	38%	32020	3261
CGCRC381	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6961936100	3287050681	47%	38749	9357
CGCRC382	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6959048700	2552325859	37%	30040	5148
CGCRC384	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7012798900	3293884583	47%	39158	3653
CGCRC385	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7542017900	3356570505	45%	39884	3686
CGCRC386	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6876059600	3064412286	45%	36431	2787
CGCRC387	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7399564700	3047254560	41%	36141	6675
CGCRC388	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6592692900	3137284885	48%	37285	5114
CGCRC389	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6651206300	3102100941	47%	36764	6123
CGCRC390	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7260616800	3376667585	47%	40048	4368
CGCRC391	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6883624500	3202877881	47%	37978	5029
CGLU316	Lung Cancer	Pre-treatment, Day -53	Y	N	100	80930	7864415100	1991331171	25%	23601	3565
CGLU316	Lung Cancer	Pre-treatment, Day -53	Y	N	100	80930	7502591600	3730963390	50%	44262	3966
CGLU316	Lung Cancer	Pre-treatment, Day -53	Y	N	100	80930	6582515900	3187059470	48%	37813	3539
CGLU316	Lung Cancer	Pre-treatment, Day -53	Y	N	100	80930	6587281800	1947630979	30%	23094	4439
CGLU344	Lung Cancer	Pre-treatment, Day -21	Y	N	100	80930	6151628500	2748983603	45%	32462	8063
CGLU344	Lung Cancer	Pre-treatment, Day -21	Y	N	100	80930	7842910900	1147703178	15%	13565	4303
CGLU344	Lung Cancer	Pre-treatment, Day -21	Y	N	100	80930	5838083100	2291108925	39%	27067	4287
CGLU344	Lung Cancer	Pre-treatment, Day -21	Y	N	100	80930	7685989200	3722274529	48%	43945	3471
CGLU369	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	7080245300	1271457982	18%	15109	2364
CGLU369	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	7078131900	1482448715	21%	17583	4275
CGLU369	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	6904701700	2124660124	31%	25230	5278
CGLU369	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	7003452200	3162195578	45%	37509	6062
CGLU373	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	6346267200	3053520676	48%	36137	6251
CGLU373	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	6517189900	3192984468	49%	38066	8040
CGLU373	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	7767146300	3572598842	46%	42378	5306
CGLU373	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	7190999100	3273648804	46%	38784	4454
CGPLBR100	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7299964400	3750278051	51%	44794	3249
CGPLBR101	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7420822800	3810365416	51%	45565	9784
CGPLBR102	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6679304900	3269688319	49%	38679	7613
CGPLBR103	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7040304400	3495542468	50%	41786	6748
CGPLBR104	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7188389200	3716096781	52%	44316	9448
CGPLBR38	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7810293900	4057576306	52%	48098	9868
CGPLBR39	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7745701500	3805623239	49%	45084	11065
CGPLBR40	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7558990500	3652442341	48%	43333	12948
CGPLBR41	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7900994600	3836600101	49%	45535	10847
CGPLBR44	Breast Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7017744200	3269110569	47%	38672	8344
CGPLBR48	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	5629044200	2611554623	46%	30860	8652
CGPLBR49	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	5784711600	2673457893	46%	31274	10429
CGPLBR55	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8309154900	4306956261	52%	51143	8328
CGPLBR57	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8636181000	4391502618	51%	52108	5857
CGPLBR59	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8799457700	4152328555	47%	49281	5855
CGPLBR61	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8163706700	3952010628	48%	46755	8522
CGPLBR63	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7020533100	3542447304	50%	41956	4773
CGPLBR67	Breast Cancer	Preoperative, Treatment naïve	Y	N	100	80930	8264353900	3686093696	45%	43516	7752
CGPLBR68	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7629312300	4078969547	53%	48389	7402
CGPLBR69	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7571501500	3857354512	51%	45322	7047

Patient	Patient Type	Timepoint	Fragment Profile Analysis	Mutation Analysis	Read Length	Bases in Target Region	Bases Mapped to Genome	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage	Distinct Coverage
CGPLBR70	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7251760700	3641333708	50%	43203	8884
CGPLBR71	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8515402600	4496696391	53%	53340	6805
CGPLBR72	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8556946900	4389761697	51%	52081	5632
CGPLBR73	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7959392300	4006933338	50%	47555	8791
CGPLBR74	Breast Cancer	Preoperative, Treatment naïve	Y	N	100	80930	8524536400	4063900599	48%	48252	7013
CGPLBR75	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8260379100	3960599885	48%	46955	6319
CGPLBR76	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7774235200	3893622420	50%	46192	9628
CGPLBR77	Breast Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7572797600	3255963429	43%	38568	8263
CGPLBR80	Breast Cancer	Preoperative, Treatment naïve	Y	N	100	80930	6845325800	3147476693	46%	37201	5595
CGPLBR82	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8236705200	4170465005	51%	49361	12319
CGPLBR83	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7434568100	3676855019	49%	43628	5458
CGPLBR86	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7616282500	3644791327	48%	43490	7048
CGPLBR87	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	6194021300	3004882010	49%	35765	5306
CGPLBR88	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	6071567200	2847926237	47%	33945	10319
CGPLBR91	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7192457700	3480203404	48%	41570	9912
CGPLBR92	Breast Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7678981800	3600279233	47%	42975	13580
CGPLBR93	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7605717800	3998713397	53%	47866	10329
CGPLBR96	Breast Cancer	Preoperative, Treatment naïve	Y	N	100	80930	6297446700	2463064737	39%	29341	7937
CGPLBR97	Breast Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7114921600	3557069027	50%	42488	10712
CGPLH35	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	6919126300	2312758764	33%	25570	1989
CGPLH36	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	6089923400	2038548115	33%	22719	1478
CGPLH37	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	5557270200	1935301929	35%	21673	2312
CGPLH42	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	5792045400	2388036949	41%	27197	2523
CGPLH43	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	5568321700	2017813329	36%	23228	1650
CGPLH45	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	8485593200	2770176078	33%	32829	3114
CGPLH46	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	5083171100	1899395790	37%	21821	1678
CGPLH47	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	6016388500	2062392156	34%	23459	1431
CGPLH48	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	4958945900	1809825992	36%	20702	1698
CGPLH49	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	7953812200	2511365904	32%	27006	1440
CGPLH50	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	6989407600	2561288100	37%	29177	2591
CGPLH51	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	7862073200	2525091396	32%	29999	1293
CGPLH52	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	6939636800	2397922699	35%	27029	2501
CGPLH54	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	10611934700	2290823134	22%	27175	3306
CGPLH55	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	9912569200	2521962244	25%	27082	3161
CGPLH56	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	5777591900	2023874863	35%	22916	1301
CGPLH57	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	9234904800	1493926244	16%	15843	1655
CGPLH59	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	9726052100	2987875484	31%	35427	2143
CGPLH63	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	8696405000	2521574759	29%	26689	1851
CGPLH64	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	5438852600	996198502	18%	11477	1443
CGPLH75	Healthy	Preoperative, Treatment naïve	Y	N	100	80930	3446444000	1505718480	44%	17805	3016
CGPLH76	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	7499116400	3685762725	49%	43682	4643
CGPLH77	Healthy	Preoperative, Treatment naïve	Y	N	100	80930	6512408400	2537359345	39%	30280	3131
CGPLH78	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	7642949300	3946069680	52%	46316	5358
CGPLH79	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	7785475700	3910639227	50%	45280	6714
CGPLH80	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	7918361500	3558236955	45%	42171	5062
CGPLH81	Healthy	Preoperative, Treatment naïve	Y	N	100	80930	6646268900	3112369850	47%	37119	3678
CGPLH82	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	7744065000	3941700596	51%	46820	5723
CGPLH83	Healthy	Preoperative, Treatment naïve	Y	N	100	80930	6957686000	1447603106	21%	17280	2875
CGPLH84	Healthy	Preoperative, Treatment naïve	Y	N	100	80930	8326493200	3969908122	48%	47464	3647
CGPLH86	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	8664194700	4470145091	52%	53398	5094
CGPLH90	Healthy	Preoperative, Treatment naïve	N	Y	100	80930	7516078800	3841504088	51%	45907	4414
CGPLLU13	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	5659546100	1721618955	30%	20587	6025
CGPLLU13	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	6199049700	2563659840	41%	30728	6514
CGPLLU13	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	5864396500	1194237002	20%	14331	3952
CGPLLU13	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	5080197700	1373550586	27%	16480	5389
CGPLLU14	Lung Cancer	Pre-treatment, Day -38	N	Y	100	80930	8668655700	3980731089	46%	48628	3148

Patient	Patient Type	Timepoint	Fragment Profile Analysis	Mutation Analysis	Read Length	Bases in Target Region	Bases Mapped to Genome	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage	Distinct Coverage
CGPLLU14	Lung Cancer	Pre-treatment, Day -16	N	Y	100	80930	8271043600	4105092738	50%	50152	4497
CGPLLU14	Lung Cancer	Pre-treatment, Day -3	N	Y	100	80930	7149809200	3405754720	48%	40382	6170
CGPLLU14	Lung Cancer	Pre-treatment, Day 0	N	Y	100	80930	6556332200	3289504484	50%	39004	4081
CGPLLU14	Lung Cancer	Post-treatment, Day 0.33	N	Y	100	80930	7410378300	3464236558	47%	41108	4259
CGPLLU14	Lung Cancer	Post-treatment, Day 7	N	Y	100	80930	7530190700	3752054349	50%	45839	2469
CGPLLU144	Lung Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8716827400	4216576624	48%	49370	10771
CGPLLU146	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	8506844200	4195033049	49%	49084	6968
CGPLLU147	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7416300600	3530746046	48%	41302	4691
CGPLLU161	Lung Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7789148700	3280139772	42%	38568	12229
CGPLLU162	Lung Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7625462000	3470147667	46%	40918	10099
CGPLLU163	Lung Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8019293200	3946533983	49%	46471	12108
CGPLLU164	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	8110030900	3592748235	44%	42161	6947
CGPLLU165	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	8389514600	4147501817	49%	48770	8996
CGPLLU168	Lung Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7690630000	3868237773	50%	45625	9711
CGPLLU169	Lung Cancer	Preoperative, Treatment naïve	N	Y	100	80930	9378353000	4800407624	51%	56547	10261
CGPLLU174	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7481844600	3067532518	41%	36321	6137
CGPLLU175	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	8532324200	4002541569	47%	47084	7862
CGPLLU176	Lung Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8143905000	4054098929	50%	47708	5588
CGPLLU177	Lung Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8421611300	4197108809	50%	49476	8780
CGPLLU178	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	8483124700	4169577489	49%	48580	6445
CGPLLU179	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7774358700	3304915738	43%	38768	6862
CGPLLU180	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	8192813800	3937552475	48%	46498	6568
CGPLLU197	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7996779200	3082397881	39%	36381	5388
CGPLLU198	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7175247200	3545719100	49%	42008	6817
CGPLLU202	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	6840112800	3427820669	50%	40670	7951
CGPLLU203	Lung Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7468749900	3762726574	50%	44500	9917
CGPLLU204	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7445026400	3703545153	50%	44317	6856
CGPLLU205	Lung Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	9205429100	4350573991	47%	51627	9810
CGPLLU206	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7397914600	3635210205	49%	43016	7124
CGPLLU207	Lung Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7133043900	3736258011	52%	44291	8499
CGPLLU208	Lung Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7346976400	3855814032	52%	45782	8940
CGPLLU209	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	6723337800	3362944595	50%	39531	11946
CGPLLU244	Lung Cancer	Pre-treatment, Day -7	N	Y	100	80930	8305560600	4182616104	50%	50851	7569
CGPLLU244	Lung Cancer	Pre-treatment, Day -1	N	Y	100	80930	7739951100	3788487116	49%	45925	8552
CGPLLU244	Lung Cancer	Post-treatment, Day 6	N	Y	100	80930	8061928000	4225322272	52%	51279	8646
CGPLLU244	Lung Cancer	Post-treatment, Day 62	N	Y	100	80930	8894936700	4437962639	50%	53862	7361
CGPLLU245	Lung Cancer	Pre-treatment, Day -32	N	Y	100	80930	7679235200	3935822054	51%	47768	7266
CGPLLU245	Lung Cancer	Pre-treatment, Day 0	N	Y	100	80930	8985252500	4824268339	54%	58338	10394
CGPLLU245	Lung Cancer	Post-treatment, Day 7	N	Y	100	80930	8518229300	4480236927	53%	54083	10125
CGPLLU245	Lung Cancer	Post-treatment, Day 21	N	Y	100	80930	9031131000	4824738475	53%	58313	10598
CGPLLU246	Lung Cancer	Pre-treatment, Day -21	N	Y	100	80930	8520360800	3509660305	41%	42349	8086
CGPLLU246	Lung Cancer	Pre-treatment, Day 0	N	Y	100	80930	5451467800	2828351657	52%	34243	8256
CGPLLU246	Lung Cancer	Post-treatment, Day 9	N	Y	100	80930	8137616600	4135036174	51%	50121	6466
CGPLLU246	Lung Cancer	Post-treatment, Day 42	N	Y	100	80930	8385724600	4413323333	53%	53495	7303
CGPLLU264	Lung Cancer	Pre-treatment, Day -1	Y	N	100	80930	6254777700	3016326208	48%	36164	12138
CGPLLU264	Lung Cancer	Pre-treatment, Day -1	Y	N	100	80930	6185331000	3087883231	50%	37003	8368
CGPLLU264	Lung Cancer	Pre-treatment, Day -1	Y	N	100	80930	6274540300	2861143666	46%	34308	6817
CGPLLU264	Lung Cancer	Pre-treatment, Day -1	Y	N	100	80930	5701274000	1241270938	22%	14886	4273
CGPLLU265	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	6091276800	2922585558	48%	35004	7742
CGPLLU265	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	6430107900	2945953499	46%	35219	8574
CGPLLU265	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	5869510300	2792208995	48%	33423	8423
CGPLLU265	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	5884330900	2588386038	44%	30977	9803
CGPLLU266	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	5807524900	2347651479	40%	28146	5793
CGPLLU266	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	6064269800	2086938782	34%	24994	6221
CGPLLU266	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	6785913900	3458588505	51%	41432	7765
CGPLLU266	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	6513702000	2096370387	32%	25142	6598

Patient	Patient Type	Timepoint	Fragment Profile Analysis	Mutation Analysis	Read Length	Bases in Target Region	Bases Mapped to Genome	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage	Distinct Coverage
CGPLLU267	Lung Cancer	Pre-treatment, Day -1	Y	N	100	80930	6610761200	2576886619	39%	31095	4485
CGPLLU267	Lung Cancer	Pre-treatment, Day -1	Y	N	100	80930	6156102000	2586081726	42%	30714	5309
CGPLLU267	Lung Cancer	Pre-treatment, Day -1	Y	N	100	80930	6180799700	2013434756	33%	23902	3885
CGPLLU269	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	6221168600	1499602843	24%	17799	6098
CGPLLU269	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	5353961600	1698331125	32%	20094	5252
CGPLLU269	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	5831612800	1521114956	26%	18067	6210
CGPLLU271	Lung Cancer	Post-treatment, Day 259	Y	N	100	80930	6229704000	1481468974	24%	17608	4633
CGPLLU271	Lung Cancer	Post-treatment, Day 259	Y	N	100	80930	6134366400	1351029627	22%	16170	7024
CGPLLU271	Lung Cancer	Post-treatment, Day 259	Y	N	100	80930	6491884900	1622578435	25%	19433	5792
CGPLLU271	Lung Cancer	Post-treatment, Day 259	Y	N	100	80930	5742881200	2349421128	41%	28171	5723
CGPLLU271	Lung Cancer	Post-treatment, Day 259	Y	N	100	80930	5503999300	1695782705	31%	20320	5907
CGPLLU43	Lung Cancer	Pre-treatment, Day -1	Y	N	100	80930	6575907000	3002048491	46%	35997	5445
CGPLLU43	Lung Cancer	Pre-treatment, Day -1	Y	N	100	80930	6204350900	3016077187	49%	36162	5704
CGPLLU43	Lung Cancer	Pre-treatment, Day -1	Y	N	100	80930	5997724300	2989608757	50%	35873	6228
CGPLLU43	Lung Cancer	Pre-treatment, Day -1	Y	N	100	80930	6026261500	2881177658	48%	34568	7221
CGPLLU86	Lung Cancer	Pre-treatment, Day 0	N	Y	100	80930	8222093400	3523035056	43%	41165	3614
CGPLLU86	Lung Cancer	Post-treatment, Day 0.5	N	Y	100	80930	8305719500	4271264008	51%	49508	6681
CGPLLU86	Lung Cancer	Post-treatment, Day 7	N	Y	100	80930	6787785300	3443658418	51%	40192	3643
CGPLLU86	Lung Cancer	Post-treatment, Day 17	N	Y	100	80930	6213229400	3120325926	50%	36413	3560
CGPLLU88	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	7252433900	3621678746	50%	42719	8599
CGPLLU88	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	7679995800	4004738253	52%	46951	6387
CGPLLU88	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	6509178000	3316053733	51%	39274	2661
CGPLLU89	Lung Cancer	Pre-treatment, Day 0	N	Y	100	80930	7662496600	3781536306	49%	44097	7909
CGPLLU89	Lung Cancer	Post-treatment, Day 7	N	Y	100	80930	7005599500	3339612564	48%	38977	5034
CGPLLU89	Lung Cancer	Post-treatment, Day 22	N	Y	100	80930	8325998600	3094796789	37%	36061	2822
CGPLOV10	Ovarian Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7073534200	3402308123	48%	39820	4059
CGPLOV11	Ovarian Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	6924062200	3324593050	48%	38796	7185
CGPLOV12	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6552080100	3181854993	49%	37340	6114
CGPLOV13	Ovarian Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	6796755500	3264897084	48%	38340	7931
CGPLOV14	Ovarian Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7856573900	3408425065	43%	39997	7712
CGPLOV15	Ovarian Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7239201500	3322285607	46%	38953	6644
CGPLOV16	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8570755900	4344288233	51%	51009	11947
CGPLOV17	Ovarian Cancer	Preoperative, Treatment naïve	Y	N	100	80930	6910310400	2805243492	41%	32828	4307
CGPLOV18	Ovarian Cancer	Preoperative, Treatment naïve	Y	N	100	80930	8173037600	4064432407	50%	47714	5182
CGPLOV19	Ovarian Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7732198900	3672564399	47%	43020	11127
CGPLOV20	Ovarian Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7559602000	3678700179	49%	43230	4872
CGPLOV21	Ovarian Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8949032900	4616255499	52%	54012	12777
CGPLOV22	Ovarian Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8680136500	4049934586	47%	46912	9715
CGPLOV23	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6660696600	3422631774	51%	40810	9460
CGPLOV24	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8634287200	4272258165	49%	50736	8689
CGPLOV25	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6978295000	3390206388	49%	40188	5856
CGPLOV26	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7041038300	3728879661	53%	44341	8950
CGPLOV28	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7429236900	3753051715	51%	45430	4155
CGPLOV31	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8981384000	4621838729	51%	55429	5458
CGPLOV32	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	9344536800	4737698323	51%	57234	6165
CGPLOV37	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8158083200	4184432898	51%	50648	6934
CGPLOV38	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8654435400	4492987085	52%	53789	6124
CGPLOV40	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	9868640700	4934400809	50%	59049	7721
CGPLOV41	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7689013600	3861448829	50%	46292	4469
CGPLOV42	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	9836516300	4864154366	49%	58302	7632
CGPLOV43	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8756507100	4515479918	52%	54661	4310
CGPLOV44	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7576310800	4120933922	54%	49903	4969
CGPLOV46	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	9346036300	5037820346	54%	61204	3927
CGPLOV47	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	10880620200	5491357828	50%	66363	6895
CGPLOV48	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7658787800	3335991337	44%	40332	4066
CGPLOV49	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	10076208000	5519656698	55%	67117	5097

Patient	Patient Type	Timepoint	Fragment Profile Analysis	Mutation Analysis	Read Length	Bases in Target Region	Bases Mapped to Genome	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage	Distinct Coverage
CGPLOV50	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8239290400	4472380276	54%	54150	3836
CGPLPA118	Bile Duct Cancer	Preoperative, Treatment naïve	N	Y	100	80930	9094827600	4828332902	53%	57021	4802
CGPLPA122	Bile Duct Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7303323100	3990160379	55%	47240	7875
CGPLPA124	Bile Duct Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7573482800	3965807442	52%	46388	8658
CGPLPA126	Bile Duct Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7904953600	4061463168	51%	47812	10498
CGPLPA128	Bile Duct Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7249238300	2244188735	31%	26436	3413
CGPLPA129	Bile Duct Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7559858900	4003725804	53%	47182	5733
CGPLPA130	Bile Duct Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6973946500	1247144905	18%	14691	1723
CGPLPA131	Bile Duct Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7226237900	3370664342	47%	39661	5054
CGPLPA134	Bile Duct Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7268866100	3754945844	52%	44306	7023
CGPLPA136	Bile Duct Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7476690700	4073978408	54%	48134	5244
CGPLPA140	Bile Duct Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7364654600	3771765342	51%	44479	7080
CGST102	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	5715504500	2644902854	46%	31309	4503
CGST110	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	9179291500	4298269268	47%	51666	3873
CGST114	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7151572200	3254967293	46%	38496	4839
CGST13	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6449701500	3198545984	50%	38515	6731
CGST141	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6781001300	3440927391	51%	40762	5404
CGST16	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6396470600	2931380289	46%	35354	8148
CGST18	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6647324000	3138967777	47%	37401	4992
CGST28	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6288486100	2884997993	46%	34538	2586
CGST30	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6141213100	3109994564	51%	37194	2555
CGST32	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6969139300	3099120469	44%	36726	3935
CGST33	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6560309400	3168371917	48%	37916	4597
CGST39	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7043791400	2992801875	42%	35620	6737
CGST41	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6975053100	3224065662	46%	38300	4016
CGST45	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6130812200	2944524278	48%	35264	4745
CGST47	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	5961400000	3083523351	52%	37008	3112
CGST48	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6418652700	1497230327	23%	17782	2410
CGST58	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	5818344500	1274708429	22%	15281	2924
CGST80	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6368064600	3298497188	52%	39692	5280
CGST81	Gastric Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8655691400	1519121452	18%	17988	6419

APPENDIX C: Table 3. Targeted cfDNA fragment analyses in cancer patients

Patient	Patient Type	Stage at Diagnosis	Alteration Type	Gene	Amino Acid (Protein)	Nucleotide	Mutation Type	Hotspot Alteration	Alteration Detected in Tissue	Mutant Allele Fraction	Wild-type Fragments				
											Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)
CGCRC291	Colorectal Cancer	IV	Tumor-derived	STK11	39R>C	chr19_1207027-1207027_C_T	Substitution	No	No	0.14%	11688	100	151	167	169
CGCRC291	Colorectal Cancer	IV	Tumor-derived	TP53	272V>M	chr17_7577124-7577124_C_T	Substitution	Yes	No	0.10%	11779	100	155	171	169
CGCRC291	Colorectal Cancer	IV	Tumor-derived	TP53	167Q>X	chr17_7578431-7578431_G_A	Substitution	Yes	Yes	22.85%	11026	100	156	166	169
CGCRC291	Colorectal Cancer	IV	Tumor-derived	KRAS	12G>A	chr12_25398284-25398284_C_G	Substitution	Yes	Yes	14.65%	7632	97	152	169	167
CGCRC291	Colorectal Cancer	IV	Tumor-derived	APC	1260Q>X	chr5_112175069-112175069_C_T	Substitution	No	Yes	11.23%	7218	101	155	167	169
CGCRC291	Colorectal Cancer	IV	Tumor-derived	APC	1450R>X	chr5_112175639-112175639_C_T	Substitution	Yes	Yes	11.05%	10757	86	154	166	167
CGCRC291	Colorectal Cancer	IV	Tumor-derived	PIK3CA	542E>K	chr3_178936082-178936082_G_A	Substitution	Yes	Yes	18.11%	5429	100	151	171	167
CGCRC292	Colorectal Cancer	IV	Tumor-derived	KRAS	146A>V	chr12_25378561-25378561_G_A	Substitution	Yes	No	1.41%	6120	101	157	167	169
CGCRC292	Colorectal Cancer	IV	Tumor-derived	CTNNB1	41T>A	chr3_41266124-41266124_A_G	Substitution	Yes	Yes	0.13%	10693	100	155	169	168
CGCRC292	Colorectal Cancer	IV	Germline	EGFR	2284-4C>G	chr7_55248982-55248982_C_G	Substitution	NA	Yes	31.99%	7587	97	158	166	171
CGCRC293	Colorectal Cancer	IV	Tumor derived	TP53	176C>S	chr17_7578404-7578404_A_T	Substitution	No	No	0.35%	7672	95	159	168	170
CGCRC294	Colorectal Cancer	II	Tumor derived	APC	213R>X	chr5_112116592-112116592_C_T	Substitution	Yes	Yes	0.14%	7339	84	155	166	167
CGCRC294	Colorectal Cancer	II	Tumor-derived	APC	1367Q>X	chr5_112175390-112175390_C_T	Substitution	Yes	Yes	0.13%	12054	89	159	167	170
CGCRC295	Colorectal Cancer	IV	Tumor-derived	PDGFRA	49+4C>T	chr4_55124988-55124988_C_T	Substitution	No	No	0.45%	5602	101	157	164	170
CGCRC295	Colorectal Cancer	IV	Hematopoietic	IDH1	104G>V	chr2_209113196-209113196_C_A	Substitution	No	Yes	0.34%	8330	100	157	166	169
CGCRC296	Colorectal Cancer	II	Germline	EGFR	922E>K	chr7_55266472-55266472_G_A	Substitution	NA	Yes	30.48%	8375	89	161	166	172
CGCRC297	Colorectal Cancer	III	Germline	KIT	18L>F	chr4_55524233-55524233_C_T	Substitution	NA	Yes	41.39%	3580	102	159	164	170
CGCRC298	Colorectal Cancer	II	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	Yes	0.08%	13032	100	159	168	171
CGCRC298	Colorectal Cancer	II	Hematopoietic	DNMT3A	714S>C	chr2_25463541-25463541_G_C	Substitution	No	No	0.11%	13475	93	158	169	170
CGCRC298	Colorectal Cancer	II	Tumor-derived	PIK3CA	414G>V	chr3_178927478-178927478_G_T	Substitution	No	No	0.55%	5815	100	156	168	169
CGCRC299	Colorectal Cancer	I	Hematopoietic	DNMT3A	735Y>C	chr2_25463289-25463289_T_C	Substitution	No	Yes	0.30%	11995	100	154	164	165
CGCRC299	Colorectal Cancer	I	Hematopoietic	DNMT3A	710C>S	chr2_25463553-25463553_C_G	Substitution	No	Yes	0.12%	15363	96	151	166	164
CGCRC300	Colorectal Cancer	I	Hematopoietic	DNMT3A	720R>G	chr2_25463524-25463524_G_C	Substitution	No	No	0.15%	7487	100	162	170	173
CGCRC301	Colorectal Cancer	I	Tumor-derived	ATM	2397Q>X	chr11_108199847-108199847_C_T	Substitution	No	No	0.21%	5681	100	156	169	169
CGCRC302	Colorectal Cancer	II	Tumor-derived	TP53	141C>Y	chr17_7578508-7578508_C_T	Substitution	Yes	Yes	0.05%	24784	84	153	165	164
CGCRC302	Colorectal Cancer	II	Tumor-derived	BRAF	600V>E	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	0.12%	11763	95	154	165	165
CGCRC303	Colorectal Cancer	III	Tumor derived	TP53	173V>L	chr17_7578413-7578413_C_A	Substitution	Yes	Yes	0.08%	13967	95	159	169	171
CGCRC303	Colorectal Cancer	III	Hematopoietic	DNMT3A	755F>S	chr2_25463229-25463229_A_G	Substitution	No	No	0.21%	10167	81	160	169	172
CGCRC303	Colorectal Cancer	III	Hematopoietic	DNMT3A	2173+1G>A	chr2_25463508-25463508_C_T	Substitution	No	No	0.17%	10845	100	160	169	172
CGCRC304	Colorectal Cancer	II	Tumor-derived	EGFR	1131T>S	chr7_55273068-55273068_A_T	Substitution	No	No	0.22%	16168	90	153	167	164
CGCRC304	Colorectal Cancer	II	Tumor-derived	ATM	3077+1G>A	chr11_108142134-108142134_G_A	Substitution	No	No	0.27%	10502	100	152	165	163
CGCRC304	Colorectal Cancer	II	Hematopoietic	ATM	3008R>C	chr11_108236086-108236086_C_T	Substitution	No	Yes	0.43%	12987	101	154	165	165
CGCRC305	Colorectal Cancer	II	Tumor-derived	GNA11	213R>Q	chr19_3118954-3118954_G_A	Substitution	No	Yes	0.11%	12507	100	159	169	171
CGCRC305	Colorectal Cancer	II	Tumor-derived	TP53	273R>H	chr17_7577120-7577120_C_T	Substitution	Yes	No	0.19%	10301	100	156	168	168
CGCRC306	Colorectal Cancer	II	Tumor-derived	TP53	196R>X	chr17_7578263-7578263_G_A	Substitution	Yes	No	0.12%	8594	101	157	165	169
CGCRC306	Colorectal Cancer	II	Tumor-derived	CDKN2A	107R>C	chr9_21971039-21971039_G_A	Substitution	No	Yes	8.02%	9437	90	159	167	171
CGCRC306	Colorectal Cancer	II	Tumor-derived	KRAS	61Q>K	chr12_25380277-25380277_G_T	Substitution	Yes	Yes	7.30%	6090	100	152	163	166
CGCRC306	Colorectal Cancer	II	Germline	PDGFRA	200T>S	chr4_55130065-55130065_C_G	Substitution	NA	Yes	34.78%	4585	103	158	167	170
CGCRC306	Colorectal Cancer	II	Tumor-derived	EGFR	618H>R	chr7_55233103-55233103_A_G	Substitution	No	Yes	6.32%	7395	81	160	166	171
CGCRC306	Colorectal Cancer	II	Tumor-derived	PIK3CA	545E>A	chr3_178936092-178936092_A_C	Substitution	Yes	No	0.96%	4885	100	152	170	167
CGCRC306	Colorectal Cancer	II	Germline	ERBB4	1155R>X	chr2_212251596-212251596_G_A	Substitution	NA	Yes	38.70%	3700	100	159	168	171
CGCRC307	Colorectal Cancer	II	Tumor-derived	JAK2	805L>V	chr9_5080662-5080662_C_G	Substitution	No	No	0.56%	6860	100	158	170	170
CGCRC307	Colorectal Cancer	II	Tumor derived	SMARCB1	501-2A>G	chr22_24145480-24145480_A_G	Substitution	No	Yes	0.34%	10065	95	157	168	169
CGCRC307	Colorectal Cancer	II	Tumor-derived	GNAS	201R>C	chr20_57484420-57484420_C_T	Substitution	Yes	Yes#	0.24%	7520	102	156	167	168
CGCRC307	Colorectal Cancer	II	Tumor-derived	BRAF	600V>E	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	0.38%	8623	76	157	169	168
CGCRC307	Colorectal Cancer	II	Tumor-derived	FBXW7	465R>C	chr4_153249385-153249385_G_A	Substitution	Yes	Yes	0.31%	10606	100	155	167	168
CGCRC307	Colorectal Cancer	II	Tumor-derived	ERBB4	17A>V	chr2_213403205-213403205_G_A	Substitution	No	No	0.15%	13189	90	158	168	171
CGCRC308	Colorectal Cancer	III	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	No	0.06%	16287	90	159	168	169
CGCRC308	Colorectal Cancer	III	Germline	EGFR	848P>L	chr7_55259485-55259485_C_T	Substitution	NA	Yes	27.69%	7729	100	160	164	170
CGCRC308	Colorectal Cancer	III	Tumor-derived	APC	1480Q>X	chr5_112175729-112175729_C_T	Substitution	No	Yes	0.11%	14067	92	157	170	169
CGCRC309	Colorectal Cancer	III	Tumor-derived	AKT1	17E>K	chr14_105246551-105246551_C_T	Substitution	Yes	Yes	2.70%	13036	85	157	170	169
CGCRC309	Colorectal Cancer	III	Tumor-derived	BRAF	600V>E	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	3.00%	9084	101	157	166	168
CGCRC310	Colorectal Cancer	II	Tumor-derived	KRAS	12G>V	chr12_25398284-25398284_C_A	Substitution	Yes	Yes	0.13%	7393	100	153	165	164
CGCRC310	Colorectal Cancer	II	Tumor-derived	APC	1513E>X	chr5_112175828-112175828_G_T	Substitution	No	Yes	0.11%	11689	100	152	166	164
CGCRC310	Colorectal Cancer	II	Tumor-derived	APC	1521E>X	chr5_112175852-112175852_G_T	Substitution	No	Yes	0.15%	10273	100	153	166	164
CGCRC311	Colorectal Cancer	I	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	No	0.86%	8456	94	160	171	172
CGCRC312	Colorectal Cancer	III	Tumor-derived	APC	960S>X	chr5_112174170-112174170_C_G	Substitution	No	Yes	0.59%	4719	100	160	165	173
CGCRC312	Colorectal Cancer	III	Tumor-derived	NRAS	61Q>K	chr1_115256530-115256530_G_T	Substitution	Yes	Yes	0.47%	3391	101	157	172	170
CGCRC313	Colorectal Cancer	III	Tumor-derived	KRAS	12G>S	chr12_25398285-25398285_C_T	Substitution	Yes	Yes	0.17%	5013	100	163	166	174
CGCRC313	Colorectal Cancer	III	Tumor derived	APC	876R>X	chr5_112173917-112173917_C_T	Substitution	Yes	Yes	0.07%	8150	72	161	171	174
CGCRC314	Colorectal Cancer	I	Tumor-derived	KRAS	12G>D	chr12_25398284-25398284_C_T	Substitution	Yes	Yes	0.30%	4684	100	158	165	169
CGCRC314	Colorectal Cancer	I	Hematopoietic	DNMT3A	738L>Q	chr2_25463280-25463280_A_T	Substitution	No	Yes	2.50%	6902	85	159	165	170
CGCRC314	Colorectal Cancer	I	Tumor-derived	APC	1379E>X	chr5_112175426-112175426_G_T	Substitution	Yes	Yes	0.38%	7229	102	158	167	170
CGCRC315	Colorectal Cancer	III	Tumor-derived	NRAS	12G>D	chr1_115258747-115258747_C_T	Substitution	Yes	Yes	0.27%	8739	94	155	167	169
CGCRC315	Colorectal Cancer	III	Tumor-derived	FBXW7	505R>C	chr4_153247289-153247289_G_A	Substitution	Yes	Yes	0.25%	9623	101	158	166	170

											Wild-type Fragments				
Patient	Patient Type	Stage at Diagnosis	Alteration Type	Gene	Amino Acid (Protein)	Nucleotide	Mutation Type	Hotspot Alteration	Alteration Detected in Tissue	Mutant Allele Fraction	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)
CGCRC316	Colorectal Cancer	III	Tumor-derived	TP53	245G>S	chr17_7577548-7577548_C_T	Substitution	Yes	Yes	6.52%	12880	100	150	166	163
CGCRC316	Colorectal Cancer	III	Tumor-derived	CDKN2A	1M>R	chr9_21974825-21974825_A_C	Substitution	No	Yes	5.74%	7479	93	157	164	168
CGCRC316	Colorectal Cancer	III	Tumor-derived	CTNNB1	37S>C	chr3_41266113-41266113_C_G	Substitution	Yes	Yes	5.47%	13682	100	149	165	162
CGCRC316	Colorectal Cancer	III	Tumor-derived	EGFR	2702-3C>T	chr7_55266407-55266407_C_T	Substitution	No	No	0.11%	16716	85	153	166	166
CGCRC316	Colorectal Cancer	III	Hematopoietic	ATM	3008R>P	chr11_108236087-108236087_G_C	Substitution	No	Yes	0.13%	17060	100	150	166	163
CGCRC317	Colorectal Cancer	III	Tumor-derived	TP53	220Y>C	chr17_7578190-7578190_T_C	Substitution	Yes	Yes	0.36%	14587	84	152	166	164
CGCRC317	Colorectal Cancer	III	Tumor-derived	ATM	1026W>R	chr11_108142132-108142132_T_C	Substitution	No	Yes	0.23%	10483	100	152	164	165
CGCRC317	Colorectal Cancer	III	Tumor-derived	APC	216R>X	chr5_112128143-112128143_C_T	Substitution	Yes	No	0.29%	3497	101	149	166	163
CGCRC318	Colorectal Cancer	I	Hematopoietic	DNMT3A	698W>X	chr2_25463589-25463589_C_T	Substitution	No	Yes	0.25%	16436	98	158	170	170
CGCRC320	Colorectal Cancer	I	Germline	KIT	18L>F	chr4_55524233-55524233_C_T	Substitution	NA	Yes	34.76%	6521	100	163	170	175
CGCRC320	Colorectal Cancer	I	Tumor-derived	ERBB4	78R>W	chr2_212989479-212989479_G_A	Substitution	No	No	0.12%	11633	100	162	174	174
CGCRC321	Colorectal Cancer	I	Tumor-derived	CDKN2A	12S>L	chr9_21974792-21974792_G_A	Substitution	No	No	0.20%	6918	88	161	167	174
CGCRC321	Colorectal Cancer	I	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	No	0.08%	9559	94	159	171	170
CGCRC321	Colorectal Cancer	I	Germline	EGFR	511S>Y	chr7_55229225-55229225_C_A	Substitution	NA	Yes	41.86%	5545	100	159	172	172
CGCRC332	Colorectal Cancer	IV	Tumor-derived	TP53	125T>R	chr17_7579313-7579313_G_C	Substitution	No	Yes	19.98%	605	104	164	170	176
CGCRC333	Colorectal Cancer	IV	Tumor-derived	TP53	673-2A>G	chr17_7577610-7577610_T_C	Substitution	No	Yes	43.03%	1265	89	159	165	171
CGCRC333	Colorectal Cancer	IV	Tumor-derived	BRAF	600V>E	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	22.26%	3338	102	153	165	169
CGCRC333	Colorectal Cancer	IV	Tumor-derived	ERBB4	691E>A	chr2_212495194-212495194_T_G	Substitution	No	No	1.00%	3008	102	153	169	169
CGCRC334	Colorectal Cancer	IV	Tumor-derived	TP53	245G>S	chr17_7577548-7577548_C_T	Substitution	Yes	Yes	13.44%	1725	105	160	170	175
CGCRC334	Colorectal Cancer	IV	Germline	EGFR	638T>M	chr7_55238900-55238900_C_T	Substitution	NA	Yes	35.28%	1168	100	159	164	174
CGCRC334	Colorectal Cancer	IV	Tumor-derived	PIK3CA	104P>R	chr3_178916924-178916924_C_G	Substitution	No	No	3.85%	1798	103	159	166	173
CGCRC335	Colorectal Cancer	IV	Tumor-derived	BRAF	600V>E	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	0.32%	2411	99	155	167	167
CGCRC336	Colorectal Cancer	IV	Tumor-derived	TP53	175R>H	chr17_7578406-7578406_C_T	Substitution	Yes	Yes	75.26%	757	104	156	171	170
CGCRC336	Colorectal Cancer	IV	Tumor-derived	KRAS	12G>V	chr12_25398284-25398284_C_A	Substitution	Yes	Yes	42.87%	1080	102	150	166	167
CGCRC336	Colorectal Cancer	IV	Tumor-derived	APC	1286E>X	chr5_112175147-112175147_G_T	Substitution	No	Yes	81.61%	391	102	161	165	171
CGCRC337	Colorectal Cancer	IV	Tumor-derived	STK11	734+2T>A	chr19_1220718-1220718_T_A	Substitution	No	No	0.12%	6497	72	153	169	177
CGCRC337	Colorectal Cancer	IV	Germline	APC	485M>I	chr5_112162851-112162851_G_A	Substitution	NA	Yes	46.26%	1686	100	147	170	163
CGCRC338	Colorectal Cancer	IV	Tumor-derived	KRAS	12G>D	chr12_25398284-25398284_C_T	Substitution	Yes	Yes	27.03%	1408	105	153	164	166
CGCRC339	Colorectal Cancer	IV	Tumor-derived	KRAS	13G>D	chr12_25398281-25398281_C_T	Substitution	Yes	Yes	1.94%	1256	106	158	168	169
CGCRC339	Colorectal Cancer	IV	Tumor-derived	APC	876R>X	chr5_112173917-112173917_C_T	Substitution	Yes	Yes	2.35%	1639	101	158	165	172
CGCRC339	Colorectal Cancer	IV	Tumor-derived	PIK3CA	407C>F	chr3_178927457-178927457_G_T	Substitution	No	Yes	3.14%	1143	100	154	170	167
CGCRC339	Colorectal Cancer	IV	Tumor-derived	PIK3CA	1047H>L	chr3_178952085-178952085_A_T	Substitution	Yes	Yes	1.71%	1584	108	161	171	173
CGCRC340	Colorectal Cancer	IV	Tumor-derived	TP53	196R>X	chr17_7578263-7578263_G_A	Substitution	Yes	Yes	18.26%	876	101	162	170	175
CGCRC340	Colorectal Cancer	IV	Tumor-derived	APC	1306E>X	chr5_112175207-112175207_G_T	Substitution	Yes	Yes	22.57%	796	105	159	164	174
CGPLBR38	Breast Cancer	I	Tumor-derived	TP53	241S>P	chr17_7577560-7577560_A_G	Substitution	No	Yes	0.53%	9684	95	156	166	168
CGPLBR40	Breast Cancer	III	Germline	AR	392P>R	chrX_66766163-66766163_C_G	Substitution	NA	Yes	28.99%	10277	78	162	168	173
CGPLBR44	Breast Cancer	III	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	Yes	1.82%	10715	99	162	171	173
CGPLBR44	Breast Cancer	III	Hematopoietic	DNMT3A	705I>T	chr2_25463568-25463568_A_G	Substitution	No	Yes	0.41%	10837	100	159	169	171
CGPLBR44	Breast Cancer	III	Tumor-derived	PDGFRA	859V>M	chr4_55153609-55153609_G_A	Substitution	No	Yes	0.13%	12640	100	159	168	171
CGPLBR48	Breast Cancer	II	Germline	ALK	1231R>Q	chr2_29436901-29436901_C_T	Substitution	NA	Yes	34.61%	5631	100	164	170	179
CGPLBR48	Breast Cancer	II	Tumor-derived	EGFR	669R>Q	chr7_55240762-55240762_G_A	Substitution	No	No	0.18%	12467	101	167	174	180
CGPLBR55	Breast Cancer	III	Hematopoietic	DNMT3A	743P>S	chr2_25463266-25463266_G_A	Substitution	No	No	0.18%	10527	101	158	169	169
CGPLBR55	Breast Cancer	III	Tumor-derived	GNAS	201R>H	chr20_57484421-57484421_G_A	Substitution	Yes	Yes	0.68%	6011	101	153	166	167
CGPLBR55	Breast Cancer	III	Tumor-derived	PIK3CA	345N>K	chr3_178921553-178921553_T_A	Substitution	Yes	Yes	0.42%	3973	101	153	166	166
CGPLBR63	Breast Cancer	II	Germline	FGFR3	403K>E	chr4_1806188-1806188_A_G	Substitution	NA	Yes	34.82%	3405	97	165	170	176
CGPLBR67	Breast Cancer	III	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	Yes	0.11%	10259	87	157	168	168
CGPLBR67	Breast Cancer	III	Tumor-derived	PIK3CA	545E>K	chr3_178936091-178936091_G_A	Substitution	Yes	Yes	0.68%	5163	100	151	167	166
CGPLBR67	Breast Cancer	III	Tumor-derived	ERBB4	1000D>A	chr2_212285302-212285302_T_G	Substitution	No	No	0.28%	6250	100	155	166	167
CGPLBR69	Breast Cancer	II	Hematopoietic	DNMT3A	774E>V	chr2_25463172-25463172_T_A	Substitution	No	No	0.29%	7558	100	159	166	170
CGPLBR69	Breast Cancer	II	Germline	CTNNB1	30Y>S	chr3_41266092-41266092_A_C	Substitution	NA	Yes	41.74%	3938	101	154	169	166
CGPLBR69	Breast Cancer	II	Germline	IDH1	231Y>N	chr2_209108158-209108158_A_T	Substitution	NA	Yes	41.66%	2387	101	157	166	168
CGPLBR70	Breast Cancer	II	Tumor-derived	ATM	2832R>H	chr11_108216546-108216546_G_A	Substitution	No	No	0.36%	6916	100	158	171	169
CGPLBR70	Breast Cancer	II	Germline	APC	1577E>D	chr5_112176022-112176022_A_C	Substitution	NA	Yes	40.28%	3580	107	160	169	173
CGPLBR71	Breast Cancer	II	Tumor-derived	TP53	273R>H	chr17_7577120-7577120_C_T	Substitution	Yes	Yes	0.10%	7930	85	156	166	168
CGPLBR72	Breast Cancer	II	Germline	APC	1532D>G	chr5_112175886-112175886_A_G	Substitution	NA	Yes	44.03%	2389	100	157	160	170
CGPLBR73	Breast Cancer	II	Tumor-derived	ALK	708S>P	chr2_29474053-29474053_A_G	Substitution	No	No	0.27%	11348	95	161	173	174
CGPLBR73	Breast Cancer	II	Germline	ERBB4	158A>E	chr2_212652833-212652833_G_T	Substitution	NA	Yes	35.58%	3422	102	157	168	169
CGPLBR74	Breast Cancer	II	Germline	AR	20+1G>T	chrX_66788865-66788865_G_T	Substitution	NA	Yes	36.23%	3784	101	163	175	174
CGPLBR75	Breast Cancer	II	Tumor-derived	PIK3CA	1047H>R	chr3_178952085-178952085_A_G	Substitution	Yes	Yes	0.14%	7290	103	162	173	172
CGPLBR76	Breast Cancer	II	Germline	KDR	1290S>N	chr4_55946310-55946310_C_T	Substitution	NA	Yes	36.57%	4342	104	166	171	179
CGPLBR76	Breast Cancer	II	Tumor-derived	PIK3CA	1047H>R	chr3_178952085-178952085_A_G	Substitution	Yes	Yes	0.12%	11785	100	165	168	177
CGPLBR77	Breast Cancer	III	Tumor-derived	PTEN	170S>I	chr10_89711891-89711891_G_T	Substitution	No	Yes	2.29%	6161	100	158	166	169
CGPLBR80	Breast Cancer	II	Tumor-derived	CDKN2A	12S>L	chr9_21974792-21974792_G_A	Substitution	No	No	0.54%	3643	96	166	166	185
CGPLBR83	Breast Cancer	II	Germline	AR	728N>D	chrX_66937328-66937328_A_G	Substitution	NA	Yes	42.66%	3479	106	162	164	174
CGPLBR83	Breast Cancer	II	Tumor-derived	ATM	322E>K	chr11_108117753-108117753_G_A	Substitution	No	No	0.28%	3496	103	165	170	177
CGPLBR83	Breast Cancer	II	Germline	ERBB4	539Y>S	chr2_212543783-212543783_T_G	Substitution	NA	Yes	44.91%	1748	100	164	173	175
CGPLBR86	Breast Cancer	II	Germline	STK11	354F>L	chr19_1223125-1223125_C_G	Substitution	NA	Yes	42.32%	4241	98	160	168	175

											Wild-type Fragments				
Patient	Patient Type	Stage at Diagnosis	Alteration Type	Gene	Amino Acid (Protein)	Nucleotide	Mutation Type	Hotspot Alteration	Alteration Detected in Tissue	Mutant Allele Fraction	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)
CGPLBR86	Breast Cancer	II	Germline	SMARCB1	795+3A>G	chr22_24159126-24159126_A_G	Substitution	NA	Yes	43.38%	3096	88	160	167	174
CGPLBR87	Breast Cancer	II	Tumor-derived	JAK2	215R>X	chr9_5054591-5054591_C_T	Substitution	No	No	0.35%	3680	101	162	168	175
CGPLBR87	Breast Cancer	II	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	No	0.31%	6180	101	163	164	175
CGPLBR87	Breast Cancer	II	Tumor-derived	SMAD4	496R>C	chr18_48604664-48604664_C_T	Substitution	No	No	0.40%	7746	86	160	167	175
CGPLBR87	Breast Cancer	II	Germline	AR	651S>N	chrX_66931310-66931310_G_A	Substitution	NA	Yes	42.94%	2266	106	160	166	172
CGPLBR88	Breast Cancer	II	Tumor-derived	CDK6	51E>K	chr7_92462487-92462487_C_T	Substitution	No	No	0.13%	17537	89	185	200	223
CGPLBR88	Breast Cancer	II	Germline	APC	1125V>A	chr5_112174665-112174665_T_C	Substitution	NA	Yes	31.19%	5919	101	162	172	173
CGPLBR92	Breast Cancer	II	Tumor-derived	TP53	257L>P	chr17_7577511-7577511_A_G	Substitution	No	Yes	0.20%	15530	77	150	164	162
CGPLBR96	Breast Cancer	II	Tumor-derived	TP53	213R>X	chr17.fa:7578212-7578212_G_A	Substitution	Yes	No	0.10%	9893	100	159	164	171
CGPLBR96	Breast Cancer	II	Hematopoietic	DNMT3A	531D>G	chr2_25467484-25467484_T_C	Substitution	No	Yes	5.81%	8620	95	162	167	173
CGPLBR96	Breast Cancer	II	Tumor-derived	AR	13R>Q	chrX_66765026-66765026_G_A	Substitution	No	No	0.60%	8036	85	162	169	175
CGPLBR97	Breast Cancer	II	Hematopoietic	DNMT3A	882R>H	chr2_25457242-25457242_C_T	Substitution	Yes	Yes	0.11%	14856	93	160	168	170
CGPLBR97	Breast Cancer	II	Germline	PDGFRA	401A>D	chr4_55136880-55136880_C_A	Substitution	NA	Yes	34.12%	5329	100	161	165	171
CGPLBR97	Breast Cancer	II	Tumor-derived	GNAS	201R>H	chr20_57484421-57484421_G_A	Substitution	Yes	Yes	0.13%	7010	97	158	169	170
CGPLLU144	Lung Cancer	II	Tumor-derived	TP53	241S>F	chr17_7577559-7577559_G_A	Substitution	Yes	Yes	1.95%	11371	100	156	165	167
CGPLLU144	Lung Cancer	II	Tumor-derived	KRAS	12G>C	chr12_25398285-25398285_C_A	Substitution	Yes	Yes	5.10%	7641	100	155	167	166
CGPLLU144	Lung Cancer	II	Tumor-derived	EGFR	373P>S	chr7_55224336-55224336_C_T	Substitution	No	Yes	0.16%	9996	100	158	168	169
CGPLLU144	Lung Cancer	II	Tumor-derived	ATM	292P>L	chr11_108115727-108115727_C_T	Substitution	No	No	0.22%	4956	101	159	166	169
CGPLLU144	Lung Cancer	II	Tumor-derived	PIK3CA	545E>K	chr3_178936091-178936091_G_A	Substitution	Yes	Yes	2.94%	6540	100	153	170	166
CGPLLU144	Lung Cancer	II	Tumor-derived	ERBB4	426R>K	chr2_212568841-212568841_C_T	Substitution	No	No	0.18%	7648	101	156	164	166
CGPLLU146	Lung Cancer	II	Hematopoietic	JAK2	617V>F	chr9_5073770-5073770_G_T	Substitution	Yes	No	0.25%	5920	100	155	164	168
CGPLLU146	Lung Cancer	II	Tumor-derived	TP53	282R>P	chr17_7577093-7577093_C_G	Substitution	No	Yes	1.30%	9356	100	155	166	168
CGPLLU146	Lung Cancer	II	Hematopoietic	DNMT3A	737L>H	chr2_25463283-25463283_A_T	Substitution	No	Yes	0.84%	7284	101	158	165	170
CGPLLU146	Lung Cancer	II	Tumor-derived	RB1	861+2T>C	chr13_48937095-48937095_T_C	Substitution	No	Yes	0.87%	4183	103	160	166	170
CGPLLU146	Lung Cancer	II	Tumor-derived	ATM	581L>F	chr11_108122699-108122699_A_T	Substitution	No	No	0.20%	6778	100	157	166	168
CGPLLU147	Lung Cancer	III	Tumor-derived	TP53	248R>Q	chr17_7577538-7577538_C_T	Substitution	Yes	No	0.15%	4807	100	155	166	170
CGPLLU147	Lung Cancer	III	Tumor-derived	TP53	201L>X	chr17_7578247-7578247_A_T	Substitution	No	Yes	0.55%	5282	100	156	167	171
CGPLLU147	Lung Cancer	III	Tumor-derived	ALK	1537G>E	chr2_29416343-29416343_C_T	Substitution	No	Yes	0.94%	7122	100	158	174	173
CGPLLU147	Lung Cancer	III	Germline	PDGFRA	200T>S	chr4_55130065-55130065_C_G	Substitution	NA	Yes	43.47%	2825	101	160	165	173
CGPLLU162	Lung Cancer	II	Tumor-derived	CDKN2A	12S>L	chr9_21974792-21974792_G_A	Substitution	No	No	0.22%	9940	95	161	164	174
CGPLLU162	Lung Cancer	II	Tumor-derived	EGFR	858L>R	chr7_55259515-55259515_T_G	Substitution	Yes	Yes	0.22%	13855	87	160	174	173
CGPLLU162	Lung Cancer	II	Tumor-derived	BRAF	354R>Q	chr7_140494187-140494187_C_T	Substitution	No	No	0.14%	11251	100	153	167	166
CGPLLU163	Lung Cancer	II	Tumor-derived	CDKN2A	12S>L	chr9_21974792-21974792_G_A	Substitution	No	No	0.21%	10805	85	159	165	173
CGPLLU163	Lung Cancer	II	Hematopoietic	DNMT3A	528Y>D	chr2_25467494-25467494_A_C	Substitution	No	Yes	0.15%	20185	83	158	166	170
CGPLLU164	Lung Cancer	II	Tumor-derived	STK11	216S>Y	chr19_1220629-1220629_C_A	Substitution	No	Yes	1.23%	6795	91	156	161	169
CGPLLU164	Lung Cancer	II	Germline	STK11	354F>L	chr19_1223125-1223125_C_G	Substitution	NA	Yes	42.52%	4561	92	157	164	169
CGPLLU164	Lung Cancer	II	Tumor-derived	GNA11	606-3C>T	chr19_3118919-3118919_C_T	Substitution	No	No	0.20%	8097	100	158	170	170
CGPLLU164	Lung Cancer	II	Tumor-derived	TP53	278P>S	chr17_7577106-7577106_G_A	Substitution	Yes	No	0.10%	9241	100	155	165	167
CGPLLU164	Lung Cancer	II	Tumor-derived	TP53	161A>S	chr17_7578449-7578449_C_A	Substitution	No	Yes	1.78%	10806	100	157	168	169
CGPLLU164	Lung Cancer	II	Tumor-derived	TP53	160M>I	chr17_7578450-7578450_C_A	Substitution	No	Yes	1.86%	10919	100	157	168	169
CGPLLU164	Lung Cancer	II	Tumor-derived	ERBB4	1299P>L	chr2_212248371-212248371_G_A	Substitution	No	Yes	0.96%	5412	103	159	175	171
CGPLLU164	Lung Cancer	II	Tumor-derived	ERBB4	253N>S	chr2_212587243-212587243_T_C	Substitution	No	No	0.22%	5151	101	160	166	169
CGPLLU165	Lung Cancer	II	Germline	STK11	354F>L	chr19_1223125-1223125_C_G	Substitution	NA	Yes	36.62%	7448	95	155	167	167
CGPLLU165	Lung Cancer	II	Tumor-derived	GNAS	201R>H	chr20_57484421-57484421_G_A	Substitution	Yes	Yes	0.16%	5822	102	154	166	166
CGPLLU168	Lung Cancer	I	Tumor-derived	TP53	136Q>X	chr17.fa:7578524-7578524_G_A	Substitution	Yes	Yes	0.06%	15985	97	152	165	166
CGPLLU168	Lung Cancer	I	Hematopoietic	DNMT3A	736R>S	chr2_25463287-25463287_G_T	Substitution	No	No	0.39%	11070	100	156	165	168
CGPLLU168	Lung Cancer	I	Tumor-derived	EGFR	858L>R	chr7.fa:55259515-55259515_T_G	Substitution	Yes	Yes	0.07%	11063	83	157	166	169
CGPLLU174	Lung Cancer	I	Tumor-derived	STK11	597+1G>T	chr19_1220505-1220505_G_T	Substitution	No	Yes	0.33%	5881	88	162	165	174
CGPLLU174	Lung Cancer	I	Tumor-derived	JAK2	160D>Y	chr9_5050695-5050695_G_T	Substitution	No	Yes	0.40%	3696	100	162	167	172
CGPLLU174	Lung Cancer	I	Tumor-derived	KRAS	12G>C	chr12_25398285-25398285_C_A	Substitution	Yes	Yes	0.16%	4941	101	162	167	172
CGPLLU174	Lung Cancer	I	Hematopoietic	DNMT3A	891R>W	chr2_25457216-25457216_G_A	Substitution	No	Yes	0.29%	7527	100	163	168	173
CGPLLU174	Lung Cancer	I	Hematopoietic	DNMT3A	715I>M	chr2_25463537-25463537_G_C	Substitution	No	Yes	0.26%	8353	101	162	168	173
CGPLLU175	Lung Cancer	I	Tumor-derived	TP53	179H>R	chr17_7578394-7578394_T_C	Substitution	Yes	Yes	8.03%	10214	100	160	166	170
CGPLLU175	Lung Cancer	I	Hematopoietic	DNMT3A	2598-1G>A	chr2_25457290-25457290_C_T	Substitution	No	No	0.21%	9739	100	157	168	168
CGPLLU175	Lung Cancer	I	Hematopoietic	DNMT3A	755F>L	chr2_25463230-25463230_A_G	Substitution	No	Yes	0.15%	9509	100	157	165	168
CGPLLU175	Lung Cancer	I	Germline	ATM	337R>C	chr11_108117798-108117798_C_T	Substitution	NA	Yes	43.84%	2710	101	157	165	167
CGPLLU175	Lung Cancer	I	Tumor-derived	ERBB4	941Q>X	chr2_212288925-212288925_G_A	Substitution	No	Yes	3.64%	6565	100	158	166	168
CGPLLU176	Lung Cancer	I	Hematopoietic	DNMT3A	750P>S	chr2_25463245-25463245_G_A	Substitution	No	Yes	0.92%	6513	101	164	168	175
CGPLLU176	Lung Cancer	I	Hematopoietic	DNMT3A	735Y>C	chr2_25463289-25463289_T_C	Substitution	No	Yes	0.21%	5962	100	164	174	175
CGPLLU177	Lung Cancer	II	Tumor-derived	KRAS	12G>V	chr12_25398284-25398284_C_A	Substitution	Yes	Yes	2.49%	7044	102	160	165	170
CGPLLU177	Lung Cancer	II	Hematopoietic	DNMT3A	897V>G	chr2_25457197-25457197_A_C	Substitution	No	Yes	1.53%	9950	88	160	169	171
CGPLLU177	Lung Cancer	II	Hematopoietic	DNMT3A	882R>C	chr2_25457243-25457243_G_A	Substitution	Yes	No	0.29%	11233	100	160	168	171
CGPLLU177	Lung Cancer	II	Hematopoietic	DNMT3A	2173+1G>A	chr2_25463508-25463508_C_T	Substitution	No	No	0.13%	10966	75	160	169	172
CGPLLU178	Lung Cancer	I	Tumor-derived	CDH1	251T>M	chr16_68844164-68844164_C_T	Substitution	No	No	0.29%	8378	100	162	176	172
CGPLLU178	Lung Cancer	I	Tumor-derived	PIK3CA	861Q>X	chr3_178947145-178947145_C_T	Substitution	No	No	0.17%	7235	101	159	167	170
CGPLLU179	Lung Cancer	I	Hematopoietic	DNMT3A	879N>D	chr2_25457252-25457252_T_C	Substitution	No	Yes	0.38%	8350	103	161	169	171
CGPLLU179	Lung Cancer	I	Germline	APC	2611T>I	chr5_112179123-112179123_C_T	Substitution	NA	Yes	39.91%	2609	108	162	171	173

Patient	Patient Type	Stage at Diagnosis	Alteration Type	Gene	Amino Acid (Protein)	Nucleotide	Mutation Type	Hotspot Alteration	Alteration Detected in Tissue	Mutant Allele Fraction	Wild-type Fragments				
											Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)
CGPLLU180	Lung Cancer	I	Tumor-derived	STK11	237D>Y	chr19_1220691-1220691_G_T	Substitution	No	Yes	2.43%	6085	91	158	165	170
CGPLLU180	Lung Cancer	I	Tumor-derived	TP53	293G>V	chr17_7577060-7577060_C_A	Substitution	No	Yes	2.07%	6680	92	158	164	169
CGPLLU180	Lung Cancer	I	Tumor-derived	TP53	282R>P	chr17_7577093-7577093_C_G	Substitution	No	Yes	1.94%	7790	92	158	167	168
CGPLLU180	Lung Cancer	I	Tumor-derived	TP53	177P>L	chr17.fa:7578400-7578400_G_A	Substitution	Yes	No	0.08%	9036	101	160	169	171
CGPLLU180	Lung Cancer	I	Tumor-derived	RB1	565S>X	chr13_48955578-48955578_C_G	Substitution	No	Yes	1.01%	4679	100	157	169	168
CGPLLU197	Lung Cancer	I	Hematopoietic	DNMT3A	882R>C	chr2_25457243-25457243_G_A	Substitution	Yes	No	0.16%	7196	102	162	166	172
CGPLLU197	Lung Cancer	I	Hematopoietic	DNMT3A	879N>D	chr2_25457252-25457252_T_C	Substitution	No	No	0.38%	7147	100	161	166	172
CGPLLU198	Lung Cancer	I	Tumor-derived	TP53	162I>N	chr17_7578445-7578445_A_T	Substitution	No	Yes	0.87%	9322	97	157	165	168
CGPLLU198	Lung Cancer	I	Tumor-derived	EGFR	858L>R	chr7_55259515-55259515_T_G	Substitution	Yes	Yes	0.52%	8303	100	160	173	172
CGPLLU202	Lung Cancer	I	Tumor-derived	EGFR	790T>M	chr7.fa:55249071-55249071_C_T	Substitution	Yes	Yes	0.05%	14197	90	151	165	166
CGPLLU202	Lung Cancer	I	Tumor-derived	EGFR	868E>X	chr7_55259544-55259544_G_T	Substitution	No	No	0.13%	9279	51	150	168	167
CGPLLU204	Lung Cancer	I	Tumor-derived	KIT	956R>Q	chr4_55604659-55604659_G_A	Substitution	No	No	0.26%	7185	100	157	165	168
CGPLLU205	Lung Cancer	II	Hematopoietic	DNMT3A	736R>C	chr2_25463287-25463287_G_A	Substitution	No	Yes	0.70%	10739	96	156	165	166
CGPLLU205	Lung Cancer	II	Hematopoietic	DNMT3A	696Q>X	chr2_25463596-25463596_G_A	Substitution	No	Yes	3.47%	12065	100	154	165	165
CGPLLU206	Lung Cancer	III	Tumor-derived	TP53	672+1G>A	chr17_7578176-7578176_C_T	Substitution	Yes	Yes	26.13%	6746	94	148	165	164
CGPLLU206	Lung Cancer	III	Tumor-derived	TP53	131N>S	chr17_7578538-7578538_T_C	Substitution	No	No	0.21%	11225	100	147	167	164
CGPLLU207	Lung Cancer	II	Tumor-derived	TP53	376-1G>A	chr17_7578555-7578555_C_T	Substitution	Yes	Yes	0.32%	11224	100	159	165	170
CGPLLU207	Lung Cancer	II	Germline	ALK	419F>L	chr2_29606625-29606625_A_G	Substitution	NA	Yes	34.58%	4960	101	160	166	170
CGPLLU207	Lung Cancer	II	Tumor-derived	EGFR	790T>M	chr7.fa:55249071-55249071_C_T	Substitution	Yes	No	0.09%	13216	85	161	165	172
CGPLLU208	Lung Cancer	II	Tumor-derived	TP53	250P>L	chr17_7577532-7577532_G_A	Substitution	Yes	Yes	1.33%	9211	101	156	166	168
CGPLLU208	Lung Cancer	II	Germline	EGFR	224R>H	chr7_55220281-55220281_G_A	Substitution	NA	Yes	39.34%	5253	100	159	164	170
CGPLLU208	Lung Cancer	II	Tumor-derived	EGFR	858L>R	chr7_55259515-55259515_T_G	Substitution	Yes	Yes	0.86%	10233	100	160	170	171
CGPLLU208	Lung Cancer	II	Tumor-derived	MYC	98R>W	chr8_128750755-128750755_C_T	Substitution	No	No	0.17%	11421	100	158	165	171
CGPLLU209	Lung Cancer	II	Germline	STK11	354F>L	chr19_1223125-1223125_C_G	Substitution	NA	Yes	26.84%	11695	96	153	166	169
CGPLLU209	Lung Cancer	II	Tumor-derived	TP53	100Q>X	chr17_7579389-7579389_G_A	Substitution	No	Yes	9.97%	12771	94	155	163	168
CGPLLU209	Lung Cancer	II	Tumor-derived	CDKN2A	88E>X	chr9_21971096-21971096_C_A	Substitution	Yes	Yes	9.13%	16557	92	157	169	170
CGPLLU209	Lung Cancer	II	Tumor-derived	PDGFRA	921A>T	chr4_55155052-55155052_G_A	Substitution	No	Yes	9.82%	13057	97	158	167	171
CGPLLU209	Lung Cancer	II	Germline	EGFR	567M>V	chr7_55231493-55231493_A_G	Substitution	NA	Yes	30.41%	8521	100	155	167	169
CGPLOV10	Ovarian Cancer	I	Tumor-derived	TP53	342R>X	chr17_7574003-7574003_G_A	Substitution	Yes	Yes	3.14%	4421	101	161	165	172
CGPLOV11	Ovarian Cancer	IV	Tumor-derived	TP53	248R>Q	chr17_7577538-7577538_C_T	Substitution	Yes	Yes	0.87%	7987	100	157	164	169
CGPLOV11	Ovarian Cancer	IV	Germline	TP53	63A>V	chr17_7579499-7579499_G_A	Substitution	NA	Yes	37.77%	3782	97	160	166	171
CGPLOV13	Ovarian Cancer	IV	Tumor-derived	ALK	444W>C	chr2_29551298-29551298_C_A	Substitution	No	Yes	0.12%	12072	88	157	165	169
CGPLOV13	Ovarian Cancer	IV	Germline	PDGFRA	401A>D	chr4_55136880-55136880_C_A	Substitution	NA	Yes	37.98%	4107	103	159	166	169
CGPLOV13	Ovarian Cancer	IV	Tumor-derived	KIT	135R>H	chr4_55564516-55564516_G_A	Substitution	No	Yes	0.35%	8427	100	161	165	171
CGPLOV14	Ovarian Cancer	I	Tumor-derived	HNF1A	230E>K	chr12_121431484-121431484_G_A	Substitution	No	No	0.14%	11418	92	154	167	171
CGPLOV15	Ovarian Cancer	III	Tumor-derived	TP53	278P>S	chr17_7577106-7577106_G_A	Substitution	Yes	Yes	3.54%	7689	102	157	164	169
CGPLOV15	Ovarian Cancer	III	Tumor-derived	EGFR	433H>D	chr7_55225445-55225445_C_G	Substitution	No	No	0.19%	7617	101	159	167	171
CGPLOV17	Ovarian Cancer	I	Tumor-derived	TP53	248R>Q	chr17_7577538-7577538_C_T	Substitution	Yes	Yes	0.32%	4463	96	156	168	169
CGPLOV17	Ovarian Cancer	I	Germline	PDGFRA	1071D>N	chr4_55161380-55161380_G_A	Substitution	NA	Yes	44.10%	2884	110	157	170	170
CGPLOV18	Ovarian Cancer	I	Germline	APC	1125V>A	chr5_112174665-112174665_T_C	Substitution	NA	Yes	40.81%	2945	101	159	164	169
CGPLOV19	Ovarian Cancer	II	Germline	FGFR3	403K>E	chr4_1806188-1806188_A_G	Substitution	NA	Yes	23.80%	9727	95	158	167	172
CGPLOV19	Ovarian Cancer	II	Tumor-derived	TP53	273R>H	chr17_7577120-7577120_C_T	Substitution	Yes	Yes	36.83%	4387	100	158	165	169
CGPLOV19	Ovarian Cancer	II	Germline	AR	176S>R	chrX_66765516-66765516_C_A	Substitution	NA	Yes	65.29%	2775	93	161	171	171
CGPLOV19	Ovarian Cancer	II	Tumor-derived	APC	1378Q>X	chr5_112175423-112175423_C_T	Substitution	Yes	Yes	46.35%	3818	102	156	170	170
CGPLOV20	Ovarian Cancer	II	Tumor-derived	TP53	195I>T	chr17_7578265-7578265_A_G	Substitution	Yes	Yes	0.21%	5404	94	159	165	170
CGPLOV20	Ovarian Cancer	II	Germline	EGFR	253K>R	chr7_55221714-55221714_A_G	Substitution	NA	Yes	44.05%	3744	102	158	166	169
CGPLOV21	Ovarian Cancer	IV	Germline	STK11	354F>L	chr19_1223125-1223125_C_G	Substitution	NA	Yes	7.68%	21823	81	158	166	169
CGPLOV21	Ovarian Cancer	IV	Tumor-derived	TP53	275C>Y	chr17_7577114-7577114_C_T	Substitution	No	Yes	2.04%	18806	101	159	165	169
CGPLOV21	Ovarian Cancer	IV	Tumor-derived	ERBB4	602S>T	chr2_212530114-212530114_C_G	Substitution	No	No	14.36%	10801	89	160	166	169
CGPLOV22	Ovarian Cancer	III	Tumor-derived	TP53	193H>P	chr17_7578271-7578271_T_G	Substitution	No	Yes	0.49%	11952	100	155	165	167
CGPLOV22	Ovarian Cancer	III	Tumor-derived	CTNNB1	41T>A	chr3_41266124-41266124_A_G	Substitution	Yes	Yes	0.34%	12399	92	150	165	164

			Mutant Fragments										
Mean cfDNA Fragment Size (bp)	75th Percentile cfDNA Fragment Size (bp)	Maximum cfDNA Fragment Size (bp)	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)	Mean cfDNA Fragment Size (bp)	75th Percentile cfDNA Fragment Size (bp)	Maximum cfDNA Fragment Size (bp)	Difference between Median Mutant and Wild-type cfDNA Fragment Sizes (bp)	Difference between Mean Mutant and Wild-type cfDNA Fragment Sizes (bp)	Adjusted P Value of Difference between Mutant and Wild-type cfDNA Fragment Sizes
179	186	400	19	100	142	233	165	180	230	305	-4.0	1.54	0.475
182	185	400	21	132	166	182	176	191	198	309	7.0	8.33	0.250
180	183	400	5411	92	152	167	169	186	191	399	0.0	5.89	0.000
177	182	400	1903	100	148	166	166	177	183	383	-1.0	-0.25	0.874
184	185	400	1344	108	155	167	170	189	191	398	1.0	5.37	0.009
181	182	400	2108	100	153	166	168	185	187	386	1.0	3.80	0.025
176	180	400	1951	101	149	175	167	179	182	397	0.0	2.65	0.148
176	183	399	75	123	162	167	172	182	190	370	3.0	5.31	0.368
177	182	400	28	101	130	130	139	164	155	345	-29.5	-12.79	0.000
183	188	399	6863	100	160	168	173	186	189	400	2.0	3.13	0.002
188	186	400	34	77	154	171	170	177	192	335	-0.5	-11.46	0.571
175	179	396	9	138	147	176	171	177	176	290	4.0	1.22	0.475
184	185	400	21	115	145	155	159	176	175	368	-11.0	-7.99	0.052
179	185	397	30	137	149	181	162	182	181	369	-8.0	3.49	0.061
179	182	397	44	125	155	155	169	185	194	338	0.0	5.78	0.623
185	188	400	8167	101	160	166	171	184	187	400	-1.0	-1.27	0.212
187	188	400	3562	102	158	168	170	185	185	399	0.0	-2.62	0.114
184	187	399	15	93	137	127	174	173	193	261	3.0	-11.00	0.507
183	185	400	26	137	163	166	167	179	180	364	-3.0	-4.34	0.430
181	182	397	35	118	147	176	163	172	176	336	-6.0	-9.35	0.166
172	175	400	71	133	152	170	165	169	173	301	0.0	-3.57	0.668
169	174	400	55	130	153	165	164	166	168	325	0.0	-2.15	0.630
189	187	399	17	149	155	326	170	221	301	387	-3.0	32.43	0.453
176	183	400	18	156	170	174	174	210	219	372	5.0	33.84	0.368
169	175	397	51	108	143	268	152	164	178	268	-12.0	-5.12	0.000
166	173	397	26	118	147	153	156	174	168	327	-9.5	8.37	0.036
184	186	400	45	116	151	168	163	175	177	346	-8.0	-8.84	0.057
185	186	400	25	157	165	191	175	207	199	350	3.0	22.93	0.465
185	187	400	25	124	168	180	180	189	191	338	8.0	4.06	0.154
167	175	394	86	121	155	169	166	168	175	309	2.0	0.46	0.445
167	173	397	45	124	143	197	162	166	168	377	-1.0	-0.91	0.482
170	175	398	108	126	147	162	162	164	174	302	-3.0	-6.74	0.064
190	189	400	23	131	148	145	166	189	205	333	-5.0	-0.80	0.297
182	182	399	42	138	155	155	174	177	187	343	5.5	-4.51	0.171
189	187	399	25	126	153	176	176	188	229	305	7.0	-0.19	0.234
192	193	400	977	101	149	189	170	182	192	380	-1.0	-9.76	0.000
173	179	391	525	102	140	168	159	168	176	382	-7.0	-5.57	0.052
181	185	399	4010	100	158	166	170	181	185	398	0.0	0.37	0.770
178	184	399	625	100	140	167	162	172	181	380	-9.0	-6.68	0.009
175	179	398	37	111	143	142	166	172	186	321	-1.0	-2.38	0.572
181	186	396	3184	102	159	168	172	182	187	400	0.5	0.95	0.564
180	183	399	47	111	148	144	169	176	183	353	-1.0	-4.83	0.598
183	184	397	39	111	146	182	162	182	185	337	-7.0	-0.44	0.064
185	184	400	24	110	146	309	182	208	284	355	14.0	22.31	0.031
176	180	400	32	117	146	154	157	167	166	298	-11.0	-8.94	0.013
180	184	399	43	111	143	144	177	187	212	319	9.0	7.22	0.062
185	187	400	29	109	140	204	159	188	204	387	-12.0	3.32	0.031
179	182	399	20	128	152	180	163	166	180	219	-6.5	-13.04	0.155
176	184	398	7515	101	160	170	171	177	185	400	1.0	1.08	0.166
182	182	399	31	85	146	137	166	167	176	316	-3.0	-14.62	0.469
181	182	395	428	100	135	138	149	158	166	340	-20.0	-23.47	0.000
175	180	397	352	97	136	132	147	149	159	326	-21.0	-26.04	0.000
165	172	397	15	131	137	132	144	163	171	323	-20.0	-1.73	0.000
170	173	398	25	107	138	159	161	175	190	299	-3.0	4.83	0.384
171	173	400	27	122	147	161	161	173	171	342	-3.0	2.54	0.354
189	189	400	91	112	165	168	173	196	192	379	1.0	6.83	0.571
189	189	400	27	124	144	154	154	167	172	320	-19.0	-22.39	0.000
178	184	399	24	105	143	132	159	183	190	367	-11.0	4.67	0.054
188	189	399	8	122	143	122	161	168	195	241	-13.0	-19.21	0.100
194	192	400	17	144	163	173	173	213	261	372	-1.0	19.22	0.587
180	183	394	15	132	159	186	166	174	185	265	-3.0	-5.62	0.461
183	185	399	233	131	162	167	172	190	187	394	2.0	7.27	0.137
186	186	398	27	136	155	183	163	170	178	262	-7.0	-16.03	0.131
192	195	399	23	137	144	175	152	190	212	327	-17.0	-1.78	0.018
182	184	399	29	131	157	177	171	183	179	319	1.0	0.74	0.564

			Mutant Fragments								Difference between Median Mutant and Wild-type cfDNA Fragment Sizes (bp)	Difference between Mean Mutant and Wild-type cfDNA Fragment Sizes (bp)	Adjusted P Value of Difference between Mutant and Wild-type cfDNA Fragment Sizes
Mean cfDNA Fragment Size (bp)	75th Percentile cfDNA Fragment Size (bp)	Maximum cfDNA Fragment Size (bp)	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)	Mean cfDNA Fragment Size (bp)	75th Percentile cfDNA Fragment Size (bp)	Maximum cfDNA Fragment Size (bp)			
166	172	396	1616	100	146	164	159	163	170	354	-3.5	-3.57	0.000
175	180	400	806	96	158	169	169	179	184	366	1.0	3.80	0.054
165	172	399	1410	102	140	149	154	164	170	398	-8.0	-0.35	0.816
170	177	397	49	99	153	143	182	206	284	333	16.0	36.25	0.000
166	173	398	33	140	155	154	170	180	180	296	7.0	14.38	0.104
180	178	400	73	95	140	140	155	173	178	324	-9.0	-6.66	0.000
172	177	400	38	115	160	164	167	182	179	329	1.5	10.09	0.479
171	174	386	6	124	137	170	156	153	168	178	-7.5	-18.98	0.411
180	183	400	70	124	151	151	164	182	183	385	-6.0	1.71	0.064
194	199	399	6586	96	162	168	175	193	196	399	0.0	-1.79	0.166
184	188	400	41	112	172	176	177	195	195	373	3.0	11.02	0.397
194	198	399	35	149	168	175	175	181	186	312	1.0	-13.40	0.587
182	184	399	20	166	180	185	191	205	219	357	21.0	23.48	0.013
183	186	397	5338	102	159	175	171	183	185	394	-1.0	0.03	0.984
202	203	393	178	101	150	168	171	198	240	357	-5.0	-4.34	0.571
195	195	397	1350	104	153	163	171	201	258	400	0.0	5.94	0.066
185	189	400	1257	100	153	168	170	189	202	392	1.0	4.37	0.064
185	189	396	30	117	163	164	172	175	179	372	3.0	-10.29	0.463
203	210	391	336	105	153	141	171	200	240	399	-4.0	-3.10	0.571
188	194	399	741	101	161	169	176	190	194	400	2.0	1.96	0.571
193	193	396	89	100	145	171	171	197	229	393	-2.0	3.42	0.479
172	179	396	12	129	143	143	153	163	166	275	-14.0	-8.99	0.084
186	188	387	3559	91	155	164	173	195	211	398	3.0	8.92	0.001
177	183	392	873	102	149	163	164	177	181	400	-3.0	-0.39	0.880
194	200	377	1909	100	158	167	176	202	242	398	5.0	7.98	0.061
202	259	400	27	122	157	164	179	199	231	350	2.0	-3.82	0.685
171	178	395	1818	103	147	169	162	173	180	396	-1.0	1.92	0.372
178	182	374	546	102	151	166	166	180	182	381	0.0	2.87	0.416
179	184	397	26	132	142	138	171	183	188	351	1.5	3.29	0.572
195	194	400	53	117	157	166	169	192	198	336	-3.0	-2.86	0.451
176	179	397	40	124	150	169	166	181	176	309	-1.0	4.53	0.539
188	191	390	38	107	153	180	174	185	210	326	0.5	-2.59	0.576
205	207	399	217	102	146	144	163	188	212	360	-12.0	-17.11	0.004
196	195	397	266	111	147	150	166	188	204	379	-8.0	-7.53	0.208
186	184	400	76	123	157	171	169	182	182	346	1.0	-3.64	0.479
179	186	400	9832	93	161	166	172	180	186	399	-1.0	1.04	0.155
191	190	400	277	104	162	160	176	201	200	384	3.0	9.95	0.061
191	189	400	65	123	165	166	172	198	192	371	1.0	7.08	0.560
187	189	400	31	136	163	171	167	201	199	387	-4.0	14.14	0.341
202	202	400	5286	102	166	168	181	201	203	400	2.0	-0.88	0.587
196	201	400	102	138	166	161	179	199	209	372	-1.5	2.90	0.679
181	182	397	30	138	158	189	185	191	191	311	16.0	9.25	0.000
181	181	400	64	113	158	163	167	179	176	318	0.0	-2.85	0.679
176	179	398	27	121	163	200	171	187	190	392	5.0	10.89	0.314
191	192	398	2943	100	165	176	176	187	192	398	0.0	-3.83	0.015
179	181	399	25	138	153	138	167	181	184	340	-1.0	2.00	0.571
171	177	399	60	110	136	147	147	161	159	327	-19.0	-9.77	0.000
172	179	399	26	139	147	180	176	176	184	344	9.0	3.52	0.015
186	184	398	35	121	149	360	161	197	195	360	-9.0	10.77	0.314
176	178	397	4000	103	155	166	167	176	178	397	0.5	0.65	0.610
176	178	385	2390	99	157	164	168	178	180	400	0.0	1.78	0.314
182	184	400	28	131	160	168	167	177	179	338	-2.0	-5.83	0.463
194	193	400	3545	100	161	169	173	194	192	399	0.0	0.40	0.825
179	180	398	15	121	146	166	166	172	204	221	-2.0	-7.32	0.564
188	187	400	2587	103	158	162	169	189	186	399	-1.0	1.12	0.598
189	192	400	86	121	165	183	177	189	193	373	3.0	-0.01	0.293
178	184	399	3339	101	157	165	169	177	184	400	0.0	-1.73	0.598
179	187	391	3193	101	163	178	173	180	186	389	-1.0	0.22	0.839
183	186	398	13	111	153	153	161	171	179	323	-11.0	-12.36	0.061
197	201	400	4140	102	166	169	179	197	200	400	0.0	-0.32	0.839
191	194	400	16	130	143	143	157	173	173	325	-20.0	-18.40	0.000
183	183	400	209	125	154	175	170	196	233	357	1.0	12.55	0.025
211	230	400	41	158	176	197	186	215	220	374	1.0	3.72	0.603
193	193	400	3445	94	162	175	174	194	194	399	0.0	0.65	0.714
197	199	400	23	123	182	248	224	232	260	359	47.0	34.97	0.000
193	195	399	1787	100	163	163	176	192	194	400	1.0	-0.85	0.718
204	207	400	4100	100	159	164	173	200	202	400	-2.0	-3.65	0.062

			Mutant Fragments										
Mean cfDNA Fragment Size (bp)	75th Percentile cfDNA Fragment Size (bp)	Maximum cfDNA Fragment Size (bp)	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)	Mean cfDNA Fragment Size (bp)	75th Percentile cfDNA Fragment Size (bp)	Maximum cfDNA Fragment Size (bp)	Difference between Median Mutant and Wild-type cfDNA Fragment Sizes (bp)	Difference between Mean Mutant and Wild-type cfDNA Fragment Sizes (bp)	Adjusted P Value of Difference between Mutant and Wild-type cfDNA Fragment Sizes
196	195	400	3096	79	159	161	173	194	191	397	-1.0	-2.45	0.251
202	203	400	73	142	178	178	184	237	338	377	9.0	35.30	0.114
205	203	400	23	161	168	168	171	189	186	380	-4.0	-16.38	0.435
195	196	400	170	125	158	173	173	188	190	400	-2.0	-6.17	0.293
195	192	400	2089	101	162	169	176	203	203	400	4.5	8.80	0.000
238	280	400	125	84	192	194	207	243	324	400	-16.0	5.51	0.574
197	194	400	5715	108	163	164	174	200	196	400	1.0	2.87	0.065
172	173	398	109	78	148	149	158	166	173	302	-4.0	-5.94	0.190
196	191	399	35	119	161	172	171	191	180	390	0.0	-4.34	0.627
189	190	400	826	102	162	166	171	187	187	395	-2.0	-1.94	0.475
194	195	400	95	135	160	161	170	182	184	400	-5.0	-11.54	0.155
184	184	400	27	128	150	150	169	174	185	319	-1.0	-9.68	0.571
179	184	399	4771	103	161	168	171	179	183	400	0.0	0.15	0.880
187	185	399	7	147	154	154	167	164	174	177	-3.0	-22.90	0.155
179	179	395	330	106	152	166	166	178	178	361	-1.0	-1.35	0.685
172	177	399	536	106	151	167	163	172	175	363	-3.0	-0.34	0.880
179	183	400	45	138	163	175	172	185	191	380	3.0	6.52	0.368
182	182	397	16	138	146	146	155	162	170	224	-14.0	-19.82	0.007
172	177	397	293	101	152	169	164	170	174	392	-2.0	-1.37	0.646
171	177	399	23	130	152	162	162	163	177	232	-4.0	-7.62	0.252
180	183	399	54	104	161	154	176	195	206	383	7.5	14.58	0.064
184	184	400	154	96	149	157	163	176	185	347	-5.5	-7.87	0.154
186	187	399	79	102	163	177	174	200	203	372	4.0	14.61	0.270
183	185	400	44	118	149	163	163	185	188	338	-7.0	1.98	0.039
182	184	400	35	136	164	204	181	194	203	369	13.0	11.80	0.039
192	191	400	13	138	164	169	169	198	173	333	-1.0	6.05	0.610
199	205	400	50	128	155	161	171	216	301	360	0.0	17.02	0.623
191	193	400	81	108	150	108	173	198	224	385	0.0	6.48	0.624
190	191	389	2597	101	159	165	172	185	187	397	-1.0	-5.17	0.005
192	197	400	58	92	173	192	192	202	200	397	18.0	9.79	0.007
183	189	400	74	90	147	142	167	176	182	391	-6.5	-6.78	0.061
175	178	400	37	144	163	185	172	192	186	375	6.0	17.15	0.005
194	202	400	61	93	164	181	181	197	211	370	8.0	3.34	0.169
184	186	400	66	104	158	194	174	189	194	379	3.5	4.60	0.270
191	190	396	101	126	155	176	176	194	213	331	7.0	2.50	0.718
188	185	394	4718	100	156	164	168	190	187	393	-1.0	2.54	0.113
186	186	399	30	134	161	175	175	190	208	339	5.0	4.07	0.302
180	180	397	34	139	163	165	170	178	175	349	3.0	-1.65	0.407
182	182	400	262	101	150	152	165	181	186	393	-4.0	-0.65	0.876
182	182	400	277	101	150	147	166	182	185	393	-3.0	0.36	0.926
180	182	395	65	121	158	161	167	186	188	338	-4.0	6.15	0.234
177	182	400	16	144	172	179	179	187	180	376	10.0	9.98	0.130
185	184	399	7186	100	154	167	166	183	181	396	-1.0	-1.73	0.154
181	179	394	21	108	164	164	173	196	200	357	7.0	14.95	0.213
177	180	400	18	111	127	127	158	189	186	352	-8.0	12.47	0.179
179	181	400	72	121	156	173	166	183	179	396	-2.0	4.31	0.427
177	182	400	30	106	160	174	174	180	186	282	5.0	3.09	0.252
200	199	399	36	131	147	143	177	196	227	298	2.5	-4.24	0.479
184	185	392	20	144	173	266	178	199	215	269	6.0	15.13	0.252
182	184	395	16	147	156	156	164	177	169	302	-8.0	-4.82	0.119
186	187	399	34	159	168	168	176	206	196	365	3.0	20.55	0.415
186	186	396	5	116	182	182	185	201	192	329	12.0	14.62	0.263
185	183	399	1073	100	142	164	152	157	164	346	-18.0	-27.67	0.000
179	180	400	46	109	151	143	175	174	183	325	7.0	-5.22	0.054
181	181	400	30	146	154	146	168	186	181	367	-0.5	5.19	0.568
176	179	392	2742	102	154	164	166	176	178	387	-1.0	-0.24	0.874
174	180	399	298	103	140	148	150	152	162	288	-18.0	-22.25	0.000
197	194	399	67	115	164	250	173	187	201	366	-2.0	-9.89	0.425
195	194	399	19	156	165	165	185	197	199	361	10.0	2.20	0.154
178	182	395	189	105	138	141	150	164	175	348	-20.0	-14.58	0.000
183	185	398	227	123	160	168	169	185	184	396	-2.0	1.68	0.706
185	184	397	53	78	161	175	175	189	188	392	4.0	3.80	0.241
190	188	395	50	130	161	168	168	184	175	377	-4.5	-5.86	0.234
186	187	398	28	139	150	173	170	170	173	354	-2.5	-15.68	0.416
179	184	400	24	130	153	176	170	193	199	359	0.0	13.13	0.598
185	185	394	48	111	154	170	168	173	183	295	-3.0	-11.80	0.270
189	187	398	2337	100	163	166	172	187	185	394	-1.0	-1.27	0.564

			Mutant Fragments										
Mean cfDNA Fragment Size (bp)	75th Percentile cfDNA Fragment Size (bp)	Maximum cfDNA Fragment Size (bp)	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)	Mean cfDNA Fragment Size (bp)	75th Percentile cfDNA Fragment Size (bp)	Maximum cfDNA Fragment Size (bp)	Difference between Median Mutant and Wild-type cfDNA Fragment Sizes (bp)	Difference between Mean Mutant and Wild-type cfDNA Fragment Sizes (bp)	Adjusted P Value of Difference between Mutant and Wild-type cfDNA Fragment Sizes
198	200	398	172	83	152	160	166	193	226	396	-4.0	-4.93	0.490
190	188	400	215	123	151	159	163	186	196	365	-6.0	-1.72	0.735
184	184	400	207	121	151	157	161	181	179	365	-7.0	-3.01	0.571
191	189	397	17	143	170	217	214	198	217	294	43.0	7.08	0.000
181	182	398	52	122	152	167	164	179	173	372	-4.5	-2.07	0.137
191	189	399	17	109	161	173	171	181	174	293	-1.0	-9.24	0.576
191	189	399	40	136	164	166	171	185	185	335	-1.0	-5.86	0.571
180	181	399	127	88	149	131	162	168	176	311	-6.0	-11.80	0.005
181	186	400	68	141	166	175	176	198	207	387	4.0	17.11	0.184
169	179	398	10	81	167	167	167	159	176	182	1.0	-10.20	0.589
170	181	398	33	107	162	167	167	174	185	322	0.0	4.57	0.636
175	181	391	23	112	156	190	164	175	190	349	-4.0	-0.92	0.308
175	177	400	109	130	153	169	166	175	178	382	0.0	-0.09	0.987
172	176	400	684	105	153	167	166	172	175	385	1.0	0.00	0.999
179	178	398	2946	100	138	157	155	172	174	398	-9.0	-7.28	0.000
175	178	399	30	121	165	165	176	198	219	325	12.0	22.37	0.007
187	186	400	63	140	155	154	167	201	215	372	-3.0	13.70	0.286
181	184	400	4754	101	160	170	170	179	181	393	0.0	-1.72	0.154
182	187	400	31	131	162	162	174	180	185	352	2.0	-2.26	0.494
181	183	400	150	110	144	166	162	176	173	385	-6.0	-5.86	0.314
179	184	400	5290	95	159	167	169	179	184	400	-1.0	0.11	0.909
181	186	400	140	101	155	175	167	179	180	352	-4.5	-2.77	0.589
187	190	397	20	92	141	241	168	178	209	283	-3.0	-9.82	0.479
190	192	400	8065	85	156	164	169	190	190	399	0.0	-0.08	0.942
174	182	400	2586	101	147	165	165	169	179	386	-3.5	-4.59	0.000
185	188	400	2808	100	150	158	167	189	200	399	-3.0	4.17	0.007
182	187	400	2227	100	154	162	171	183	190	398	0.0	1.00	0.564
176	183	396	8425	100	155	165	169	176	184	400	0.0	0.54	0.568
186	188	399	142	112	146	140	159	180	193	352	-13.0	-5.41	0.463
186	185	399	104	132	158	159	167	189	180	331	-2.0	3.05	0.657
183	185	392	3462	101	160	173	172	184	187	396	1.0	0.82	0.576
182	183	399	25	94	140	140	158	159	163	341	-11.0	-23.47	0.027
177	181	399	3789	101	159	168	169	176	181	395	0.0	-0.66	0.576
181	184	400	57	131	152	170	170	179	184	327	-1.0	-2.41	0.568
183	191	400	36	118	154	201	182	187	201	328	11.0	3.60	0.114
187	185	399	362	110	152	143	180	207	268	389	11.0	20.70	0.000
182	188	400	20	158	163	311	174	198	209	311	3.0	15.25	0.475
186	187	397	23	126	151	184	168	185	185	328	-1.0	-1.49	0.571
188	189	400	2980	100	158	169	170	187	189	398	0.0	-0.84	0.637
183	183	391	2793	91	158	167	170	181	182	389	1.0	-2.30	0.171
185	189	395	7357	100	158	175	171	182	187	399	-1.0	-2.37	0.008
184	184	398	5186	101	157	165	170	185	186	400	1.0	1.72	0.240
182	187	400	15595	64	159	167	170	181	185	397	-1.0	-1.39	0.245
186	185	400	6749	101	158	167	170	185	187	400	0.0	-0.52	0.702
193	190	400	23	127	148	148	194	222	292	378	24.0	29.58	0.027
182	185	394	3901	101	160	167	171	182	185	398	2.0	0.32	0.821
179	180	400	4633	100	158	169	170	185	187	400	1.0	6.16	0.000
175	179	400	734	101	151	155	165	176	178	366	-4.0	0.48	0.823
175	180	394	4022	101	159	167	168	172	178	399	-1.0	-2.84	0.000
184	182	400	117	116	156	156	172	199	184	399	5.0	15.08	0.084
172	176	395	65	109	145	177	167	181	181	306	3.0	9.11	0.293

APPENDIX - D: Table 4. Summary of whole genome cfDNA analyses

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGCRC291	Preoperative treatment naïve	WGS	Colorectal Cancer	100	7232125000	4695396600	1.86
CGCRC292	Preoperative treatment naïve	WGS	Colorectal Cancer	100	6794092800	4471065400	1.77
CGCRC293	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8373899600	5686176000	2.26
CGCRC294	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8081312000	5347045800	2.12
CGCRC296	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10072029200	6770998200	2.69
CGCRC299	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10971591600	7632723200	3.03
CGCRC300	Preoperative treatment naïve	WGS	Colorectal Cancer	100	9894332600	6699951000	2.66
CGCRC301	Preoperative treatment naïve	WGS	Colorectal Cancer	100	7857346200	5021002000	1.99
CGCRC302	Preoperative treatment naïve	WGS	Colorectal Cancer	100	11671913000	8335275800	3.31
CGCRC304	Preoperative treatment naïve	WGS	Colorectal Cancer	100	19011739200	12957614200	5.14
CGCRC305	Preoperative treatment naïve	WGS	Colorectal Cancer	100	7177341400	4809957200	1.91
CGCRC306	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8302233200	5608043600	2.23
CGCRC307	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8034729400	5342620000	2.12
CGCRC308	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8670084800	5934037200	2.35
CGCRC311	Preoperative treatment naïve	WGS	Colorectal Cancer	100	6947634400	4704601800	1.87
CGCRC315	Preoperative treatment naïve	WGS	Colorectal Cancer	100	5205544000	3419565400	1.36
CGCRC316	Preoperative treatment naïve	WGS	Colorectal Cancer	100	6405388600	4447534800	1.76
CGCRC317	Preoperative treatment naïve	WGS	Colorectal Cancer	100	6060390400	4104616600	1.63
CGCRC318	Preoperative treatment naïve	WGS	Colorectal Cancer	100	6848768600	4439404800	1.76
CGCRC319	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10545294400	7355181600	2.92
CGCRC320	Preoperative treatment naïve	WGS	Colorectal Cancer	100	5961999200	3945054000	1.57
CGCRC321	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8248095400	5614355000	2.23
CGCRC333	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10540267600	6915490600	2.74
CGCRC336	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10675581800	7087691800	2.81
CGCRC338	Preoperative treatment naïve	WGS	Colorectal Cancer	100	13788172600	8970308600	3.56
CGCRC341	Preoperative treatment naïve	WGS	Colorectal Cancer	100	10753467600	7311539200	2.90
CGCRC342	Preoperative treatment naïve	WGS	Colorectal Cancer	100	11836966000	7552793200	3.00
CGH14	Human adult elutriated lymphocytes	WGS	Healthy	100	36525427600	24950300200	9.90
CGH15	Human adult elutriated lymphocytes	WGS	Healthy	100	29930855000	23754049400	9.43
CGLU316	Pre-treatment, Day -53	WGS	Lung Cancer	100	10354123200	6896471400	2.74
CGLU316	Pre-treatment, Day -4	WGS	Lung Cancer	100	7870039200	5254938800	2.09
CGLU316	Post-treatment, Day 18	WGS	Lung Cancer	100	8155322000	5416262400	2.15
CGLU316	Post-treatment, Day 87	WGS	Lung Cancer	100	9442310400	6087893400	2.42
CGLU344	Pre-treatment, Day -21	WGS	Lung Cancer	100	8728318600	5769097200	2.29
CGLU344	Pre-treatment, Day 0	WGS	Lung Cancer	100	11710249400	7826902600	3.11
CGLU344	Post-treatment, Day 0.1875	WGS	Lung Cancer	100	11569683000	7654701600	3.04
CGLU344	Post-treatment, Day 59	WGS	Lung Cancer	100	11042459200	6320138800	2.51
CGLU369	Pre-treatment, Day -2	WGS	Lung Cancer	100	8630932800	5779595800	2.29
CGLU369	Post-treatment, Day 12	WGS	Lung Cancer	100	9227709600	6136755200	2.44
CGLU369	Post-treatment, Day 68	WGS	Lung Cancer	100	7995282600	5239077200	2.08
CGLU369	Post-treatment, Day 110	WGS	Lung Cancer	100	8750541000	5626139000	2.23
CGLU373	Pre-treatment, Day -2	WGS	Lung Cancer	100	11746059600	7547485800	3.00
CGLU373	Post-treatment, Day 0.125	WGS	Lung Cancer	100	13801136800	9255579400	3.67
CGLU373	Post-treatment, Day 7	WGS	Lung Cancer	100	11537896800	7654111200	3.04
CGLU373	Post-treatment, Day 47	WGS	Lung Cancer	100	8046326400	5397702400	2.14
CGPLBR100	Preoperative treatment naïve	WGS	Breast Cancer	100	8440532400	5729474800	2.27
CGPLBR101	Preoperative treatment naïve	WGS	Breast Cancer	100	9786253600	6673495200	2.65
CGPLBR102	Preoperative treatment naïve	WGS	Breast Cancer	100	8664980400	5669781600	2.25
CGPLBR103	Preoperative treatment naïve	WGS	Breast Cancer	100	9846936200	6662883400	2.64
CGPLBR104	Preoperative treatment naïve	WGS	Breast Cancer	100	9443375400	6497061000	2.58
CGPLBR12	Preoperative treatment naïve	WGS	Breast Cancer	100	7017577800	4823327400	1.91
CGPLBR18	Preoperative treatment naïve	WGS	Breast Cancer	100	10309652800	7130386000	2.83
CGPLBR23	Preoperative treatment naïve	WGS	Breast Cancer	100	9034484800	6219625800	2.47
CGPLBR24	Preoperative treatment naïve	WGS	Breast Cancer	100	9891454200	6601857400	2.62
CGPLBR28	Preoperative treatment naïve	WGS	Breast Cancer	100	7997607200	5400803200	2.14
CGPLBR30	Preoperative treatment naïve	WGS	Breast Cancer	100	8502597200	5885822400	2.34
CGPLBR31	Preoperative treatment naïve	WGS	Breast Cancer	100	12660085600	8551995600	3.39
CGPLBR32	Preoperative treatment naïve	WGS	Breast Cancer	100	8773498600	5839034600	2.32
CGPLBR33	Preoperative treatment naïve	WGS	Breast Cancer	100	10931742800	6967030600	2.76
CGPLBR34	Preoperative treatment naïve	WGS	Breast Cancer	100	10861398600	7453225800	2.96
CGPLBR35	Preoperative treatment naïve	WGS	Breast Cancer	100	9180193600	6158440200	2.44
CGPLBR36	Preoperative treatment naïve	WGS	Breast Cancer	100	9159948400	6091817800	2.42
CGPLBR37	Preoperative treatment naïve	WGS	Breast Cancer	100	10307505800	6929530600	2.75
CGPLBR38	Preoperative treatment naïve	WGS	Breast Cancer	100	9983824000	6841725400	2.71
CGPLBR40	Preoperative treatment naïve	WGS	Breast Cancer	100	10148823800	7024345400	2.79
CGPLBR41	Preoperative treatment naïve	WGS	Breast Cancer	100	11168192000	7562945800	3.00
CGPLBR45	Preoperative treatment naïve	WGS	Breast Cancer	100	8793780600	6011109400	2.39
CGPLBR46	Preoperative treatment naïve	WGS	Breast Cancer	100	7228607600	4706130000	1.87
CGPLBR47	Preoperative treatment naïve	WGS	Breast Cancer	100	7906911400	5341655000	2.12
CGPLBR48	Preoperative treatment naïve	WGS	Breast Cancer	100	6992032000	4428636200	1.76
CGPLBR49	Preoperative treatment naïve	WGS	Breast Cancer	100	7311195000	4559460200	1.81
CGPLBR50	Preoperative treatment naïve	WGS	Breast Cancer	100	11107960600	7582776600	3.01

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGPLBR51	Preoperative treatment naïve	WGS	Breast Cancer	100	8393547400	5102069000	2.02
CGPLBR52	Preoperative treatment naïve	WGS	Breast Cancer	100	9491894800	6141729000	2.44
CGPLBR55	Preoperative treatment naïve	WGS	Breast Cancer	100	9380109800	6518855200	2.59
CGPLBR56	Preoperative treatment naïve	WGS	Breast Cancer	100	12191816800	8293011200	3.29
CGPLBR57	Preoperative treatment naïve	WGS	Breast Cancer	100	9847584400	6713638000	2.66
CGPLBR59	Preoperative treatment naïve	WGS	Breast Cancer	100	7476477000	5059878200	2.01
CGPLBR60	Preoperative treatment naïve	WGS	Breast Cancer	100	6531354600	4331253800	1.72
CGPLBR61	Preoperative treatment naïve	WGS	Breast Cancer	100	9311029200	6430920800	2.55
CGPLBR63	Preoperative treatment naïve	WGS	Breast Cancer	100	8971949000	6044009600	2.40
CGPLBR65	Preoperative treatment naïve	WGS	Breast Cancer	100	7197301400	4835015200	1.92
CGPLBR68	Preoperative treatment naïve	WGS	Breast Cancer	100	10003774000	6974918800	2.77
CGPLBR69	Preoperative treatment naïve	WGS	Breast Cancer	100	10080881800	6903459200	2.74
CGPLBR70	Preoperative treatment naïve	WGS	Breast Cancer	100	8824002800	6002533800	2.38
CGPLBR71	Preoperative treatment naïve	WGS	Breast Cancer	100	10164136800	6994668600	2.78
CGPLBR72	Preoperative treatment naïve	WGS	Breast Cancer	100	18416841400	12328783000	4.89
CGPLBR73	Preoperative treatment naïve	WGS	Breast Cancer	100	10281460200	7078613200	2.81
CGPLBR76	Preoperative treatment naïve	WGS	Breast Cancer	100	10105270400	6800705000	2.70
CGPLBR81	Preoperative treatment naïve	WGS	Breast Cancer	100	5087126000	3273367200	1.30
CGPLBR82	Preoperative treatment naïve	WGS	Breast Cancer	100	10576496600	7186662600	2.85
CGPLBR83	Preoperative treatment naïve	WGS	Breast Cancer	100	8977124400	5947525000	2.36
CGPLBR84	Preoperative treatment naïve	WGS	Breast Cancer	100	6272538600	4066870600	1.61
CGPLBR87	Preoperative treatment naïve	WGS	Breast Cancer	100	8460954800	5375710200	2.13
CGPLBR88	Preoperative treatment naïve	WGS	Breast Cancer	100	8665810400	5499898200	2.18
CGPLBR90	Preoperative treatment naïve	WGS	Breast Cancer	100	6663469200	4392442400	1.74
CGPLBR91	Preoperative treatment naïve	WGS	Breast Cancer	100	10933002400	7647842000	3.03
CGPLBR92	Preoperative treatment naïve	WGS	Breast Cancer	100	10392674000	6493598000	2.58
CGPLBR93	Preoperative treatment naïve	WGS	Breast Cancer	100	5659836000	3931106800	1.56
CGPLH189	Preoperative treatment naïve	WGS	Healthy	100	11400610400	7655568800	3.04
CGPLH190	Preoperative treatment naïve	WGS	Healthy	100	11444671600	7581175200	3.01
CGPLH192	Preoperative treatment naïve	WGS	Healthy	100	12199010800	8126804800	3.22
CGPLH193	Preoperative treatment naïve	WGS	Healthy	100	10201897600	6635285400	2.63
CGPLH194	Preoperative treatment naïve	WGS	Healthy	100	11005087400	7081652600	2.81
CGPLH196	Preoperative treatment naïve	WGS	Healthy	100	12891462800	8646881800	3.43
CGPLH197	Preoperative treatment naïve	WGS	Healthy	100	11961841600	8052855200	3.20
CGPLH198	Preoperative treatment naïve	WGS	Healthy	100	13605489000	8885716000	3.53
CGPLH199	Preoperative treatment naïve	WGS	Healthy	100	1818090200	5615316000	2.23
CGPLH200	Preoperative treatment naïve	WGS	Healthy	100	14400027600	9310342000	3.69
CGPLH201	Preoperative treatment naïve	WGS	Healthy	100	6208766800	4171848400	1.66
CGPLH202	Preoperative treatment naïve	WGS	Healthy	100	11282922800	7363530600	2.92
CGPLH203	Preoperative treatment naïve	WGS	Healthy	100	13540689600	9068747600	3.60
CGPLH205	Preoperative treatment naïve	WGS	Healthy	100	10343537800	6696988600	2.66
CGPLH208	Preoperative treatment naïve	WGS	Healthy	100	12796300000	8272073400	3.28
CGPLH209	Preoperative treatment naïve	WGS	Healthy	100	13123035400	8531813600	3.39
CGPLH210	Preoperative treatment naïve	WGS	Healthy	100	10184218800	6832204600	2.71
CGPLH211	Preoperative treatment naïve	WGS	Healthy	100	14655260200	8887067600	3.53
CGPLH300	Preoperative treatment naïve	WGS	Healthy	100	7062083400	4553351200	1.81
CGPLH307	Preoperative treatment naïve	WGS	Healthy	100	7239128200	4547697200	1.80
CGPLH308	Preoperative treatment naïve	WGS	Healthy	100	8512551400	5526653600	2.19
CGPLH309	Preoperative treatment naïve	WGS	Healthy	100	11664474200	7431836600	2.95
CGPLH310	Preoperative treatment naïve	WGS	Healthy	100	11045691000	7451506200	2.96
CGPLH311	Preoperative treatment naïve	WGS	Healthy	100	10406803200	6786479600	2.69
CGPLH314	Preoperative treatment naïve	WGS	Healthy	100	10371343800	6925866600	2.75
CGPLH315	Preoperative treatment naïve	WGS	Healthy	100	9508538400	6208744600	2.46
CGPLH316	Preoperative treatment naïve	WGS	Healthy	100	10131063600	6891181000	2.73
CGPLH317	Preoperative treatment naïve	WGS	Healthy	100	8364314400	5302232600	2.10
CGPLH319	Preoperative treatment naïve	WGS	Healthy	100	8780528200	5585897000	2.22
CGPLH320	Preoperative treatment naïve	WGS	Healthy	100	8956232600	5784619200	2.30
CGPLH322	Preoperative treatment naïve	WGS	Healthy	100	9563837800	6445517800	2.56
CGPLH324	Preoperative treatment naïve	WGS	Healthy	100	6765038600	4469201600	1.77
CGPLH325	Preoperative treatment naïve	WGS	Healthy	100	8008213400	5099262800	2.02
CGPLH326	Preoperative treatment naïve	WGS	Healthy	100	9554226200	6112544800	2.43
CGPLH327	Preoperative treatment naïve	WGS	Healthy	100	8239168800	5351280200	2.12
CGPLH328	Preoperative treatment naïve	WGS	Healthy	100	7197086800	4516894800	1.79
CGPLH329	Preoperative treatment naïve	WGS	Healthy	100	8921554800	5493709800	2.18
CGPLH330	Preoperative treatment naïve	WGS	Healthy	100	10693603400	7077793600	2.81
CGPLH331	Preoperative treatment naïve	WGS	Healthy	100	8982792000	5538096200	2.20
CGPLH333	Preoperative treatment naïve	WGS	Healthy	100	7856985400	5178829600	2.06
CGPLH335	Preoperative treatment naïve	WGS	Healthy	100	9370663400	6035739400	2.40
CGPLH336	Preoperative treatment naïve	WGS	Healthy	100	8002498200	5340331400	2.12
CGPLH337	Preoperative treatment naïve	WGS	Healthy	100	7399022000	4954467600	1.97
CGPLH338	Preoperative treatment naïve	WGS	Healthy	100	8917121600	6170927200	2.45
CGPLH339	Preoperative treatment naïve	WGS	Healthy	100	8591130800	5866411400	2.33
CGPLH340	Preoperative treatment naïve	WGS	Healthy	100	8046351000	5368062000	2.13
CGPLH341	Preoperative treatment naïve	WGS	Healthy	100	7914788600	5200304800	2.06

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGPLH342	Preoperative treatment naïve	WGS	Healthy	100	8633473000	5701972400	2.26
CGPLH343	Preoperative treatment naïve	WGS	Healthy	100	6694769800	4410670800	1.75
CGPLH344	Preoperative treatment naïve	WGS	Healthy	100	7628192400	4961476600	1.97
CGPLH345	Preoperative treatment naïve	WGS	Healthy	100	7121569400	4747223000	1.88
CGPLH346	Preoperative treatment naïve	WGS	Healthy	100	7707924600	4873321600	1.93
CGPLH35	Preoperative treatment naïve	WGS	Healthy	100	47305985200	4774186200	12.63
CGPLH350	Preoperative treatment naïve	WGS	Healthy	100	9745839800	6054055200	2.40
CGPLH351	Preoperative treatment naïve	WGS	Healthy	100	13317435800	8714465000	3.46
CGPLH352	Preoperative treatment naïve	WGS	Healthy	100	7659351600	4752309400	1.89
CGPLH353	Preoperative treatment naïve	WGS	Healthy	100	8435782400	5275098200	2.09
CGPLH354	Preoperative treatment naïve	WGS	Healthy	100	8018644000	4857577600	1.93
CGPLH355	Preoperative treatment naïve	WGS	Healthy	100	8624675800	5709726400	2.27
CGPLH356	Preoperative treatment naïve	WGS	Healthy	100	8817952800	5729595200	2.27
CGPLH357	Preoperative treatment naïve	WGS	Healthy	100	11931696200	7690004400	3.05
CGPLH358	Preoperative treatment naïve	WGS	Healthy	100	12802561200	8451274800	3.35
CGPLH36	Preoperative treatment naïve	WGS	Healthy	100	40173545600	3974810400	10.52
CGPLH360	Preoperative treatment naïve	WGS	Healthy	100	7280078400	4918566200	1.95
CGPLH361	Preoperative treatment naïve	WGS	Healthy	100	7493498400	4966813800	1.97
CGPLH362	Preoperative treatment naïve	WGS	Healthy	100	11345644200	7532133600	2.99
CGPLH363	Preoperative treatment naïve	WGS	Healthy	100	6117382800	3965952400	1.57
CGPLH364	Preoperative treatment naïve	WGS	Healthy	100	10823498400	7195657000	2.86
CGPLH365	Preoperative treatment naïve	WGS	Healthy	100	5938367400	3954556200	1.57
CGPLH366	Preoperative treatment naïve	WGS	Healthy	100	7063168600	4731853000	1.88
CGPLH367	Preoperative treatment naïve	WGS	Healthy	100	7119631800	4627888200	1.84
CGPLH368	Preoperative treatment naïve	WGS	Healthy	100	7726718400	4975233400	1.97
CGPLH369	Preoperative treatment naïve	WGS	Healthy	100	10967584200	7130956800	2.83
CGPLH37	Preoperative treatment naïve	WGS	Healthy	100	45970545400	4591328800	12.15
CGPLH370	Preoperative treatment naïve	WGS	Healthy	100	9237170600	6106373800	2.42
CGPLH371	Preoperative treatment naïve	WGS	Healthy	100	8077798800	5237070600	2.08
CGPLH380	Preoperative treatment naïve	WGS	Healthy	100	14049589200	8614241200	3.42
CGPLH381	Preoperative treatment naïve	WGS	Healthy	100	16743792000	10767882800	4.27
CGPLH382	Preoperative treatment naïve	WGS	Healthy	100	18474025200	12276437200	4.87
CGPLH383	Preoperative treatment naïve	WGS	Healthy	100	13215954000	8430420600	3.35
CGPLH384	Preoperative treatment naïve	WGS	Healthy	100	8481814000	5463636200	2.17
CGPLH385	Preoperative treatment naïve	WGS	Healthy	100	9596118800	6445445600	2.56
CGPLH386	Preoperative treatment naïve	WGS	Healthy	100	7399540400	4915484800	1.95
CGPLH387	Preoperative treatment naïve	WGS	Healthy	100	6860332600	4339724400	1.72
CGPLH388	Preoperative treatment naïve	WGS	Healthy	100	8679705600	5463945400	2.17
CGPLH389	Preoperative treatment naïve	WGS	Healthy	100	7266863600	4702386000	1.87
CGPLH390	Preoperative treatment naïve	WGS	Healthy	100	7509035600	4913901800	1.95
CGPLH391	Preoperative treatment naïve	WGS	Healthy	100	7252286000	4702404800	1.87
CGPLH392	Preoperative treatment naïve	WGS	Healthy	100	7302618200	4722407000	1.87
CGPLH393	Preoperative treatment naïve	WGS	Healthy	100	8879138000	5947871800	2.36
CGPLH394	Preoperative treatment naïve	WGS	Healthy	100	8737031000	5599777400	2.22
CGPLH395	Preoperative treatment naïve	WGS	Healthy	100	7783904800	4907146000	1.95
CGPLH396	Preoperative treatment naïve	WGS	Healthy	100	7585567200	5076638200	2.01
CGPLH398	Preoperative treatment naïve	WGS	Healthy	100	13001418200	8607025000	3.42
CGPLH399	Preoperative treatment naïve	WGS	Healthy	100	9867699200	5526646000	2.19
CGPLH400	Preoperative treatment naïve	WGS	Healthy	100	10573939000	6290438200	2.50
CGPLH401	Preoperative treatment naïve	WGS	Healthy	100	9415150000	6139638000	2.44
CGPLH402	Preoperative treatment naïve	WGS	Healthy	100	5541458000	2972027800	1.18
CGPLH403	Preoperative treatment naïve	WGS	Healthy	100	6470913200	3549772600	1.41
CGPLH404	Preoperative treatment naïve	WGS	Healthy	100	7369651800	4120205000	1.64
CGPLH405	Preoperative treatment naïve	WGS	Healthy	100	7360239000	4293522600	1.70
CGPLH406	Preoperative treatment naïve	WGS	Healthy	100	6026125400	3426007400	1.36
CGPLH407	Preoperative treatment naïve	WGS	Healthy	100	7073375200	4079286800	1.62
CGPLH408	Preoperative treatment naïve	WGS	Healthy	100	8006103200	5121285600	2.03
CGPLH409	Preoperative treatment naïve	WGS	Healthy	100	7343124600	4432335600	1.76
CGPLH410	Preoperative treatment naïve	WGS	Healthy	100	7551842000	4818779600	1.91
CGPLH411	Preoperative treatment naïve	WGS	Healthy	100	6119676400	3636478400	1.44
CGPLH412	Preoperative treatment naïve	WGS	Healthy	100	7960821200	4935752200	1.96
CGPLH413	Preoperative treatment naïve	WGS	Healthy	100	7623405400	4827888400	1.92
CGPLH414	Preoperative treatment naïve	WGS	Healthy	100	7381312400	4743337200	1.88
CGPLH415	Preoperative treatment naïve	WGS	Healthy	100	7240754200	4162208800	1.65
CGPLH416	Preoperative treatment naïve	WGS	Healthy	100	7745658600	4670226000	1.85
CGPLH417	Preoperative treatment naïve	WGS	Healthy	100	7627498600	4403085600	1.75
CGPLH418	Preoperative treatment naïve	WGS	Healthy	100	9090285000	5094814000	2.02
CGPLH419	Preoperative treatment naïve	WGS	Healthy	100	7914120200	5078389800	2.02
CGPLH42	Preoperative treatment naïve	WGS	Healthy	100	39492040600	3901039400	10.32
CGPLH420	Preoperative treatment naïve	WGS	Healthy	100	7014307800	4711393600	1.87
CGPLH422	Preoperative treatment naïve	WGS	Healthy	100	9103972800	6053559800	2.40
CGPLH423	Preoperative treatment naïve	WGS	Healthy	100	10154714200	6128800200	2.43
CGPLH424	Preoperative treatment naïve	WGS	Healthy	100	11002394000	6573756000	2.61
CGPLH425	Preoperative treatment naïve	WGS	Healthy	100	14681352600	9272557000	3.68

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGPLH426	Preoperative treatment naïve	WGS	Healthy	100	8336731000	5177430800	2.05
CGPLH427	Preoperative treatment naïve	WGS	Healthy	100	8242924400	5632991800	2.24
CGPLH428	Preoperative treatment naïve	WGS	Healthy	100	8512550400	5604756600	2.22
CGPLH429	Preoperative treatment naïve	WGS	Healthy	100	8369802800	5477121400	2.17
CGPLH43	Preoperative treatment naïve	WGS	Healthy	100	38513193400	3815698400	10.10
CGPLH430	Preoperative treatment naïve	WGS	Healthy	100	10357365400	6841611000	2.71
CGPLH431	Preoperative treatment naïve	WGS	Healthy	100	7599875800	5006909000	1.99
CGPLH432	Preoperative treatment naïve	WGS	Healthy	100	7932532400	4932304200	1.96
CGPLH434	Preoperative treatment naïve	WGS	Healthy	100	10417028600	6965998800	2.76
CGPLH435	Preoperative treatment naïve	WGS	Healthy	100	8747793800	5677115200	2.25
CGPLH436	Preoperative treatment naïve	WGS	Healthy	100	7990589400	5228737800	2.07
CGPLH437	Preoperative treatment naïve	WGS	Healthy	100	10156991200	6935537200	2.75
CGPLH438	Preoperative treatment naïve	WGS	Healthy	100	9473604000	6445455600	2.56
CGPLH439	Preoperative treatment naïve	WGS	Healthy	100	8303723400	5439877200	2.16
CGPLH440	Preoperative treatment naïve	WGS	Healthy	100	9055233800	6018631400	2.39
CGPLH441	Preoperative treatment naïve	WGS	Healthy	100	10290682000	6896415200	2.74
CGPLH442	Preoperative treatment naïve	WGS	Healthy	100	9876551600	6591249800	2.62
CGPLH443	Preoperative treatment naïve	WGS	Healthy	100	9837225800	6360740800	2.52
CGPLH444	Preoperative treatment naïve	WGS	Healthy	100	9199271400	5755941600	2.28
CGPLH445	Preoperative treatment naïve	WGS	Healthy	100	8089236400	5218259800	2.07
CGPLH446	Preoperative treatment naïve	WGS	Healthy	100	7890664200	5181606000	2.06
CGPLH447	Preoperative treatment naïve	WGS	Healthy	100	7775775000	5120239800	2.03
CGPLH448	Preoperative treatment naïve	WGS	Healthy	100	8686964800	5605079200	2.22
CGPLH449	Preoperative treatment naïve	WGS	Healthy	100	8604545400	5527726600	2.19
CGPLH45	Preoperative treatment naïve	WGS	Healthy	100	39029653000	3771601200	9.98
CGPLH450	Preoperative treatment naïve	WGS	Healthy	100	8428254800	5439950000	2.16
CGPLH451	Preoperative treatment naïve	WGS	Healthy	100	8128977600	5186265600	2.06
CGPLH452	Preoperative treatment naïve	WGS	Healthy	100	6474313400	4216316400	1.67
CGPLH453	Preoperative treatment naïve	WGS	Healthy	100	9831832800	6224917600	2.47
CGPLH455	Preoperative treatment naïve	WGS	Healthy	100	7373753000	4593473600	1.82
CGPLH456	Preoperative treatment naïve	WGS	Healthy	100	8455416200	5457148200	2.17
CGPLH457	Preoperative treatment naïve	WGS	Healthy	100	8647618000	5534503800	2.20
CGPLH458	Preoperative treatment naïve	WGS	Healthy	100	6633156400	4415186000	1.75
CGPLH459	Preoperative treatment naïve	WGS	Healthy	100	8361048200	5497193800	2.18
CGPLH46	Preoperative treatment naïve	WGS	Healthy	100	35361484600	3516232800	9.30
CGPLH460	Preoperative treatment naïve	WGS	Healthy	100	6788835400	4472282800	1.77
CGPLH463	Preoperative treatment naïve	WGS	Healthy	100	8534880800	5481759200	2.18
CGPLH464	Preoperative treatment naïve	WGS	Healthy	100	6692520000	4184463400	1.66
CGPLH465	Preoperative treatment naïve	WGS	Healthy	100	7772884600	4878430800	1.94
CGPLH466	Preoperative treatment naïve	WGS	Healthy	100	9056275000	5830877400	2.31
CGPLH467	Preoperative treatment naïve	WGS	Healthy	100	6931419200	4585861000	1.82
CGPLH468	Preoperative treatment naïve	WGS	Healthy	100	9334067400	6314830400	2.51
CGPLH469	Preoperative treatment naïve	WGS	Healthy	100	7376691000	4545246600	1.80
CGPLH47	Preoperative treatment naïve	WGS	Healthy	100	38485647600	3534883600	9.35
CGPLH470	Preoperative treatment naïve	WGS	Healthy	100	7899727600	5221650600	2.07
CGPLH471	Preoperative treatment naïve	WGS	Healthy	100	9200430600	6102371000	2.42
CGPLH472	Preoperative treatment naïve	WGS	Healthy	100	8143742400	5399946600	2.14
CGPLH473	Preoperative treatment naïve	WGS	Healthy	100	8123924600	5419825400	2.15
CGPLH474	Preoperative treatment naïve	WGS	Healthy	100	8853071400	6084059400	2.41
CGPLH475	Preoperative treatment naïve	WGS	Healthy	100	8115374000	5291718000	2.10
CGPLH476	Preoperative treatment naïve	WGS	Healthy	100	8163162600	5096869600	2.02
CGPLH477	Preoperative treatment naïve	WGS	Healthy	100	8350093200	5465468600	2.17
CGPLH478	Preoperative treatment naïve	WGS	Healthy	100	8259642200	5406516200	2.15
CGPLH479	Preoperative treatment naïve	WGS	Healthy	100	8027598600	5417376800	2.15
CGPLH48	Preoperative treatment naïve	WGS	Healthy	100	42232410000	4165893400	11.02
CGPLH480	Preoperative treatment naïve	WGS	Healthy	100	7632983200	5020127000	1.99
CGPLH481	Preoperative treatment naïve	WGS	Healthy	100	7578518800	4883280800	1.94
CGPLH482	Preoperative treatment naïve	WGS	Healthy	100	8279364800	5652263600	2.24
CGPLH483	Preoperative treatment naïve	WGS	Healthy	100	8660338800	5823859200	2.31
CGPLH484	Preoperative treatment naïve	WGS	Healthy	100	8445420000	5794328000	2.30
CGPLH485	Preoperative treatment naïve	WGS	Healthy	100	8371255400	5490207800	2.18
CGPLH486	Preoperative treatment naïve	WGS	Healthy	100	8216712200	5506871000	2.19
CGPLH487	Preoperative treatment naïve	WGS	Healthy	100	7936294200	5309250200	2.11
CGPLH488	Preoperative treatment naïve	WGS	Healthy	100	8355603600	5453160000	2.16
CGPLH49	Preoperative treatment naïve	WGS	Healthy	100	33912191800	3310056000	8.76
CGPLH490	Preoperative treatment naïve	WGS	Healthy	100	7768712400	5175567800	2.05
CGPLH491	Preoperative treatment naïve	WGS	Healthy	100	9070904000	6011275000	2.39
CGPLH492	Preoperative treatment naïve	WGS	Healthy	100	7208727200	4753213800	1.89
CGPLH493	Preoperative treatment naïve	WGS	Healthy	100	10542882600	7225870800	2.87
CGPLH494	Preoperative treatment naïve	WGS	Healthy	100	10908197600	7046645000	2.80
CGPLH495	Preoperative treatment naïve	WGS	Healthy	100	8945040400	5891697800	2.34
CGPLH496	Preoperative treatment naïve	WGS	Healthy	100	10859729400	7549608000	3.00
CGPLH497	Preoperative treatment naïve	WGS	Healthy	100	9630507400	6473162800	2.57
CGPLH498	Preoperative treatment naïve	WGS	Healthy	100	10060232600	6744622800	2.68

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGPLH499	Preoperative treatment naïve	WGS	Healthy	100	10221293600	6951282800	2.76
CGPLH50	Preoperative treatment naïve	WGS	Healthy	100	41248860600	4073272800	10.78
CGPLH500	Preoperative treatment naïve	WGS	Healthy	100	9703168200	6239893800	2.48
CGPLH501	Preoperative treatment naïve	WGS	Healthy	100	9104779800	6161602800	2.45
CGPLH502	Preoperative treatment naïve	WGS	Healthy	100	8514467400	5290881400	2.10
CGPLH503	Preoperative treatment naïve	WGS	Healthy	100	9019992200	6100383400	2.42
CGPLH504	Preoperative treatment naïve	WGS	Healthy	100	9320330200	6199750200	2.46
CGPLH505	Preoperative treatment naïve	WGS	Healthy	100	7499497400	4914559000	1.95
CGPLH506	Preoperative treatment naïve	WGS	Healthy	100	10526142000	6963312600	2.76
CGPLH507	Preoperative treatment naïve	WGS	Healthy	100	9091018400	6146678600	2.44
CGPLH508	Preoperative treatment naïve	WGS	Healthy	100	10989315600	7360201400	2.92
CGPLH509	Preoperative treatment naïve	WGS	Healthy	100	9729084600	6702691600	2.66
CGPLH51	Preoperative treatment naïve	WGS	Healthy	100	35967451400	3492833200	9.24
CGPLH510	Preoperative treatment naïve	WGS	Healthy	100	11162691600	7626795400	3.03
CGPLH511	Preoperative treatment naïve	WGS	Healthy	100	11888619600	8110427600	3.22
CGPLH512	Preoperative treatment naïve	WGS	Healthy	100	10726438400	7110078000	2.82
CGPLH513	Preoperative treatment naïve	WGS	Healthy	100	10701564200	7155271400	2.84
CGPLH514	Preoperative treatment naïve	WGS	Healthy	100	8822067000	5958773800	2.36
CGPLH515	Preoperative treatment naïve	WGS	Healthy	100	7792074800	5317464600	2.11
CGPLH516	Preoperative treatment naïve	WGS	Healthy	100	8642620000	5846439400	2.32
CGPLH517	Preoperative treatment naïve	WGS	Healthy	100	11915929600	8013937000	3.18
CGPLH518	Preoperative treatment naïve	WGS	Healthy	100	12804517400	8606661600	3.42
CGPLH519	Preoperative treatment naïve	WGS	Healthy	100	11513222200	7922798400	3.14
CGPLH52	Preoperative treatment naïve	WGS	Healthy	100	49247304200	4849631400	12.83
CGPLH520	Preoperative treatment naïve	WGS	Healthy	100	8942102400	6030683400	2.39
CGPLH54	Preoperative treatment naïve	WGS	Healthy	100	45399346400	4466164600	11.82
CGPLH55	Preoperative treatment naïve	WGS	Healthy	100	42547725000	4283337600	11.33
CGPLH56	Preoperative treatment naïve	WGS	Healthy	100	33460308000	3226338000	8.53
CGPLH57	Preoperative treatment naïve	WGS	Healthy	100	36504735200	3509125000	9.28
CGPLH59	Preoperative treatment naïve	WGS	Healthy	100	39642810600	3820011000	10.11
CGPLH625	Preoperative treatment naïve	WGS	Healthy	100	6408225000	4115487600	1.63
CGPLH626	Preoperative treatment naïve	WGS	Healthy	100	9915193600	6391657000	2.54
CGPLH63	Preoperative treatment naïve	WGS	Healthy	100	37447047600	3506737000	9.28
CGPLH639	Preoperative treatment naïve	WGS	Healthy	100	8158965800	5216049600	2.07
CGPLH64	Preoperative treatment naïve	WGS	Healthy	100	34275506800	3264508000	8.63
CGPLH640	Preoperative treatment naïve	WGS	Healthy	100	8058876800	5333551800	2.12
CGPLH642	Preoperative treatment naïve	WGS	Healthy	100	7545555600	4909732800	1.95
CGPLH643	Preoperative treatment naïve	WGS	Healthy	100	7865776800	5254772000	2.09
CGPLH644	Preoperative treatment naïve	WGS	Healthy	100	6890139000	4599387400	1.83
CGPLH646	Preoperative treatment naïve	WGS	Healthy	100	7757219400	5077408200	2.01
CGPLH75	Preoperative treatment naïve	WGS	Healthy	100	23882926000	2250344400	5.95
CGPLH76	Preoperative treatment naïve	WGS	Healthy	100	30631483600	3086042200	8.16
CGPLH77	Preoperative treatment naïve	WGS	Healthy	100	31651741400	3041290200	8.04
CGPLH78	Preoperative treatment naïve	WGS	Healthy	100	31165831200	3130079800	8.28
CGPLH79	Preoperative treatment naïve	WGS	Healthy	100	31935043000	3128488200	8.27
CGPLH80	Preoperative treatment naïve	WGS	Healthy	100	32965093000	3311371800	8.76
CGPLH81	Preoperative treatment naïve	WGS	Healthy	100	27035311200	2455084400	6.49
CGPLH82	Preoperative treatment naïve	WGS	Healthy	100	28447051200	2893358200	7.65
CGPLH83	Preoperative treatment naïve	WGS	Healthy	100	26702240200	2459494000	6.50
CGPLH84	Preoperative treatment naïve	WGS	Healthy	100	25176861400	2524467400	6.68
CGPLLU13	Pre-treatment, Day -2	WGS	Lung Cancer	100	9126585600	5915061800	2.35
CGPLLU13	Post-treatment, Day 5	WGS	Lung Cancer	100	7739120200	5071745800	2.01
CGPLLU13	Post-treatment, Day 28	WGS	Lung Cancer	100	9081585400	5764371600	2.29
CGPLLU13	Post-treatment, Day 91	WGS	Lung Cancer	100	9576557000	6160760200	2.44
CGPLLU14	Pre-treatment, Day -38	WGS	Lung Cancer	100	13659198400	9033455800	3.58
CGPLLU14	Pre-treatment, Day -16	WGS	Lung Cancer	100	7178855800	4856648600	1.93
CGPLLU14	Pre-treatment, Day -3	WGS	Lung Cancer	100	7653473000	4816193600	1.91
CGPLLU14	Pre-treatment, Day 0	WGS	Lung Cancer	100	7851997400	5193256600	2.06
CGPLLU14	Post-treatment, Day 0.33	WGS	Lung Cancer	100	7193040800	4869701600	1.93
CGPLLU14	Post-treatment, Day 7	WGS	Lung Cancer	100	7102050000	4741432600	1.88
CGPLLU144	Preoperative treatment naïve	WGS	Lung Cancer	100	4934813600	3415936400	1.36
CGPLLU147	Preoperative treatment naïve	WGS	Lung Cancer	100	24409561000	2118672800	5.61
CGPLLU161	Preoperative treatment naïve	WGS	Lung Cancer	100	8998813400	6016145000	2.39
CGPLLU162	Preoperative treatment naïve	WGS	Lung Cancer	100	9709792400	6407866400	2.54
CGPLLU163	Preoperative treatment naïve	WGS	Lung Cancer	100	9150620200	6063569800	2.41
CGPLLU165	Preoperative treatment naïve	WGS	Lung Cancer	100	28374436400	2651138600	7.01
CGPLLU168	Preoperative treatment naïve	WGS	Lung Cancer	100	5692739400	3695191000	1.47
CGPLLU169	Preoperative treatment naïve	WGS	Lung Cancer	100	9093975600	5805320800	2.30
CGPLLU175	Preoperative treatment naïve	WGS	Lung Cancer	100	33794816800	3418750400	9.04
CGPLLU176	Preoperative treatment naïve	WGS	Lung Cancer	100	8778553800	5794950200	2.30
CGPLLU177	Preoperative treatment naïve	WGS	Lung Cancer	100	3734614800	2578696200	1.02
CGPLLU180	Preoperative treatment naïve	WGS	Lung Cancer	100	28305936600	2756034200	7.29
CGPLLU198	Preoperative treatment naïve	WGS	Lung Cancer	100	23244959200	2218577200	5.86
CGPLLU202	Preoperative treatment naïve	WGS	Lung Cancer	100	21110128200	1831279400	4.84

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGPLLU203	Preoperative treatment naïve	WGS	Lung Cancer	100	4304235600	2896429000	1.15
CGPLLU205	Preoperative treatment naïve	WGS	Lung Cancer	100	10502467000	7386984800	2.93
CGPLLU206	Preoperative treatment naïve	WGS	Lung Cancer	100	21888248200	2026666000	5.36
CGPLLU207	Preoperative treatment naïve	WGS	Lung Cancer	100	10806230600	7363049000	2.92
CGPLLU208	Preoperative treatment naïve	WGS	Lung Cancer	100	7795426800	5199545800	2.06
CGPLLU209	Preoperative treatment naïve	WGS	Lung Cancer	100	26174542000	2621961800	6.93
CGPLLU244	Pre-treatment, Day -7	WGS	Lung Cancer	100	9967531400	6704365800	2.66
CGPLLU244	Pre-treatment, Day -1	WGS	Lung Cancer	100	9547119200	5785172600	2.30
CGPLLU244	Post-treatment, Day 6	WGS	Lung Cancer	100	9535898600	6452174000	2.56
CGPLLU244	Post-treatment, Day 62	WGS	Lung Cancer	100	8783628600	5914149000	2.35
CGPLLU245	Pre-treatment, Day -32	WGS	Lung Cancer	100	10025823200	6313303800	2.51
CGPLLU245	Pre-treatment, Day 0	WGS	Lung Cancer	100	9462480400	6612867800	2.62
CGPLLU245	Post-treatment, Day 7	WGS	Lung Cancer	100	9143825000	6431013200	2.55
CGPLLU245	Post-treatment, Day 21	WGS	Lung Cancer	100	9072713800	6368533000	2.53
CGPLLU246	Pre-treatment, Day -21	WGS	Lung Cancer	100	9579787000	6458003400	2.56
CGPLLU246	Pre-treatment, Day 0	WGS	Lung Cancer	100	9512703600	6440535600	2.56
CGPLLU246	Post-treatment, Day 9	WGS	Lung Cancer	100	9512646000	6300939200	2.50
CGPLLU246	Post-treatment, Day 42	WGS	Lung Cancer	100	11136103000	7358747400	2.92
CGPLLU264	Pre-treatment, Day -1	WGS	Lung Cancer	100	9196305000	6239803600	2.48
CGPLLU264	Post-treatment, Day 6	WGS	Lung Cancer	100	8247416600	5600454200	2.22
CGPLLU264	Post-treatment, Day 27	WGS	Lung Cancer	100	8681022200	5856109000	2.32
CGPLLU264	Post-treatment, Day 69	WGS	Lung Cancer	100	8931976400	5974246000	2.37
CGPLLU265	Pre-treatment, Day 0	WGS	Lung Cancer	100	9460534000	6111185200	2.43
CGPLLU265	Post-treatment, Day 3	WGS	Lung Cancer	100	8051601200	4984166600	1.98
CGPLLU265	Post-treatment, Day 7	WGS	Lung Cancer	100	8082224600	5110092600	2.03
CGPLLU265	Post-treatment, Day 84	WGS	Lung Cancer	100	8368637400	5369526400	2.13
CGPLLU266	Pre-treatment, Day 0	WGS	Lung Cancer	100	8583766400	5846473600	2.32
CGPLLU266	Post-treatment, Day 16	WGS	Lung Cancer	100	8795793600	5984531400	2.37
CGPLLU266	Post-treatment, Day 83	WGS	Lung Cancer	100	9157947600	6227735000	2.47
CGPLLU266	Post-treatment, Day 328	WGS	Lung Cancer	100	7299455400	5049379000	2.00
CGPLLU267	Pre-treatment, Day -1	WGS	Lung Cancer	100	10658657800	6892067000	2.73
CGPLLU267	Post-treatment, Day 34	WGS	Lung Cancer	100	8492833400	5101097800	2.02
CGPLLU267	Post-treatment, Day 90	WGS	Lung Cancer	100	12030314800	7757930400	3.08
CGPLLU269	Pre-treatment, Day 0	WGS	Lung Cancer	100	9170168000	5830454400	2.31
CGPLLU269	Post-treatment, Day 9	WGS	Lung Cancer	100	8905640400	5298461400	2.10
CGPLLU269	Post-treatment, Day 28	WGS	Lung Cancer	100	8455306600	5387927400	2.14
CGPLLU271	Post-treatment, Day 259	WGS	Lung Cancer	100	8112060400	5404979000	2.14
CGPLLU271	Pre-treatment, Day 0	WGS	Lung Cancer	100	13150818200	8570453400	3.40
CGPLLU271	Post-treatment, Day 6	WGS	Lung Cancer	100	9008880600	5854051400	2.32
CGPLLU271	Post-treatment, Day 20	WGS	Lung Cancer	100	8670913000	5461577000	2.17
CGPLLU271	Post-treatment, Day 104	WGS	Lung Cancer	100	8887441400	5609039000	2.23
CGPLLU43	Pre-treatment, Day -1	WGS	Lung Cancer	100	8407811200	5203486400	2.06
CGPLLU43	Post-treatment, Day 6	WGS	Lung Cancer	100	9264335200	5626714400	2.23
CGPLLU43	Post-treatment, Day 27	WGS	Lung Cancer	100	8902283000	5485656200	2.18
CGPLLU43	Post-treatment, Day 83	WGS	Lung Cancer	100	9201509200	5875084200	2.33
CGPLLU86	Pre-treatment, Day 0	WGS	Lung Cancer	100	9152729200	6248173200	2.48
CGPLLU86	Post-treatment, Day 0.5	WGS	Lung Cancer	100	6703253000	4663026800	1.85
CGPLLU86	Post-treatment, Day 7	WGS	Lung Cancer	100	6590121400	4559562400	1.81
CGPLLU86	Post-treatment, Day 17	WGS	Lung Cancer	100	8653551800	5900136000	2.34
CGPLLU88	Pre-treatment, Day 0	WGS	Lung Cancer	100	8096528000	5505475400	2.18
CGPLLU88	Post-treatment, Day 7	WGS	Lung Cancer	100	8283192200	5784217600	2.30
CGPLLU88	Post-treatment, Day 297	WGS	Lung Cancer	100	9297110800	6407258000	2.54
CGPLLU89	Pre-treatment, Day 0	WGS	Lung Cancer	100	7842145200	5356095400	2.13
CGPLLU89	Post-treatment, Day 7	WGS	Lung Cancer	100	7234220200	4930375200	1.96
CGPLLU89	Post-treatment, Day 22	WGS	Lung Cancer	100	6242889800	4057361000	1.61
CGPLOV11	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8985130400	5871959600	2.33
CGPLOV12	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9705820000	6430505400	2.55
CGPLOV13	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10307949400	7029712000	2.79
CGPLOV15	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8472829400	5562142400	2.21
CGPLOV16	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10977781000	7538581600	2.99
CGPLOV19	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8800876200	5855304000	2.32
CGPLOV20	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8714443600	5695165800	2.26
CGPLOV21	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10180394800	7120260400	2.83
CGPLOV22	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10107760000	6821916800	2.71
CGPLOV23	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10643399800	7206330800	2.86
CGPLOV24	Preoperative treatment naïve	WGS	Ovarian Cancer	100	6780929000	4623300400	1.83
CGPLOV25	Preoperative treatment naïve	WGS	Ovarian Cancer	100	7817548600	5359975200	2.13
CGPLOV26	Preoperative treatment naïve	WGS	Ovarian Cancer	100	11763101400	8178024400	3.25
CGPLOV28	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9522546400	6259423400	2.48
CGPLOV31	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9104831200	6109358400	2.42
CGPLOV32	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9222073600	6035150000	2.39
CGPLOV37	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8898328600	5971018200	2.37
CGPLOV38	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8756825200	5861536600	2.33
CGPLOV40	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9709391600	6654707200	2.64

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGPLOV41	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8923625000	5973070400	2.37
CGPLOV42	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10719380400	7353214200	2.92
CGPLOV43	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10272189000	6423288600	2.55
CGPLOV44	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9861862600	6769185800	2.69
CGPLOV46	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8788956400	5789863400	2.30
CGPLOV47	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9380561800	6480763600	2.57
CGPLOV48	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9258552600	6380106400	2.53
CGPLOV49	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8787025400	6134503600	2.43
CGPLOV50	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10144154400	6984721400	2.77
CGPLPA112	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	12740651400	9045622000	3.59
CGPLPA113	Preoperative treatment naïve	WGS	Duodenal Cancer	100	8802479000	5909030800	2.34
CGPLPA114	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8792313600	6019061000	2.39
CGPLPA115	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8636551400	5958809000	2.36
CGPLPA117	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	9128885200	6288833200	2.50
CGPLPA118	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	7931485800	5407532800	2.15
CGPLPA122	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	10888985000	7530118800	2.99
CGPLPA124	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8562012400	5860171000	2.33
CGPLPA125	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	9715576600	6390321000	2.54
CGPLPA126	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8056768800	5651600800	2.24
CGPLPA127	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8000301000	5382987600	2.14
CGPLPA128	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	6165751600	4256521400	1.69
CGPLPA129	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	7143147400	4917370400	1.95
CGPLPA130	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	5664335000	3603919400	1.43
CGPLPA131	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8292982000	5844942000	2.32
CGPLPA134	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	7088917000	5048887600	2.00
CGPLPA135	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8759665600	5800618200	2.30
CGPLPA136	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	7539715800	5248227600	2.08
CGPLPA137	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8391815400	5901273800	2.34
CGPLPA139	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8992280200	6328314400	2.51
CGPLPA14	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8787706200	5731317600	2.27
CGPLPA140	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	16365641800	11216732000	4.45
CGPLPA141	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	15086298000	10114790200	4.01
CGPLPA15	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8255566800	5531677600	2.20
CGPLPA155	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	9457155800	6621881800	2.63
CGPLPA156	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9845385800	6728653000	2.67
CGPLPA165	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8356604600	5829895800	2.31
CGPLPA168	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	10365661600	7048115600	2.80
CGPLPA17	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8073547400	4687808000	1.86
CGPLPA184	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	9014218400	6230922200	2.47
CGPLPA187	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8883536200	6140874400	2.44
CGPLPA23	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9835452000	6246525400	2.48
CGPLPA25	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	10077515400	6103322200	2.42
CGPLPA26	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8354272400	5725781000	2.27
CGPLPA28	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8477461600	5688846800	2.26
CGPLPA33	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7287615600	4596723800	1.82
CGPLPA34	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	6122902400	4094828000	1.62
CGPLPA37	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	12714888200	8527779200	3.38
CGPLPA38	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8525500600	5501341400	2.18
CGPLPA39	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	10502663600	6812333000	2.70
CGPLPA40	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9083670000	5394717800	2.14
CGPLPA42	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	5972126600	3890395200	1.54
CGPLPA46	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	4720090200	2626298800	1.04
CGPLPA47	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7317385800	4543833000	1.80
CGPLPA48	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7553856200	5022695600	1.99
CGPLPA52	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	5655875000	3551861600	1.41
CGPLPA53	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9504749000	6323344800	2.51
CGPLPA58	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8088090200	5118138200	2.03
CGPLPA59	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	14547364600	9617778600	3.82
CGPLPA67	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8222177400	5351172600	2.12
CGPLPA69	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7899181400	5006114800	1.99
CGPLPA71	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7349620400	4955417400	1.97
CGPLPA74	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	6666371400	4571394200	1.81
CGPLPA76	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9755658600	6412606800	2.54
CGPLPA85	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	10856223000	7309498600	2.90
CGPLPA86	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8744365400	5514523200	2.19
CGPLPA92	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8073791200	5390492800	2.14
CGPLPA93	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	10390273000	7186589400	2.85
CGPLPA94	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	11060347600	7641336400	3.03
CGPLPA95	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	12416627200	7206503800	2.86
CGST102	Preoperative treatment naïve	WGS	Gastric cancer	100	6637004600	4545072600	1.80
CGST11	Preoperative treatment naïve	WGS	Gastric cancer	100	9718427800	6259679600	2.48
CGST110	Preoperative treatment naïve	WGS	Gastric cancer	100	9319661600	6359317400	2.52
CGST114	Preoperative treatment naïve	WGS	Gastric cancer	100	6865213000	4841171600	1.92
CGST13	Preoperative treatment naïve	WGS	Gastric cancer	100	9284554800	6360843800	2.52

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGST131	Preoperative treatment naïve	WGS	Gastric cancer	100	5924382000	3860677200	1.53
CGST141	Preoperative treatment naïve	WGS	Gastric cancer	100	8486380800	5860491000	2.33
CGST16	Preoperative treatment naïve	WGS	Gastric cancer	100	13820725800	9377828000	3.72
CGST18	Preoperative treatment naïve	WGS	Gastric cancer	100	7781288000	5278862400	2.09
CGST21	Preoperative treatment naïve	WGS	Gastric cancer	100	7171165400	4103970800	1.63
CGST26	Preoperative treatment naïve	WGS	Gastric cancer	100	8983961800	6053405600	2.40
CGST28	Preoperative treatment naïve	WGS	Gastric cancer	100	9683035400	6745116400	2.68
CGST30	Preoperative treatment naïve	WGS	Gastric cancer	100	8684086600	5741416000	2.28
CGST32	Preoperative treatment naïve	WGS	Gastric cancer	100	8568194600	5783369200	2.29
CGST33	Preoperative treatment naïve	WGS	Gastric cancer	100	9351699600	6448718400	2.56
CGST38	Preoperative treatment naïve	WGS	Gastric cancer	100	8409876400	5770989200	2.29
CGST39	Preoperative treatment naïve	WGS	Gastric cancer	100	10573763000	7597016000	3.01
CGST41	Preoperative treatment naïve	WGS	Gastric cancer	100	9434854200	6609415400	2.62
CGST45	Preoperative treatment naïve	WGS	Gastric cancer	100	8203868600	5625223000	2.23
CGST47	Preoperative treatment naïve	WGS	Gastric cancer	100	8938597600	6178990600	2.45
CGST48	Preoperative treatment naïve	WGS	Gastric cancer	100	9106628800	6517085200	2.59
CGST53	Preoperative treatment naïve	WGS	Gastric cancer	100	9005374200	5854996200	2.32
CGST58	Preoperative treatment naïve	WGS	Gastric cancer	100	10020368600	6133458400	2.43
CGST67	Preoperative treatment naïve	WGS	Gastric cancer	100	9198135600	5911071000	2.35
CGST77	Preoperative treatment naïve	WGS	Gastric cancer	100	8228789400	5119116800	2.03
CGST80	Preoperative treatment naïve	WGS	Gastric cancer	100	10596963400	7283152800	2.89
CGST81	Preoperative treatment naïve	WGS	Gastric cancer	100	8494881200	5838064000	2.32

APPENDIX E: Table 5. High coverage whole genome cfDNA analyses of healthy individuals and lung cancer patients

Patient	Patient Type	Analysis Type	Timepoint	Stage at Diagnosis	Median cfDNA Fragment Size (bp)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Correlation of GC Corrected Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Lymphocytes	Correlation of Fragment Ratio Profile to Lymphocyte Nucleosome Distances
CGPLH75	Healthy	WGS	Preoperative treatment naïve	NA	168	0.977	0.952	0.920	-0.886
CGPLH77	Healthy	WGS	Preoperative treatment naïve	NA	166	0.970	0.960	0.904	-0.912
CGPLH80	Healthy	WGS	Preoperative treatment naïve	NA	168	0.955	0.949	0.960	-0.917
CGPLH81	Healthy	WGS	Preoperative treatment naïve	NA	167	0.949	0.953	0.869	-0.883
CGPLH82	Healthy	WGS	Preoperative treatment naïve	NA	166	0.969	0.949	0.954	-0.917
CGPLH83	Healthy	WGS	Preoperative treatment naïve	NA	167	0.949	0.939	0.919	-0.904
CGPLH84	Healthy	WGS	Preoperative treatment naïve	NA	168	0.967	0.948	0.951	-0.913
CGPLH52	Healthy	WGS	Preoperative treatment naïve	NA	167	0.946	0.968	0.952	-0.924
CGPLH35	Healthy	WGS	Preoperative treatment naïve	NA	166	0.981	0.973	0.945	-0.921
CGPLH37	Healthy	WGS	Preoperative treatment naïve	NA	168	0.968	0.970	0.951	-0.922
CGPLH54	Healthy	WGS	Preoperative treatment naïve	NA	167	0.968	0.976	0.948	-0.925
CGPLH55	Healthy	WGS	Preoperative treatment naïve	NA	166	0.947	0.964	0.948	-0.917
CGPLH48	Healthy	WGS	Preoperative treatment naïve	NA	168	0.959	0.965	0.960	-0.923
CGPLH50	Healthy	WGS	Preoperative treatment naïve	NA	167	0.960	0.968	0.952	-0.921
CGPLH36	Healthy	WGS	Preoperative treatment naïve	NA	168	0.955	0.954	0.955	-0.919
CGPLH42	Healthy	WGS	Preoperative treatment naïve	NA	167	0.973	0.963	0.948	-0.918
CGPLH43	Healthy	WGS	Preoperative treatment naïve	NA	166	0.952	0.958	0.953	-0.928
CGPLH59	Healthy	WGS	Preoperative treatment naïve	NA	168	0.970	0.965	0.951	-0.925
CGPLH45	Healthy	WGS	Preoperative treatment naïve	NA	168	0.965	0.950	0.949	-0.911
CGPLH47	Healthy	WGS	Preoperative treatment naïve	NA	167	0.952	0.944	0.954	-0.921
CGPLH46	Healthy	WGS	Preoperative treatment naïve	NA	168	0.966	0.965	0.953	-0.923
CGPLH63	Healthy	WGS	Preoperative treatment naïve	NA	168	0.977	0.968	0.939	-0.920
CGPLH51	Healthy	WGS	Preoperative treatment naïve	NA	168	0.935	0.955	0.957	-0.914
CGPLH57	Healthy	WGS	Preoperative treatment naïve	NA	169	0.965	0.954	0.955	-0.917
CGPLH49	Healthy	WGS	Preoperative treatment naïve	NA	168	0.958	0.951	0.950	-0.924
CGPLH56	Healthy	WGS	Preoperative treatment naïve	NA	166	0.940	0.957	0.959	-0.911
CGPLH64	Healthy	WGS	Preoperative treatment naïve	NA	169	0.960	0.940	0.949	-0.918
CGPLH78	Healthy	WGS	Preoperative treatment naïve	NA	166	0.956	0.936	0.958	-0.911
CGPLH79	Healthy	WGS	Preoperative treatment naïve	NA	168	0.960	0.957	0.953	-0.917
CGPLH76	Healthy	WGS	Preoperative treatment naïve	NA	167	0.969	0.965	0.953	-0.917
CGPLLU175	Lung Cancer	WGS	Preoperative treatment naïve	I	165	0.316	0.284	0.244	-0.262
CGPLLU180	Lung Cancer	WGS	Preoperative treatment naïve	I	166	0.907	0.846	0.826	-0.819
CGPLLU198	Lung Cancer	WGS	Preoperative treatment naïve	I	166	0.972	0.946	0.928	-0.911
CGPLLU202	Lung Cancer	WGS	Preoperative treatment naïve	I	163	0.821	0.605	0.905	-0.843
CGPLLU165	Lung Cancer	WGS	Preoperative treatment naïve	II	163	0.924	0.961	0.815	-0.851
CGPLLU209	Lung Cancer	WGS	Preoperative treatment naïve	II	163	0.578	0.526	0.513	-0.534
CGPLLU147	Lung Cancer	WGS	Preoperative treatment naïve	III	166	0.953	0.919	0.939	-0.912
CGPLLU206	Lung Cancer	WGS	Preoperative treatment naïve	III	158	0.488	0.343	0.460	-0.481

APPENDIX F: Table 6. Monitoring response to therapy using whole genome analyses of cfDNA fragmentation profiles and targeted mutations analyses

Patient	Patient Type	Analysis Type	Timepoint	Stage	Progression-free Survival (months)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Correlation of Fragment Ratio Profile to Lymphocyte Nucleosome Distances	Targeted Mutation	Maximum Mutant Allele Fraction
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -38	IV	15.4	0.941	-0.841	EGFR 861L>Q	0.89%
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -16	IV	15.4	0.933	-0.833	EGFR 861L>Q	0.18%
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -3	IV	15.4	0.908	-0.814	EGFR 719G>S	0.49%
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	15.4	0.883	-0.752	EGFR 861L>Q	1.39%
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 0.33	IV	15.4	0.820	-0.692	EGFR 719G>S	1.05%
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	15.4	0.927	-0.887	EGFR 861L>Q	0.00%
CGPLLU88	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	18.0	0.657	-0.584	EGFR 745KELREA>T	9.06%
CGPLLU88	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	18.0	0.939	-0.799	EGFR 790T>M	0.15%
CGPLLU88	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 297	IV	18.0	0.946	-0.869	EGFR 745KELREA>T	0.93%
CGPLLU244	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -7	IV	1.2	0.850	-0.706	EGFR 858L>R	4.98%
CGPLLU244	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -1	IV	1.2	0.867	-0.764	EGFR 62L>R	3.41%
CGPLLU244	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 6	IV	1.2	0.703	-0.639	EGFR 858L>R	5.57%
CGPLLU244	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 62	IV	1.2	0.659	-0.660	EGFR 858L>R	11.80%
CGPLLU245	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -32	IV	1.7	0.871	-0.724	EGFR 745KELREA>K	10.60%
CGPLLU245	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	1.7	0.736	-0.608	EGFR 745KELREA>K	14.10%
CGPLLU245	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	1.7	0.731	-0.559	EGFR 745KELREA>K	8.56%
CGPLLU245	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 21	IV	1.7	0.613	-0.426	EGFR 745KELREA>K	10.69%
CGPLLU246	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -21	IV	1.3	0.897	-0.757	EGFR 790T>M	0.49%
CGPLLU246	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	1.3	0.469	-0.376	EGFR 858L>R	6.17%
CGPLLU246	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 9	IV	1.3	0.874	-0.746	EGFR 858L>R	1.72%
CGPLLU246	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 42	IV	1.3	0.775	-0.665	EGFR 858L>R	5.29%
CGPLLU86	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	12.4	0.817	-0.630	EGFR 746ELREATS>D	0.00%
CGPLLU86	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 0.5	IV	12.4	0.916	-0.811	EGFR 746ELREATS>D	0.19%
CGPLLU86	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	12.4	0.859	-0.694	EGFR 746ELREATS>D	0.00%
CGPLLU86	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 17	IV	12.4	0.932	-0.848	EGFR 746ELREATS>D	0.00%
CGPLLU89	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	6.7	0.864	-0.729	EGFR 747LREATS>-	0.42%
CGPLLU89	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	6.7	0.908	-0.803	EGFR 747LREATS>-	0.20%
CGPLLU89	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 22	IV	6.7	0.853	-0.881	EGFR 747LREATS>-	0.00%
CGLU316	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -53	IV	1.4	0.331	-0.351	EGFR L861Q	15.72%
CGLU316	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -4	IV	1.4	0.225	-0.253	EGFR L861Q	45.67%
CGLU316	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 18	IV	1.4	0.336	-0.364	EGFR G719A	33.38%
CGLU316	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 87	IV	1.4	0.340	-0.364	EGFR L861Q	66.01%
CGLU344	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -21	IV	Ongoing	0.935	-0.818	EGFR E746_A750del	0.00%
CGLU344	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	Ongoing	0.919	-0.774	EGFR E746_A750del	0.22%
CGLU344	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 0.1875	IV	Ongoing	0.953	-0.860	EGFR E746_A750del	0.40%
CGLU344	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 59	IV	Ongoing	0.944	-0.832	EGFR E746_A750del	0.00%
CGLU369	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -2	IV	7.5	0.825	-0.826	EGFR L858R	20.61%
CGLU369	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 12	IV	7.5	0.950	-0.903	EGFR L858R	0.22%
CGLU369	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 68	IV	7.5	0.945	-0.889	EGFR L858R	0.16%
CGLU369	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 110	IV	7.5	0.886	-0.883	EGFR L858R	0.10%
CGLU373	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -2	IV	Ongoing	0.922	-0.804	EGFR E746_A750del	0.82%
CGLU373	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 0.125	IV	Ongoing	0.959	-0.853	EGFR E746_A750del	0.00%
CGLU373	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	Ongoing	0.967	-0.886	EGFR E746_A750del	0.15%
CGLU373	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 47	IV	Ongoing	0.951	-0.890	EGFR E746_A750del	0.00%
CGPLLU13	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -2	IV	1.5	0.425	-0.400	EGFR E746_A750del	7.66%
CGPLLU13	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 5	IV	1.5	0.272	-0.257	EGFR E746_A750del	13.10%
CGPLLU13	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 28	IV	1.5	0.584	-0.536	EGFR E746_A750del	6.09%
CGPLLU13	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 91	IV	1.5	0.530	-0.513	EGFR E746_A750del	9.28%
CGPLLU264	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -1	IV	Ongoing	0.946	-0.824	EGFR D761N	0.00%
CGPLLU264	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 6	IV	Ongoing	0.927	-0.788	EGFR D761N	0.16%
CGPLLU264	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 27	IV	Ongoing	0.962	-0.856	EGFR D761N	0.00%
CGPLLU264	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 69	IV	Ongoing	0.960	-0.894	EGFR D761N	0.00%
CGPLLU265	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	Ongoing	0.953	-0.859	EGFR L858R	0.21%
CGPLLU265	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 3	IV	Ongoing	0.949	-0.842	EGFR L858R	0.21%
CGPLLU265	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	Ongoing	0.955	-0.844	EGFR T790M	0.21%
CGPLLU265	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 84	IV	Ongoing	0.946	-0.825	EGFR L858R	0.00%
CGPLLU266	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	9.6	0.961	-0.904	NA	0.00%
CGPLLU266	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 16	IV	9.6	0.959	-0.886	NA	0.00%
CGPLLU266	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 83	IV	9.6	0.961	-0.880	NA	0.00%
CGPLLU266	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 328	IV	9.6	0.958	-0.855	NA	0.00%

Patient	Patient Type	Analysis Type	Timepoint	Stage	Progression-free Survival (months)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Correlation of Fragment Ratio Profile to Lymphocyte Nucleosome Distances	Targeted Mutation	Maximum Mutant Allele Fraction
CGPLLU267	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -1	IV	3.9	0.919	-0.863	EGFR L858R	1.93%
CGPLLU267	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 34	IV	3.9	0.863	-0.889	EGFR L858R	0.14%
CGPLLU267	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 90	IV	3.9	0.962	-0.876	EGFR L858R	0.38%
CGPLLU269	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	Ongoing	0.951	-0.864	EGFR L858R	0.10%
CGPLLU269	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 9	IV	Ongoing	0.941	-0.894	EGFR L858R	0.00%
CGPLLU269	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 28	IV	Ongoing	0.957	-0.876	EGFR L858R	0.00%
CGPLLU271	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	8.2	0.371	-0.284	EGFR E746_A750del	3.36%
CGPLLU271	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 6	IV	8.2	0.947	-0.826	EGFR E746_A750del	0.17%
CGPLLU271	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 20	IV	8.2	0.952	-0.839	EGFR E746_A750del	0.00%
CGPLLU271	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 104	IV	8.2	0.944	-0.810	EGFR E746_A750del	0.00%
CGPLLU271	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 259	IV	8.2	0.950	-0.831	EGFR E746_A750del	0.44%
CGPLLU43	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day -1	IV	Ongoing	0.944	-0.903	NA	0.00%
CGPLLU43	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 6	IV	Ongoing	0.956	-0.899	NA	0.00%
CGPLLU43	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 27	IV	Ongoing	0.959	-0.901	NA	0.00%
CGPLLU43	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 83	IV	Ongoing	0.965	-0.896	NA	0.00%

APPENDIX G: Table 7. Whole genome cfDNA analyses in healthy individuals and cancer patients

Patient	Patient Type	Analysis Type	Timepoint	Stage at Diagnosis	Median cfDNA Fragment Size (bp)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Correlation of GC Corrected Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Fraction of Reads Mapped to Mitochondrial Genome	DELFI Score	Detected using DELFI (95% specificity)	Detected using DELFI (98% specificity)	Mutant Alelle Fraction Detected using Targeted sequencing*
CGCRC291	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	163	0.1972	0.5268	0.0484%	0.9976	Y	Y	22.85%
CGCRC292	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	166	0.7804	0.8835	0.0270%	0.7299	Y	N	1.41%
CGCRC293	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	166	0.9335	0.9205	0.0748%	0.5234	N	N	0.35%
CGCRC294	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.6531	0.8904	0.0188%	0.8757	Y	Y	0.17%
CGCRC296	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.8161	0.8695	0.0369%	0.9951	Y	Y	ND
CGCRC299	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	162	0.7325	0.9268	0.0392%	0.9648	Y	Y	ND
CGCRC300	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.9382	0.9303	0.0235%	0.4447	N	N	ND
CGCRC301	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	165	0.8252	0.9151	0.0310%	0.2190	N	N	0.21%
CGCRC302	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	163	0.7499	0.9243	0.0112%	0.9897	Y	Y	0.12%
CGCRC304	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	162	0.4642	0.9360	0.0093%	0.9358	Y	Y	0.27%
CGCRC305	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.8909	0.9250	0.0120%	0.8988	Y	Y	0.19%
CGCRC306	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.8523	0.8186	0.0781%	0.9466	Y	Y	8.02%
CGCRC307	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.9140	0.9342	0.0181%	0.7042	Y	N	0.56%
CGCRC308	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	165	0.8734	0.9324	0.0078%	0.9082	Y	Y	0.11%
CGCRC311	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.8535	0.9156	0.0173%	0.1867	N	N	ND
CGCRC315	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	167	0.6083	0.8846	0.0241%	0.6422	Y	N	0.27%
CGCRC316	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	161	0.1546	0.5879	0.0315%	0.9971	Y	Y	6.52%
CGCRC317	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	163	0.6242	0.8944	0.0184%	0.9855	Y	Y	0.36%
CGCRC318	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.8824	0.9140	0.0156%	0.5615	N	N	ND
CGCRC319	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	160	0.5979	0.8230	0.1259%	0.9925	Y	Y	0.11%
CGCRC320	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.7949	0.9101	0.0363%	0.8019	Y	Y	0.64%
CGCRC321	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	164	0.7804	0.9091	0.0829%	0.9759	Y	Y	0.20%
CGCRC333	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	163	0.4263	0.4355	0.4284%	0.9974	Y	Y	43.03%
CGCRC336	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	162	0.6466	0.6856	0.1154%	0.9887	Y	Y	81.61%
CGCRC338	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	162	0.7740	0.7573	0.1436%	0.9976	Y	Y	36.00%
CGCRC341	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	164	0.8995	0.9191	0.0197%	0.9670	Y	Y	ND
CGCRC342	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	158	0.2524	0.1845	0.1732%	0.9987	Y	Y	30.72%
CGPLBR100	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	166	0.9440	0.8946	0.1234%	0.8664	Y	Y	ND
CGPLBR101	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.8864	0.9304	0.0709%	0.9385	Y	Y	ND
CGPLBR102	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9617	0.9345	0.4742%	0.9052	Y	Y	0.25%
CGPLBR103	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	168	0.9498	0.9251	0.0775%	0.5994	N	N	ND
CGPLBR104	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.8490	0.9192	0.0532%	0.9950	Y	Y	0.13%
CGPLBR12	Breast Cancer	WGS	Preoperative treatment naïve	III	164	0.8350	0.7760	0.1407%	0.7598	Y	Y	-
CGPLBR18	Breast Cancer	WGS	Preoperative treatment naïve	III	163	0.8411	0.9534	0.0267%	0.3886	N	N	-
CGPLBR23	Breast Cancer	WGS	Preoperative treatment naïve	II	166	0.9714	0.9312	0.0144%	0.1235	N	N	-
CGPLBR24	Breast Cancer	WGS	Preoperative treatment naïve	II	156	0.8402	0.8766	0.0210%	0.7480	Y	Y	-
CGPLBR28	Breast Cancer	WGS	Preoperative treatment naïve	III	166	0.9584	0.9120	0.1456%	0.9630	Y	Y	-
CGPLBR30	Breast Cancer	WGS	Preoperative treatment naïve	II	161	0.6951	0.6611	0.0952%	0.9956	Y	Y	-
CGPLBR31	Breast Cancer	WGS	Preoperative treatment naïve	II	167	0.9719	0.9556	0.0427%	0.2227	N	N	-
CGPLBR32	Breast Cancer	WGS	Preoperative treatment naïve	II	166	0.9590	0.9229	0.0306%	0.9815	Y	Y	-
CGPLBR33	Breast Cancer	WGS	Preoperative treatment naïve	II	166	0.9706	0.9432	0.0617%	0.2863	N	N	-
CGPLBR34	Breast Cancer	WGS	Preoperative treatment naïve	II	163	0.8735	0.9425	0.0115%	0.1637	N	N	-
CGPLBR35	Breast Cancer	WGS	Preoperative treatment naïve	II	168	0.9655	0.9348	0.1371%	0.5057	N	N	-
CGPLBR36	Breast Cancer	WGS	Preoperative treatment naïve	II	169	0.9394	0.8884	0.0813%	0.4017	N	N	-
CGPLBR37	Breast Cancer	WGS	Preoperative treatment naïve	II	167	0.9691	0.9496	0.0518%	0.0314	N	N	-
CGPLBR38	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	165	0.9105	0.9349	0.1352%	0.8983	Y	Y	0.53%
CGPLBR40	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	167	0.9273	0.9244	0.0929%	0.9046	Y	Y	ND
CGPLBR41	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	168	0.9626	0.9346	0.0544%	0.9416	Y	Y	0.32%
CGPLBR45	Breast Cancer	WGS	Preoperative treatment naïve	II	164	0.9615	0.9286	0.0296%	0.3860	N	N	-
CGPLBR46	Breast Cancer	WGS	Preoperative treatment naïve	III	168	0.9322	0.9005	0.0345%	0.7270	Y	N	-
CGPLBR47	Breast Cancer	WGS	Preoperative treatment naïve	I	166	0.9461	0.9028	0.0591%	0.8247	Y	Y	-
CGPLBR48	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.7686	0.8246	0.0504%	0.9973	Y	Y	0.18%
CGPLBR49	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	171	0.8867	0.7887	0.0377%	0.9946	Y	Y	ND
CGPLBR50	Breast Cancer	WGS	Preoperative treatment naïve	I	160	0.8593	0.9332	0.0137%	0.6820	Y	N	-
CGPLBR51	Breast Cancer	WGS	Preoperative treatment naïve	II	165	0.9359	0.9160	0.0863%	0.6915	Y	N	-
CGPLBR52	Breast Cancer	WGS	Preoperative treatment naïve	III	164	0.8688	0.9196	0.0165%	0.6390	Y	N	-
CGPLBR55	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	165	0.9634	0.9341	0.0356%	0.9494	Y	Y	0.68%
CGPLBR56	Breast Cancer	WGS	Preoperative treatment naïve	II	163	0.9469	0.9428	0.2025%	0.4700	N	N	-
CGPLBR57	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	166	0.9672	0.9416	0.0902%	0.9090	Y	Y	ND
CGPLBR59	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.9438	0.9130	0.0761%	0.5828	N	N	ND
CGPLBR60	Breast Cancer	WGS	Preoperative treatment naïve	II	167	0.9479	0.8916	0.0626%	0.8779	Y	Y	-
CGPLBR61	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.9611	0.9422	0.0601%	0.4417	N	N	0.44%
CGPLBR63	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	168	0.9555	0.9132	0.0514%	0.8788	Y	Y	ND
CGPLBR65	Breast Cancer	WGS	Preoperative treatment naïve	II	167	0.9506	0.8970	0.0264%	0.9048	Y	Y	-
CGPLBR68	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	163	0.9154	0.9532	0.0164%	0.7863	Y	Y	ND
CGPLBR69	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.9460	0.9474	0.0279%	0.0600	N	N	ND
CGPLBR70	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	168	0.9651	0.9388	0.0171%	0.6447	Y	N	0.36%
CGPLBR71	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.9577	0.9368	0.0271%	0.6706	Y	N	0.10%
CGPLBR72	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.9786	0.9640	0.0263%	0.6129	N	N	ND
CGPLBR73	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.9576	0.9421	0.0142%	0.0746	N	N	0.27%

Patient	Patient Type	Analysis Type	Timepoint	Stage at Diagnosis	Median cfDNA Fragment Size (bp)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Correlation of GC Corrected Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Fraction of Reads Mapped to Mitochondrial Genome	DELFI Score	Detected using DELFI (95% specificity)	Detected using DELFI (98% specificity)	Mutant Allele Fraction Detected using Targeted sequencing*
CGPLBR76	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	170	0.9410	0.9254	0.0775%	0.9334	Y	Y	0.12%
CGPLBR81	Breast Cancer	WGS	Preoperative treatment naïve	II	170	0.9043	0.8193	0.0241%	0.9899	Y	Y	-
CGPLBR82	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.9254	0.9288	0.1640%	0.9834	Y	Y	0.12%
CGPLBR83	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9451	0.9138	0.0419%	0.9810	Y	Y	0.28%
CGPLBR84	Breast Cancer	WGS	Preoperative treatment naïve	III	169	0.9315	0.8659	0.0274%	0.9901	Y	Y	-
CGPLBR87	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9154	0.8797	0.0294%	0.9968	Y	Y	0.45%
CGPLBR88	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9370	0.8547	0.0181%	0.9988	Y	Y	0.38%
CGPLBR90	Breast Cancer	WGS	Preoperative treatment naïve	II	169	0.9002	0.8330	0.0417%	0.9667	Y	Y	-
CGPLBR91	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	164	0.7955	0.9408	0.0799%	0.8710	Y	Y	ND
CGPLBR92	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	162	0.6774	0.8835	0.1042%	0.9866	Y	Y	0.20%
CGPLBR93	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.8773	0.9072	0.0352%	0.7253	Y	N	ND
CGPLH189	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9325	0.8947	0.0591%	0.1748	N	N	-
CGPLH190	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9433	0.9369	0.1193%	0.5168	N	N	-
CGPLH192	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9646	0.9487	0.0276%	0.0178	N	N	-
CGPLH193	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9423	0.9442	0.0420%	0.5794	N	N	-
CGPLH194	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9567	0.9289	0.0407%	0.1616	N	N	-
CGPLH196	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9709	0.9512	0.0266%	0.0999	N	N	-
CGPLH197	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9605	0.9416	0.0334%	0.4699	N	N	-
CGPLH198	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9238	0.9457	0.0302%	0.6571	Y	N	-
CGPLH199	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9618	0.9439	0.0170%	0.5564	N	N	-
CGPLH200	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9183	0.9391	0.0362%	0.3833	N	N	-
CGPLH201	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9548	0.9180	0.0470%	0.8395	Y	Y	-
CGPLH202	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9471	0.9436	0.0501%	0.1088	N	N	-
CGPLH203	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9534	0.9575	0.0455%	0.2485	N	N	-
CGPLH205	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9075	0.9283	0.0409%	0.4401	N	N	-
CGPLH208	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9422	0.9409	0.0371%	0.2706	N	N	-
CGPLH209	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9556	0.9367	0.0427%	0.2213	N	N	-
CGPLH210	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9447	0.9181	0.0279%	0.3500	N	N	-
CGPLH211	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9538	0.9410	0.0317%	0.1752	N	N	-
CGPLH300	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9019	0.9200	0.0397%	0.0226	N	N	-
CGPLH307	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9576	0.9167	0.0388%	0.1789	N	N	-
CGPLH308	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9481	0.9352	0.0311%	0.0185	N	N	-
CGPLH309	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9672	0.9451	0.0226%	0.0441	N	N	-
CGPLH310	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9547	0.9527	0.0145%	0.7135	Y	N	-
CGPLH311	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9302	0.9348	0.0202%	0.2589	N	N	-
CGPLH314	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9482	0.9491	0.0212%	0.1632	N	N	-
CGPLH315	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8659	0.9427	0.0071%	0.3450	N	N	-
CGPLH316	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9374	0.9552	0.0191%	0.4697	N	N	-
CGPLH317	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9542	0.9352	0.0232%	0.1330	N	N	-
CGPLH319	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9578	0.9189	0.0263%	0.2232	N	N	-
CGPLH320	Healthy	WGS	Preoperative treatment naïve	NA	164	0.8913	0.9166	0.0222%	0.1095	N	N	-
CGPLH322	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8751	0.9411	0.0248%	0.0749	N	N	-
CGPLH324	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9519	0.9133	0.0402%	0.0126	N	N	-
CGPLH325	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9124	0.9202	0.0711%	0.0102	N	N	-
CGPLH326	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9574	0.9408	0.0213%	0.0475	N	N	-
CGPLH327	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9533	0.9071	0.1275%	0.4891	N	N	-
CGPLH328	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9643	0.9332	0.0256%	0.0234	N	N	-
CGPLH329	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9609	0.9396	0.0269%	0.0139	N	N	-
CGPLH330	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9118	0.9403	0.0203%	0.2642	N	N	-
CGPLH331	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9679	0.9377	0.0314%	0.0304	N	N	-
CGPLH333	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9474	0.9132	0.0350%	0.1633	N	N	-
CGPLH335	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8909	0.9333	0.0285%	0.0096	N	N	-
CGPLH336	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9248	0.9159	0.0159%	0.3872	N	N	-
CGPLH337	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9533	0.9262	0.0367%	0.2976	N	N	-
CGPLH338	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9388	0.9303	0.0103%	0.0431	N	N	-
CGPLH339	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9396	0.9338	0.0280%	0.0379	N	N	-
CGPLH340	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9488	0.9321	0.0210%	0.0379	N	N	-
CGPLH341	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9533	0.9187	0.0448%	0.1775	N	N	-
CGPLH342	Healthy	WGS	Preoperative treatment naïve	NA	166	0.7858	0.8986	0.0283%	0.0904	N	N	-
CGPLH343	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9421	0.9067	0.0632%	0.0160	N	N	-
CGPLH344	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9192	0.8998	0.0257%	0.0120	N	N	-
CGPLH345	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9345	0.9107	0.0445%	0.0031	N	N	-
CGPLH346	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9475	0.9074	0.0208%	0.0686	N	N	-
CGPLH350	Healthy	WGS	Preoperative treatment naïve	NA	171	0.9570	0.9288	0.0284%	0.0071	N	N	-
CGPLH351	Healthy	WGS	Preoperative treatment naïve	NA	168	0.8176	0.9294	0.0223%	0.0207	N	N	-
CGPLH352	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9521	0.9190	0.0613%	0.0512	N	N	-
CGPLH353	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9435	0.9130	0.0408%	0.0132	N	N	-
CGPLH354	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9481	0.9121	0.0318%	0.0082	N	N	-
CGPLH355	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9613	0.9308	0.0400%	0.6407	Y	N	-
CGPLH356	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9474	0.9312	0.0427%	0.2437	N	N	-
CGPLH357	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9255	0.9540	0.0217%	0.0070	N	N	-
CGPLH358	Healthy	WGS	Preoperative treatment naïve	NA	167	0.7777	0.9372	0.0174%	0.1451	N	N	-

Patient	Patient Type	Analysis Type	Timepoint	Stage at Diagnosis	Median cfDNA Fragment Size (bp)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Correlation of GC Corrected Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Fraction of Reads Mapped to Mitochondrial Genome	DELFI Score	Detected using DELFI (95% specificity)	Detected using DELFI (98% specificity)	Mutant Allele Fraction Detected using Targeted sequencing*
CGPLH360	Healthy	WGS	Preoperative treatment naïve	NA	168	0.8500	0.8775	0.0395%	0.0048	N	N	-
CGPLH361	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9261	0.9263	0.0268%	0.1524	N	N	-
CGPLH362	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9236	0.9503	0.0309%	0.4832	N	N	-
CGPLH363	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9488	0.9187	0.0620%	0.0199	N	N	-
CGPLH364	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9311	0.9480	0.0282%	0.8719	Y	Y	-
CGPLH365	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9371	0.9051	0.1740%	0.9683	Y	Y	-
CGPLH366	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9536	0.9170	0.0344%	0.0952	N	N	-
CGPLH367	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8748	0.9181	0.0353%	0.1235	N	N	-
CGPLH368	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9490	0.9076	0.1073%	0.1252	N	N	-
CGPLH369	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9428	0.9541	0.0246%	0.2621	N	N	-
CGPLH370	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9642	0.9423	0.0410%	0.0989	N	N	-
CGPLH371	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9621	0.9414	0.0734%	0.2173	N	N	-
CGPLH380	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9652	0.9424	0.0523%	0.0128	N	N	-
CGPLH381	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9541	0.9501	0.0435%	0.0152	N	N	-
CGPLH382	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9380	0.9584	0.0340%	0.0326	N	N	-
CGPLH383	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9700	0.9407	0.0389%	0.0035	N	N	-
CGPLH384	Healthy	WGS	Preoperative treatment naïve	NA	169	0.8061	0.9043	0.0207%	0.0258	N	N	-
CGPLH385	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8866	0.9246	0.0165%	0.0566	N	N	-
CGPLH386	Healthy	WGS	Preoperative treatment naïve	NA	167	0.6920	0.8859	0.0502%	0.2677	N	N	-
CGPLH387	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9583	0.9223	0.0375%	0.0081	N	N	-
CGPLH388	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9348	0.9266	0.0527%	0.0499	N	N	-
CGPLH389	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9409	0.9035	0.0667%	0.6565	Y	N	-
CGPLH390	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9216	0.9162	0.0229%	0.0837	N	N	-
CGPLH391	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9334	0.9162	0.0223%	0.0716	N	N	-
CGPLH392	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9165	0.9014	0.0424%	0.1305	N	N	-
CGPLH393	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9256	0.9045	0.0407%	0.0037	N	N	-
CGPLH394	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9257	0.9292	0.0522%	0.1073	N	N	-
CGPLH395	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8611	0.9254	0.0424%	0.0171	N	N	-
CGPLH396	Healthy	WGS	Preoperative treatment naïve	NA	167	0.7884	0.8928	0.0393%	0.0303	N	N	-
CGPLH398	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9463	0.9578	0.0242%	0.3195	N	N	-
CGPLH399	Healthy	WGS	Preoperative treatment naïve	NA	169	0.8780	0.9195	0.0679%	0.0685	N	N	-
CGPLH400	Healthy	WGS	Preoperative treatment naïve	NA	168	0.6862	0.9047	0.0300%	0.2103	N	N	-
CGPLH401	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9428	0.9339	0.0146%	0.0620	N	N	-
CGPLH402	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9353	0.8800	0.1516%	0.0395	N	N	-
CGPLH403	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9329	0.8829	0.0515%	0.0223	N	N	-
CGPLH404	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9402	0.8948	0.0528%	0.0027	N	N	-
CGPLH405	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9579	0.9204	0.0359%	0.0188	N	N	-
CGPLH406	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8188	0.8592	0.0667%	0.0206	N	N	-
CGPLH407	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9527	0.9099	0.0229%	0.0040	N	N	-
CGPLH408	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9584	0.9192	0.0415%	0.1257	N	N	-
CGPLH409	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9220	0.8950	0.0302%	0.0056	N	N	-
CGPLH410	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9102	0.9006	0.0453%	0.0019	N	N	-
CGPLH411	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9392	0.8857	0.0621%	0.0188	N	N	-
CGPLH412	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9561	0.9191	0.0140%	0.0417	N	N	-
CGPLH413	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9461	0.9145	0.0355%	0.0084	N	N	-
CGPLH414	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9258	0.9127	0.0290%	0.0284	N	N	-
CGPLH415	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9217	0.9025	0.0296%	0.0131	N	N	-
CGPLH416	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9672	0.9368	0.0198%	0.0645	N	N	-
CGPLH417	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9576	0.9192	0.0241%	0.0636	N	N	-
CGPLH418	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9376	0.9234	0.0306%	0.0052	N	N	-
CGPLH419	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9226	0.9295	0.0260%	0.0469	N	N	-
CGPLH420	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9164	0.9108	0.0187%	0.0420	N	N	-
CGPLH422	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9069	0.9006	0.0209%	0.0324	N	N	-
CGPLH423	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9606	0.9289	0.0832%	0.0139	N	N	-
CGPLH424	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9553	0.9265	0.1119%	0.0864	N	N	-
CGPLH425	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9722	0.9488	0.0722%	0.0156	N	N	-
CGPLH426	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9560	0.9080	0.0548%	0.1075	N	N	-
CGPLH427	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9594	0.9257	0.0182%	0.0470	N	N	-
CGPLH428	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9591	0.9272	0.0346%	0.0182	N	N	-
CGPLH429	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9358	0.8757	0.0593%	0.8143	Y	Y	-
CGPLH430	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9639	0.9307	0.0258%	0.0369	N	N	-
CGPLH431	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9570	0.9165	0.0234%	0.0174	N	N	-
CGPLH432	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9485	0.9082	0.0433%	0.0181	N	N	-
CGPLH434	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9671	0.9442	0.0297%	0.0060	N	N	-
CGPLH435	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9133	0.9097	0.0179%	0.0441	N	N	-
CGPLH436	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9360	0.9158	0.0290%	0.0958	N	N	-
CGPLH437	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9445	0.9245	0.0156%	0.0136	N	N	-
CGPLH438	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9537	0.9138	0.0169%	0.1041	N	N	-
CGPLH439	Healthy	WGS	Preoperative treatment naïve	NA	171	0.9547	0.9028	0.0226%	0.0078	N	N	-
CGPLH440	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9562	0.9295	0.0330%	0.0867	N	N	-
CGPLH441	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9660	0.9430	0.0178%	0.0085	N	N	-
CGPLH442	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9569	0.9406	0.0169%	0.0562	N	N	-

Patient	Patient Type	Analysis Type	Timepoint	Stage at Diagnosis	Median cfDNA Fragment Size (bp)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Correlation of GC Corrected Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Fraction of Reads Mapped to Mitochondrial Genome	DELFI Score	Detected using DELFI (95% specificity)	Detected using DELFI (98% specificity)	Mutant Allele Fraction Detected using Targeted sequencing*
CGPLH443	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9431	0.8801	0.0207%	0.0578	N	N	-
CGPLH444	Healthy	WGS	Preoperative treatment naïve	NA	171	0.9429	0.9066	0.0464%	0.0097	N	N	-
CGPLH445	Healthy	WGS	Preoperative treatment naïve	NA	171	0.9446	0.8750	0.0267%	0.1939	N	N	-
CGPLH446	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9502	0.9257	0.0281%	0.0340	N	N	-
CGPLH447	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9421	0.8968	0.0167%	0.0017	N	N	-
CGPLH448	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9553	0.9191	0.0401%	0.0389	N	N	-
CGPLH449	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9550	0.9254	0.0236%	0.0116	N	N	-
CGPLH450	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9572	0.9195	0.0331%	0.0597	N	N	-
CGPLH451	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9548	0.9167	0.0262%	0.0104	N	N	-
CGPLH452	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9498	0.8948	0.0480%	0.4722	N	N	-
CGPLH453	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9572	0.9339	0.0186%	0.3419	N	N	-
CGPLH455	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9626	0.9322	0.0455%	0.4536	N	N	-
CGPLH456	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9537	0.9098	0.0207%	0.0365	N	N	-
CGPLH457	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9429	0.9022	0.0298%	0.0364	N	N	-
CGPLH458	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9511	0.9275	0.0298%	0.1891	N	N	-
CGPLH459	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9609	0.9209	0.0281%	0.0371	N	N	-
CGPLH460	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9331	0.8863	0.0227%	0.1157	N	N	-
CGPLH463	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9506	0.9372	0.0130%	0.0865	N	N	-
CGPLH464	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9133	0.8511	0.0659%	0.2040	N	N	-
CGPLH465	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9251	0.9164	0.0325%	0.0124	N	N	-
CGPLH466	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9679	0.9408	0.0155%	0.1733	N	N	-
CGPLH467	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9273	0.9024	0.0229%	0.2303	N	N	-
CGPLH468	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8353	0.9345	0.0247%	0.5427	N	N	-
CGPLH469	Healthy	WGS	Preoperative treatment naïve	NA	169	0.8225	0.8799	0.0201%	0.5351	N	N	-
CGPLH470	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9073	0.9228	0.0715%	0.0327	N	N	-
CGPLH471	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9354	0.9333	0.0150%	0.0406	N	N	-
CGPLH472	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8509	0.8915	0.0481%	0.6152	N	N	-
CGPLH473	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9206	0.9128	0.0443%	0.2995	N	N	-
CGPLH474	Healthy	WGS	Preoperative treatment naïve	NA	168	0.8474	0.9245	0.0316%	0.6246	Y	N	-
CGPLH475	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9155	0.9233	0.0269%	0.0736	N	N	-
CGPLH476	Healthy	WGS	Preoperative treatment naïve	NA	169	0.8807	0.9059	0.0236%	0.0143	N	N	-
CGPLH477	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9129	0.9376	0.0382%	0.1111	N	N	-
CGPLH478	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9586	0.9344	0.0256%	0.0828	N	N	-
CGPLH479	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9303	0.9207	0.0221%	0.0648	N	N	-
CGPLH480	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9522	0.9046	0.0672%	0.7473	Y	N	-
CGPLH481	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9568	0.9113	0.0311%	0.0282	N	N	-
CGPLH482	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9379	0.9336	0.0162%	0.0058	N	N	-
CGPLH483	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9518	0.9275	0.0251%	0.0495	N	N	-
CGPLH484	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9630	0.9366	0.0261%	0.0048	N	N	-
CGPLH485	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9547	0.9128	0.0291%	0.1064	N	N	-
CGPLH486	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9199	0.9042	0.0220%	0.0820	N	N	-
CGPLH487	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9575	0.9098	0.0594%	0.2154	N	N	-
CGPLH488	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9618	0.9298	0.0409%	0.0903	N	N	-
CGPLH490	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8950	0.8794	0.0432%	0.0424	N	N	-
CGPLH491	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9631	0.9332	0.0144%	0.0223	N	N	-
CGPLH492	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9335	0.8799	0.0322%	0.0311	N	N	-
CGPLH493	Healthy	WGS	Preoperative treatment naïve	NA	168	0.8718	0.9330	0.0065%	0.0280	N	N	-
CGPLH494	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9623	0.9303	0.0232%	0.0824	N	N	-
CGPLH495	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8777	0.8908	0.0513%	0.0465	N	N	-
CGPLH496	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8788	0.9398	0.0208%	0.0572	N	N	-
CGPLH497	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9576	0.9330	0.0335%	0.0404	N	N	-
CGPLH498	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9526	0.9315	0.0403%	0.0752	N	N	-
CGPLH499	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9733	0.9442	0.0198%	0.0149	N	N	-
CGPLH500	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9542	0.9240	0.0433%	0.0754	N	N	-
CGPLH501	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9526	0.9308	0.0300%	0.0159	N	N	-
CGPLH502	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9512	0.9200	0.0351%	0.0841	N	N	-
CGPLH503	Healthy	WGS	Preoperative treatment naïve	NA	169	0.8947	0.8939	0.0398%	0.0649	N	N	-
CGPLH504	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9561	0.9324	0.0440%	0.1231	N	N	-
CGPLH505	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9554	0.9243	0.0605%	0.1869	N	N	-
CGPLH506	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9733	0.9498	0.0264%	0.0180	N	N	-
CGPLH507	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9222	0.9192	0.0186%	0.0848	N	N	-
CGPLH508	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9674	0.9410	0.0150%	0.1077	N	N	-
CGPLH509	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9475	0.9323	0.0163%	0.0828	N	N	-
CGPLH510	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9459	0.9548	0.0128%	0.0378	N	N	-
CGPLH511	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9714	0.9493	0.0224%	0.1779	N	N	-
CGPLH512	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9442	0.9244	0.0094%	0.0076	N	N	-
CGPLH513	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9705	0.9595	0.0441%	0.5250	N	N	-
CGPLH514	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9690	0.9369	0.0114%	0.3131	N	N	-
CGPLH515	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9568	0.9283	0.0352%	0.4936	N	N	-
CGPLH516	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9508	0.9298	0.0175%	0.0916	N	N	-
CGPLH517	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9635	0.9494	0.0161%	0.0059	N	N	-
CGPLH518	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9647	0.9432	0.0274%	0.0130	N	N	-

Patient	Patient Type	Analysis Type	Timepoint	Stage at Diagnosis	Median cfDNA Fragment Size (bp)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Correlation of GC Corrected Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Fraction of Reads Mapped to Mitochondrial Genome	DELFI Score	Detected using DELFI (95% specificity)	Detected using DELFI (98% specificity)	Mutant Allele Fraction Detected using Targeted sequencing*
CGPLH519	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9366	0.9351	0.0171%	0.0949	N	N	-
CGPLH520	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9649	0.9476	0.0241%	0.0944	N	N	-
CGPLH625	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8766	0.9231	0.0697%	0.4977	N	N	-
CGPLH626	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9011	0.9269	0.0231%	0.3100	N	N	-
CGPLH639	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9482	0.9410	0.0549%	0.0773	N	N	-
CGPLH640	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9131	0.9264	0.0232%	0.0327	N	N	-
CGPLH642	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9641	0.9376	0.0768%	0.0555	N	N	-
CGPLH643	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9450	0.9271	0.0579%	0.1325	N	N	-
CGPLH644	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9398	0.8948	0.0621%	0.3819	N	N	-
CGPLH646	Healthy	WGS	Preoperative treatment naïve	NA	172	0.9296	0.8691	0.0462%	0.2423	N	N	-
CGPLLU144	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.8702	0.8681	0.0423%	0.9892	Y	Y	5.10%
CGPLLU161	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.9126	0.9187	0.0273%	0.9955	Y	Y	0.20%
CGPLLU162	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.7753	0.8836	0.1410%	0.9986	Y	Y	0.22%
CGPLLU163	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.4770	0.3033	0.0724%	0.9940	Y	Y	0.21%
CGPLLU168	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	163	0.9164	0.8842	0.0712%	0.9861	Y	Y	0.07%
CGPLLU169	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	163	0.9326	0.9169	0.0846%	0.9866	Y	Y	0.13%
CGPLLU176	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.9572	0.9081	0.0626%	0.8769	Y	Y	ND
CGPLLU177	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.8472	0.6790	0.0564%	0.9924	Y	Y	3.22%
CGPLLU203	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.9119	0.8741	0.0568%	0.9178	Y	Y	0.11%
CGPLLU205	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	163	0.9518	0.9476	0.0495%	0.9877	Y	Y	ND
CGPLLU207	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9344	0.9379	0.0421%	0.9908	Y	Y	0.32%
CGPLLU208	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.9091	0.8942	0.0815%	0.9273	Y	Y	1.33%
CGPLOV11	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	166	0.8902	0.8872	0.0469%	0.9343	Y	Y	0.87%
CGPLOV12	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.8779	0.8973	0.2767%	0.9764	Y	Y	ND
CGPLOV13	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	166	0.7560	0.9146	0.1017%	0.9690	Y	Y	0.35%
CGPLOV15	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	165	0.8585	0.8552	0.0876%	0.9945	Y	Y	3.54%
CGPLOV16	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	165	0.9052	0.9046	0.0400%	0.9983	Y	Y	1.12%
CGPLOV19	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.7854	0.7578	0.1089%	0.9989	Y	Y	46.35%
CGPLOV20	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.8711	0.9154	0.0581%	0.9749	Y	Y	0.21%
CGPLOV21	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	167	0.8942	0.8869	0.0677%	0.9961	Y	Y	14.36%
CGPLOV22	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	164	0.8944	0.9355	0.0251%	0.9775	Y	Y	0.49%
CGPLOV23	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	169	0.8510	0.8850	0.1520%	0.9916	Y	Y	1.39%
CGPLOV24	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.9449	0.8995	0.0303%	0.9856	Y	Y	ND
CGPLOV25	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.9590	0.9228	0.0141%	0.8544	Y	Y	ND
CGPLOV26	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	161	0.8148	0.9351	0.0646%	0.9946	Y	Y	ND
CGPLOV28	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.9635	0.9378	0.0647%	0.8160	Y	Y	ND
CGPLOV31	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	167	0.9461	0.9293	0.1606%	0.9795	Y	Y	ND
CGPLOV32	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.9582	0.9338	0.1351%	0.8609	Y	Y	ND
CGPLOV37	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	170	0.9397	0.8831	0.0986%	0.9849	Y	Y	0.29%
CGPLOV38	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.5779	0.6502	0.0490%	0.9990	Y	Y	4.89%
CGPLOV40	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	170	0.6097	0.8127	0.6145%	0.9983	Y	Y	6.73%
CGPLOV41	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	167	0.9403	0.8929	0.1110%	0.9484	Y	Y	0.60%
CGPLOV42	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.9265	0.9086	0.0469%	0.9979	Y	Y	1.24%
CGPLOV43	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.9626	0.9342	0.0432%	0.6042	N	N	ND
CGPLOV44	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	164	0.9536	0.9173	0.1946%	0.9962	Y	Y	0.37%
CGPLOV46	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.9622	0.9291	0.0801%	0.9128	Y	Y	ND
CGPLOV47	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	165	0.9704	0.9461	0.0270%	0.3410	N	N	3.20%
CGPLOV48	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.9675	0.9429	0.0422%	0.4874	N	N	10.70%
CGPLOV49	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	164	0.8998	0.8083	0.1527%	0.9897	Y	Y	2.03%
CGPLOV50	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	165	0.9682	0.9382	0.0807%	0.9955	Y	Y	ND
CGPLPA112	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	164	0.8914	0.9429	0.0268%	0.0856	N	N	-
CGPLPA113	Duodenal Cancer	WGS	Preoperative treatment naïve	I	170	0.8751	0.7674	1.0116%	0.9935	Y	Y	-
CGPLPA114	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	166	0.9098	0.9246	0.0836%	0.7598	Y	Y	-
CGPLPA115	Bile Duct Cancer	WGS	Preoperative treatment naïve	IV	165	0.8053	0.8310	0.0763%	0.9974	Y	Y	-
CGPLPA117	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	165	0.9395	0.8767	0.1084%	0.9049	Y	Y	-
CGPLPA118	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.9406	0.9001	0.1842%	0.9859	Y	Y	0.14%
CGPLPA122	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.8231	0.8058	0.2047%	0.9983	Y	Y	37.22%
CGPLPA124	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9108	0.9238	0.1542%	0.8791	Y	Y	0.62%
CGPLPA125	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	166	0.9675	0.9373	0.0273%	0.0226	N	N	-
CGPLPA126	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9155	0.9139	0.4349%	0.9908	Y	Y	ND
CGPLPA127	Bile Duct Cancer	WGS	Preoperative treatment naïve	IV	167	0.8916	0.8117	0.4371%	0.9789	Y	Y	-
CGPLPA128	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.9262	0.9003	0.1317%	0.9812	Y	Y	ND
CGPLPA129	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9220	0.9155	0.0642%	0.9839	Y	Y	ND
CGPLPA130	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.8586	0.8499	0.1005%	0.9895	Y	Y	ND
CGPLPA131	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.7707	0.9195	0.0780%	0.9885	Y	Y	0.21%
CGPLPA134	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	160	0.7502	0.8847	0.0260%	0.9896	Y	Y	0.93%
CGPLPA135	Bile Duct Cancer	WGS	Preoperative treatment naïve	I	165	0.9495	0.9184	0.0558%	0.6594	Y	N	-
CGPLPA136	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.9289	0.9050	0.0769%	0.9596	Y	Y	0.10%
CGPLPA137	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	166	0.9568	0.9320	0.0499%	0.7282	Y	N	-
CGPLPA139	Bile Duct Cancer	WGS	Preoperative treatment naïve	IV	166	0.9511	0.9374	0.0465%	0.0743	N	N	-
CGPLPA14	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.8718	0.9069	0.0515%	0.9824	Y	Y	-
CGPLPA140	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9215	0.9548	0.0330%	0.9761	Y	Y	0.21%

Patient	Patient Type	Analysis Type	Timepoint	Stage at Diagnosis	Median cfDNA Fragment Size (bp)	Correlation of Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Correlation of GC Corrected Fragment Ratio Profile to Median Fragment Ratio Profile of Healthy Individuals	Fraction of Reads Mapped to Mitochondrial Genome	DELFI Score	Detected using DELFI (95% specificity)	Detected using DELFI (98% specificity)	Mutant Allele Fraction Detected using Targeted sequencing*
CGPLPA141	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	165	0.9172	0.9381	0.0920%	0.9988	Y	Y	-
CGPLPA15	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9111	0.8927	0.0160%	0.8737	Y	Y	-
CGPLPA155	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	165	0.9496	0.9313	0.0260%	0.8013	Y	Y	-
CGPLPA156	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9479	0.9432	0.0290%	0.0159	N	N	-
CGPLPA165	Bile Duct Cancer	WGS	Preoperative treatment naïve	I	168	0.9596	0.9309	0.0558%	0.2158	N	N	-
CGPLPA168	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	162	0.7838	0.7757	0.3123%	0.9878	Y	Y	-
CGPLPA17	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.8624	0.6771	1.2600%	0.9956	Y	Y	-
CGPLPA184	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	165	0.9100	0.9203	0.0897%	0.9926	Y	Y	-
CGPLPA187	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	165	0.8577	0.8968	0.0658%	0.9675	Y	Y	-
CGPLPA23	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.7887	0.6938	0.5785%	0.9984	Y	Y	-
CGPLPA25	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.9549	0.9239	0.0380%	0.8103	Y	Y	-
CGPLPA26	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.9598	0.9356	0.0247%	0.8231	Y	Y	-
CGPLPA28	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.9069	0.8938	0.0546%	0.9036	Y	Y	-
CGPLPA33	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.8361	0.8553	0.0894%	0.9967	Y	Y	-
CGPLPA34	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	168	0.8946	0.8885	0.0439%	0.7977	Y	Y	-
CGPLPA37	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.8840	0.9294	0.0410%	0.9924	Y	Y	-
CGPLPA38	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.8746	0.8941	0.0372%	0.9851	Y	Y	-
CGPLPA39	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.8562	0.7972	0.5058%	0.9951	Y	Y	-
CGPLPA40	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.8563	0.8865	0.2268%	0.9920	Y	Y	-
CGPLPA42	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9126	0.8863	0.0283%	0.3544	N	N	-
CGPLPA46	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	169	0.8274	0.7525	1.0982%	0.9952	Y	Y	-
CGPLPA47	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.8376	0.8439	0.1596%	0.9946	Y	Y	-
CGPLPA48	Pancreatic Cancer	WGS	Preoperative treatment naïve	I	167	0.9391	0.9207	1.0232%	0.2251	N	N	-
CGPLPA52	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9452	0.8863	0.0154%	0.0963	N	N	-
CGPLPA53	Pancreatic Cancer	WGS	Preoperative treatment naïve	I	163	0.9175	0.8776	0.1824%	0.8946	Y	Y	-
CGPLPA58	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.9587	0.9224	0.0803%	0.9056	Y	Y	-
CGPLPA59	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	163	0.9230	0.9193	0.1479%	0.9759	Y	Y	-
CGPLPA67	Pancreatic Cancer	WGS	Preoperative treatment naïve	III	166	0.9574	0.9248	0.0329%	0.6716	Y	N	-
CGPLPA69	Pancreatic Cancer	WGS	Preoperative treatment naïve	I	168	0.9172	0.8592	0.0459%	0.1245	N	N	-
CGPLPA71	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9424	0.8888	0.0479%	0.0524	N	N	-
CGPLPA74	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.9688	0.9372	0.0292%	0.0108	N	N	-
CGPLPA76	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	163	0.9681	0.9441	0.0345%	0.0897	N	N	-
CGPLPA85	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.9137	0.9337	0.0363%	0.0508	N	N	-
CGPLPA86	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.8875	0.8042	0.7564%	0.9864	Y	Y	-
CGPLPA92	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9389	0.9003	0.1458%	0.7061	Y	N	-
CGPLPA93	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.8585	0.8023	0.6250%	0.9978	Y	Y	-
CGPLPA94	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	162	0.9365	0.9433	0.0180%	0.9025	Y	Y	-
CGPLPA95	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	163	0.8542	0.8571	0.0815%	0.9941	Y	Y	-
CGST102	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.9496	0.9057	0.0704%	0.8581	Y	Y	0.43%
CGST11	Gastric cancer	WGS	Preoperative treatment naïve	IV	169	0.9419	0.9161	0.0651%	0.1435	N	N	-
CGST110	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	167	0.9626	0.9232	0.0817%	0.8900	Y	Y	ND
CGST114	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	164	0.9535	0.9038	0.0317%	0.5693	N	N	ND
CGST13	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9369	0.9156	0.0321%	0.9754	Y	Y	ND
CGST131	Gastric cancer	WGS	Preoperative treatment naïve	III	171	0.9428	0.8886	0.2752%	0.9409	Y	Y	-
CGST141	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	168	0.9621	0.9206	0.0388%	0.2008	N	N	ND
CGST16	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	166	0.7804	0.8355	0.1744%	0.9974	Y	Y	0.93%
CGST18	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9523	0.9111	0.0299%	0.3842	N	N	0.14%
CGST21	Gastric cancer	WGS	Preoperative treatment naïve	II	165	-0.4778	0.2687	0.2299%	0.9910	Y	Y	-
CGST26	Gastric cancer	WGS	Preoperative treatment naïve	IV	166	0.9554	0.9140	0.0399%	0.5009	N	N	-
CGST28	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	X	169	0.9076	0.7832	0.1295%	0.9955	Y	Y	1.62%
CGST30	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	169	0.9246	0.9121	0.0338%	0.9183	Y	Y	0.42%
CGST32	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9431	0.8639	0.0247%	0.9612	Y	Y	2.99%
CGST33	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.7999	0.7770	0.0799%	0.9805	Y	Y	2.32%
CGST38	Gastric cancer	WGS	Preoperative treatment naïve	0	168	0.9368	0.8758	0.0640%	0.9416	Y	Y	-
CGST39	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	164	0.8742	0.9401	0.0287%	0.8480	Y	Y	ND
CGST41	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	168	0.8194	0.9284	0.0398%	0.9263	Y	Y	ND
CGST45	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	168	0.9576	0.9036	0.0220%	0.9713	Y	Y	ND
CGST47	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.9611	0.9096	0.0157%	0.9687	Y	Y	0.45%
CGST48	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	167	0.7469	0.5445	0.0220%	0.9975	Y	Y	4.21%
CGST53	Gastric cancer	WGS	Preoperative treatment naïve	0	173	-0.0019	0.7888	0.1140%	0.9914	Y	Y	-
CGST58	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	169	0.9470	0.9094	0.0696%	0.9705	Y	Y	ND
CGST67	Gastric cancer	WGS	Preoperative treatment naïve	I	170	0.9352	0.8853	0.3245%	0.9032	Y	Y	-
CGST77	Gastric cancer	WGS	Preoperative treatment naïve	IV	170	0.0043	0.8295	0.1851%	0.9981	Y	Y	-
CGST80	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	168	0.9313	0.8846	0.0490%	0.9513	Y	Y	1.04%
CGST81	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.9480	0.8851	0.0138%	0.9748	Y	Y	0.20%

*ND indicates not detected. Please see reference 10 for additional information on targeted sequencing analyes. DELFI cancer detection at 95% and 98% specificity is based on scores greater than 0.6200 and 0.7500, respectively.

WHAT IS CLAIMED IS:

1. A method of determining a cell free DNA (cfDNA) fragmentation profile of a mammal, the method comprising:

processing cfDNA fragments obtained from a sample obtained from the mammal into sequencing libraries;

subjecting the sequencing libraries to low-coverage whole genome sequencing to obtain sequenced fragments;

mapping the sequenced fragments to a genome to obtain windows of mapped sequences; and

analyzing the windows of mapped sequences to determine cfDNA fragment lengths.

2. The method of claim 1, wherein the mapped sequences comprise tens to thousands of windows.

3. The method of claims 1-2, wherein the windows are non-overlapping windows.

4. The method of any one of claims 1-3, wherein the windows each comprise about 5 million base pairs.

5. The method of any one of claims 1-4, wherein a cfDNA fragmentation profile is determined within each window.

6. The method of any one of claims 1-5, wherein cfDNA fragmentation profile comprises a median fragment size.

7. The method of any one of claims 1-5, wherein cfDNA fragmentation profile comprises a fragment size distribution.

8. The method of any one of claims 1-5, wherein the cfDNA fragmentation profile comprises a ratio of small cfDNA fragments to large cfDNA fragments in said windows of mapped sequences.

9. The method of any one of claims 1-5, wherein the cfDNA fragmentation profile comprises the sequence coverage of small cfDNA fragments in windows across the genome.

10. The method of any one of claims 1-5, wherein the cfDNA fragmentation profile comprises the sequence coverage of large cfDNA fragments in windows across the genome.

11. The method of any one of claims 1-5, wherein the cfDNA fragmentation profile comprises the sequence coverage of small and large cfDNA fragments in windows across the genome.

12. The method of any one of claims 1-11, wherein the cfDNA fragmentation profile is over the whole genome.

13. The method of any one of claims 1-11, wherein the cfDNA fragmentation profile is over a subgenomic interval.

14. A method of identifying a mammal as having cancer, the method comprising:

determining a cell free DNA (cfDNA) fragmentation profile in a sample obtained from the mammal;

comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile; and

identifying the mammal as having cancer when the cfDNA fragmentation profile obtained from the mammal is different from the reference cfDNA fragmentation profile.

15. The method of claim 14, wherein the reference cfDNA fragmentation profile is a cfDNA fragmentation profile of a healthy mammal.

16. The method of claim 15, wherein the reference cfDNA fragmentation profile is generated by determining a cfDNA fragmentation profile in a sample obtained from the healthy mammal.

17. The method of claim 14, wherein the reference DNA fragmentation pattern is a reference nucleosome cfDNA fragmentation profile.

18. The method of any one of claims 14-17, wherein the cfDNA fragmentation profile comprises a median fragment size, and wherein a median fragment size of the cfDNA fragmentation profile is shorter than a median fragment size of the reference cfDNA fragmentation profile.

19. The method of any one of claims 14-17, wherein the cfDNA fragmentation profile comprises a fragment size distribution, and wherein a fragment size distribution of the cfDNA fragmentation profile differs by at least 10 nucleotides as compared to a fragment size distribution of the reference cfDNA fragmentation profile.

20. The method of any one of claims 14-17, wherein the cfDNA fragmentation profile comprises a ratio of small cfDNA fragments to large cfDNA fragments in said windows of mapped sequences, wherein a small cfDNA fragment is 100 base pairs (bp) to 150 bp in length, wherein a large cfDNA fragments is 151 bp to 220 bp in length, and wherein a correlation of fragment ratios in the cfDNA fragmentation profile is lower than a correlation of fragment ratios of the reference cfDNA fragmentation profile.

21. The method of any one of claims 14-17, wherein the cfDNA fragmentation profile comprises the sequence coverage of small cfDNA fragments in windows across the genome.

22. The method of any one of claims 14-17, wherein the cfDNA fragmentation profile comprises the sequence coverage of large cfDNA fragments in windows across the genome.

23. The method of any one of claims 14-17, wherein the cfDNA fragmentation profile comprises the sequence coverage of small and large cfDNA fragments in windows across the genome.

24. The method of any one of claims 14-17, wherein the cancer is selected from the group consisting of: colorectal cancer, lung cancer, breast cancer, gastric cancers, pancreatic cancers, bile duct cancers, and ovarian cancer.

25. The method of claim 14, wherein the step of comparing comprises comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile over the whole genome.

26. The method of claim 14, wherein the step of comparing comprises comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile over a subgenomic interval.

27. The method of any one of claim 14-23, wherein the mammal has previously been administered a cancer treatment to treat the cancer.

28. The method of claim 27, wherein the cancer treatment is selected from the group consisting of: surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy, targeted therapy, and combinations thereof.

29. The method of any one of claims 14-28, further comprising administering to the mammal a cancer treatment selected from the group consisting of: surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy, targeted therapy, and combinations thereof.

30. The method of claim 29, wherein the mammal is monitored for the presence of cancer after administration of the cancer treatment.

31. The method of any one of claim 14 to claim 30, the method further comprising identifying one or more cancer-specific sequence alterations in the sample.

32. The method of any one of claim 14 to claim 30, the method further comprising identifying one or more chromosomal abnormalities in the sample.

33. The method of claim 32, wherein the one or more chromosomal abnormalities comprises a copy number change in one or more chromosome arms.

34. A method of identifying the tissue of origin of a cancer in a mammal identified as having a cancer, the method comprising:

determining a cell free DNA (cfDNA) fragmentation profile in a sample obtained from the mammal;

comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile; and

identifying the tissue of origin of the cancer in a mammal when the cfDNA fragmentation profile obtained from the mammal matches a reference cfDNA fragmentation profiles from a mammal identified as having a cancer with the same tissue of origin.

35. The method of claim 34, wherein the reference cfDNA fragmentation profile comprises reference cfDNA fragmentation profiles from mammals identified as having one or more of colorectal cancer, lung cancer, breast cancer, gastric cancers, pancreatic cancers, bile duct cancers, and ovarian cancer.

36. The method of claim 35, wherein the reference cfDNA fragmentation profile is generated by determining a cfDNA fragmentation profile in a sample obtained from the mammals

identified as having one or more or colorectal cancer, lung cancer, breast cancer, gastric cancers, pancreatic cancers, bile duct cancers, and ovarian cancer.

37. The method of claim 34, wherein the reference DNA fragmentation pattern is a reference nucleosome cfDNA fragmentation profile.

38. The method of any one of claims 34-37, wherein the cfDNA fragmentation profile comprises a median fragment size, and wherein a median fragment size of the cfDNA fragmentation profile is shorter than a median fragment size of the reference cfDNA fragmentation profile.

39. The method of any one of claims 34-37, wherein the cfDNA fragmentation profile comprises a fragment size distribution, and wherein a fragment size distribution of the cfDNA fragmentation profile differs by at least 10 nucleotides as compared to a fragment size distribution of the reference cfDNA fragmentation profile.

40. The method of any one of claims 34-37, wherein the cfDNA fragmentation profile comprises a ratio of small cfDNA fragments to large cfDNA fragments in said windows of mapped sequences, wherein a small cfDNA fragment is 100 base pairs (bp) to 150 bp in length, wherein a large cfDNA fragments is 151 bp to 220 bp in length, and wherein a correlation of fragment ratios in the cfDNA fragmentation profile is lower than a correlation of fragment ratios of the reference cfDNA fragmentation profile.

41. The method of any one of claims 34-37, wherein the cfDNA fragmentation profile comprises the sequence coverage of small cfDNA fragments in windows across the genome.

42. The method of any one of claims 34-37, wherein the cfDNA fragmentation profile comprises the sequence coverage of large cfDNA fragments in windows across the genome.

43. The method of any one of claims 34-37, wherein the cfDNA fragmentation profile comprises the sequence coverage of small and large cfDNA fragments in windows across the genome.

44. The method of any one of claims 34-37, wherein the cancer is selected from the group consisting of: colorectal cancer, lung cancer, breast cancer, gastric cancers, pancreatic cancers, bile duct cancers, and ovarian cancer.

45. The method of claim 34, wherein the step of comparing comprises comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile over the whole genome.

46. The method of claim 34, wherein the step of comparing comprises comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile over a subgenomic interval.

47. The method of any one of claims 34-46, the method further comprising identifying one or more cancer-specific sequence alterations in the sample.

48. The method of any one of claims 34-46, the method further comprising identifying one or more chromosomal abnormalities in the sample.

49. The method of claim 48, wherein the one or more chromosomal abnormalities comprises a copy number change in one or more chromosome arms.

50. A method treating a mammal having cancer, the method comprising:

identifying said mammal as having cancer, wherein said identifying comprises:

determining a cell free DNA (cfDNA) fragmentation profile in a sample obtained from the mammal;

comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile; and

identifying the mammal as having cancer when the cfDNA fragmentation profile obtained from the mammal is different from the reference cfDNA fragmentation profile; and

administering a cancer treatment to said mammal.

51. The method of claim 50, wherein said mammal is a human.

52. The method of any one of claims 50-51, wherein the cancer is selected from the group consisting of: colorectal cancer, lung cancer, breast cancer, gastric cancers, pancreatic cancers, bile duct cancers, and ovarian cancer.

53. The method of any one of claims 50-52, wherein said cancer treatment is selected from the group consisting of: surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy, targeted therapy, and combinations thereof.

54. The method of any one of claims 50-53, wherein the reference cfDNA fragmentation profile is a cfDNA fragmentation profile of a healthy mammal.

55. The method of claim 54, wherein the reference cfDNA fragmentation profile is generated by determining a cfDNA fragmentation profile in a sample obtained from the healthy mammal.

56. The method of any one of claims 50-53, wherein the reference DNA fragmentation pattern is a reference nucleosome cfDNA fragmentation profile.

57. The method of any one of claims 50-56, wherein the cfDNA fragmentation profile comprises a median fragment size, and wherein a median fragment size of the cfDNA

fragmentation profile is shorter than a median fragment size of the reference cfDNA fragmentation profile.

58. The method of any one of claims 50-56, wherein the cfDNA fragmentation profile comprises a fragment size distribution, and wherein a fragment size distribution of the cfDNA fragmentation profile differs by at least 10 nucleotides as compared to a fragment size distribution of the reference cfDNA fragmentation profile.

59. The method of any one of claims 50-56, wherein the cfDNA fragmentation profile comprises a ratio of small cfDNA fragments to large cfDNA fragments in said windows of mapped sequences, wherein a small cfDNA fragment is 100 base pairs (bp) to 150 bp in length, wherein a large cfDNA fragments is 151 bp to 220 bp in length, and wherein a correlation of fragment ratios in the cfDNA fragmentation profile is lower than a correlation of fragment ratios of the reference cfDNA fragmentation profile.

60. The method of any one of claims 50-56, wherein the cfDNA fragmentation profile comprises the sequence coverage of small cfDNA fragments in windows across the genome.

61. The method of any one of claims 50-56, wherein the cfDNA fragmentation profile comprises the sequence coverage of large cfDNA fragments in windows across the genome.

62. The method of any one of claims 50-56, wherein the cfDNA fragmentation profile comprises the sequence coverage of small and large cfDNA fragments in windows across the genome.

63. The method of any one of claims 50-62, wherein the step of comparing comprises comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile over the whole genome.

64. The method of any one of claims 50-62, wherein the step of comparing comprises comparing the cfDNA fragmentation profile to a reference cfDNA fragmentation profile over a subgenomic interval.

65. The method of any one of claims 50-64, wherein the mammal has previously been administered a cancer treatment to treat the cancer.

66. The method of claim 65, wherein the cancer treatment is selected from the group consisting of: surgery, adjuvant chemotherapy, neoadjuvant chemotherapy, radiation therapy, hormone therapy, cytotoxic therapy, immunotherapy, adoptive T cell therapy, targeted therapy, and combinations thereof.

67. The method of any one of claims 50-66, wherein the mammal is monitored for the presence of cancer after administration of the cancer treatment.

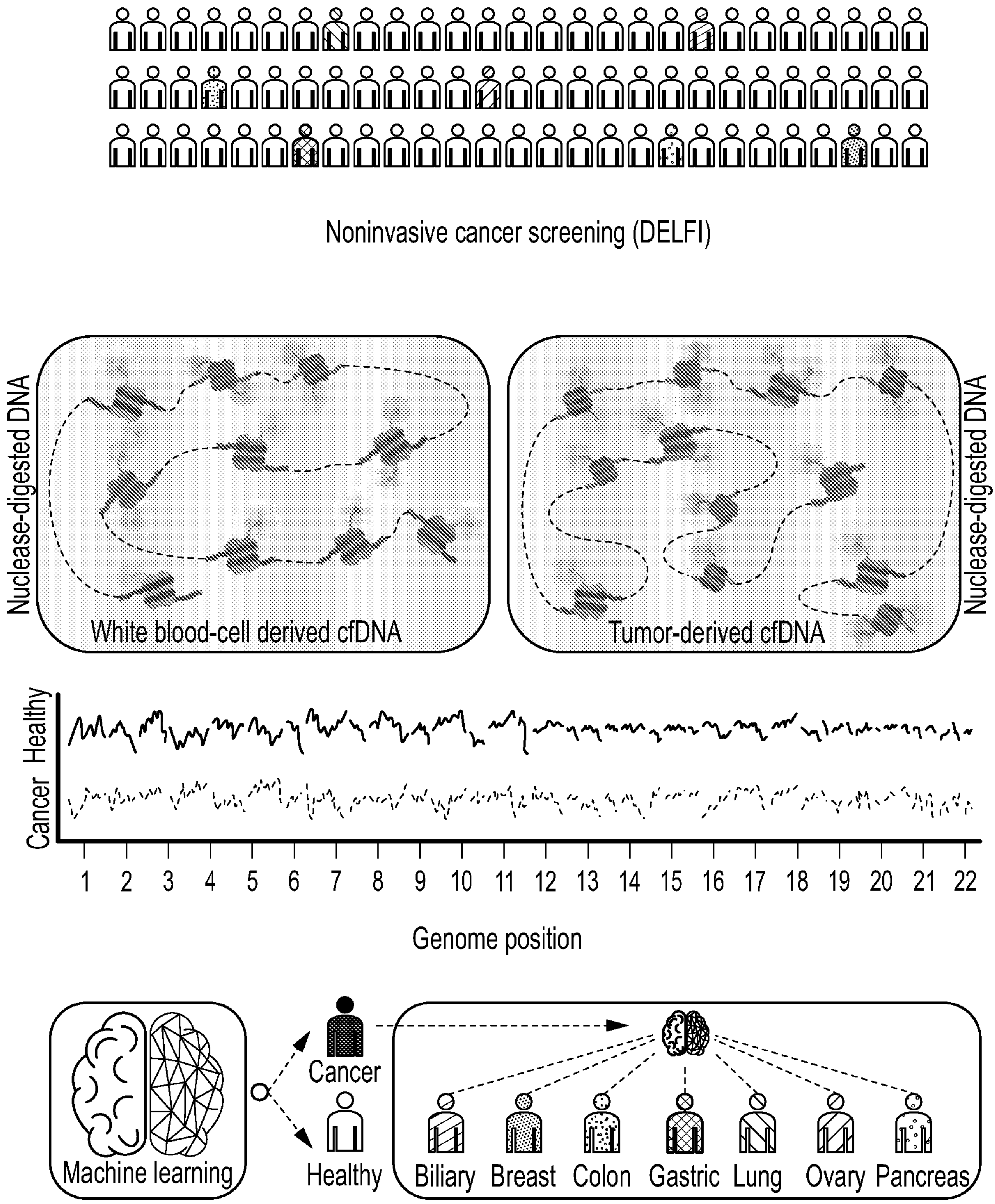

Noninvasive cancer screening (DELFI)
Nuclease-digested DNA
White blood-cell derived cfDNA
Tumor-derived cfDNA
Nuclease-digested DNA
Healthy
Cancer
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
Genome position
Machine learning
Cancer
Healthy
Biliary
Breast
Colon
Gastric
Lung
Ovary
Pancreas

FIG. 1

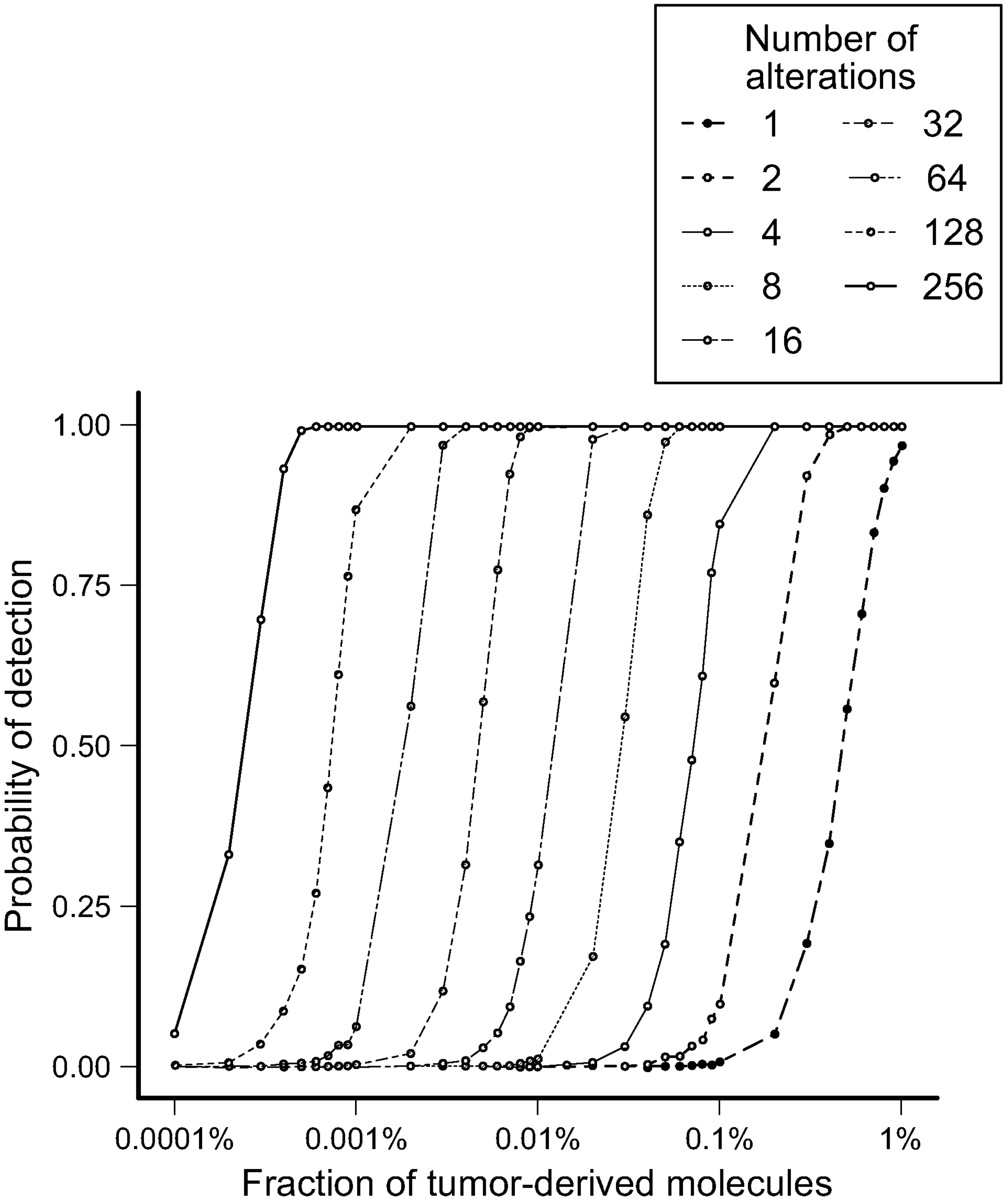

Number of alterations
1
2
4
8
16
32
64
128
256
Probability of detection
1.00
0.75
0.50
0.25
0.00
0.0001%
0.001%
0.01%
0.1%
1%
Fraction of tumor-derived molecules

FIG. 2

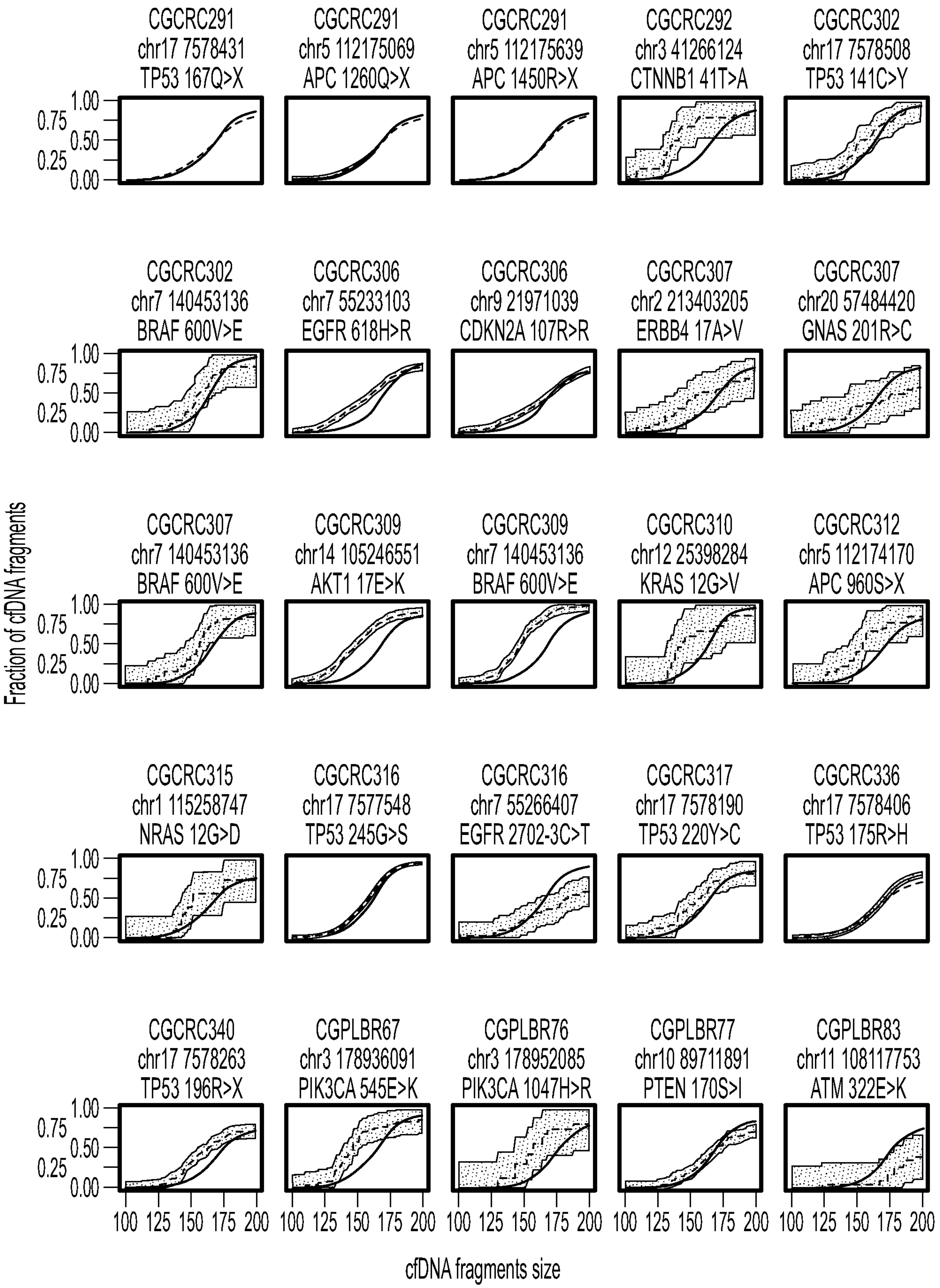

CGCRC291
chr17 7578431
TP53 167Q>X
CGCRC291
chr5 112175069
APC 1260Q>X
CGCRC291
chr5 112175639
APC 1450R>X
CGCRC292
chr3 41266124
CTNNB1 41T>A
CGCRC302
chr17 7578508
TP53 141C>Y
CGCRC302
chr7 140453136
BRAF 600V>E
CGCRC306
chr7 55233103
EGFR 618H>R
CGCRC306
chr9 21971039
CDKN2A 107R>R
CGCRC307
chr2 213403205
ERBB4 17A>V
CGCRC307
chr20 57484420
GNAS 201R>C
CGCRC307
chr7 140453136
BRAF 600V>E
CGCRC309
chr14 105246551
AKT1 17E>K
CGCRC309
chr7 140453136
BRAF 600V>E
CGCRC310
chr12 25398284
KRAS 12G>V
CGCRC312
chr5 112174170
APC 960S>X
CGCRC315
chr1 115258747
NRAS 12G>D
CGCRC316
chr17 7577548
TP53 245G>S
CGCRC316
chr7 55266407
EGFR 2702-3C>T
CGCRC317
chr17 7578190
TP53 220Y>C
CGCRC336
chr17 7578406
TP53 175R>H
CGCRC340
chr17 7578263
TP53 196R>X
CGPLBR67
chr3 178936091
PIK3CA 545E>K
CGPLBR76
chr3 178952085
PIK3CA 1047H>R
CGPLBR77
chr10 89711891
PTEN 170S>I
CGPLBR83
chr11 108117753
ATM 322E>K
Fraction of cfDNA fragments
1.00
0.75
0.50
0.25
0.00
100 125 150 175 200
cfDNA fragments size

FIG. 3

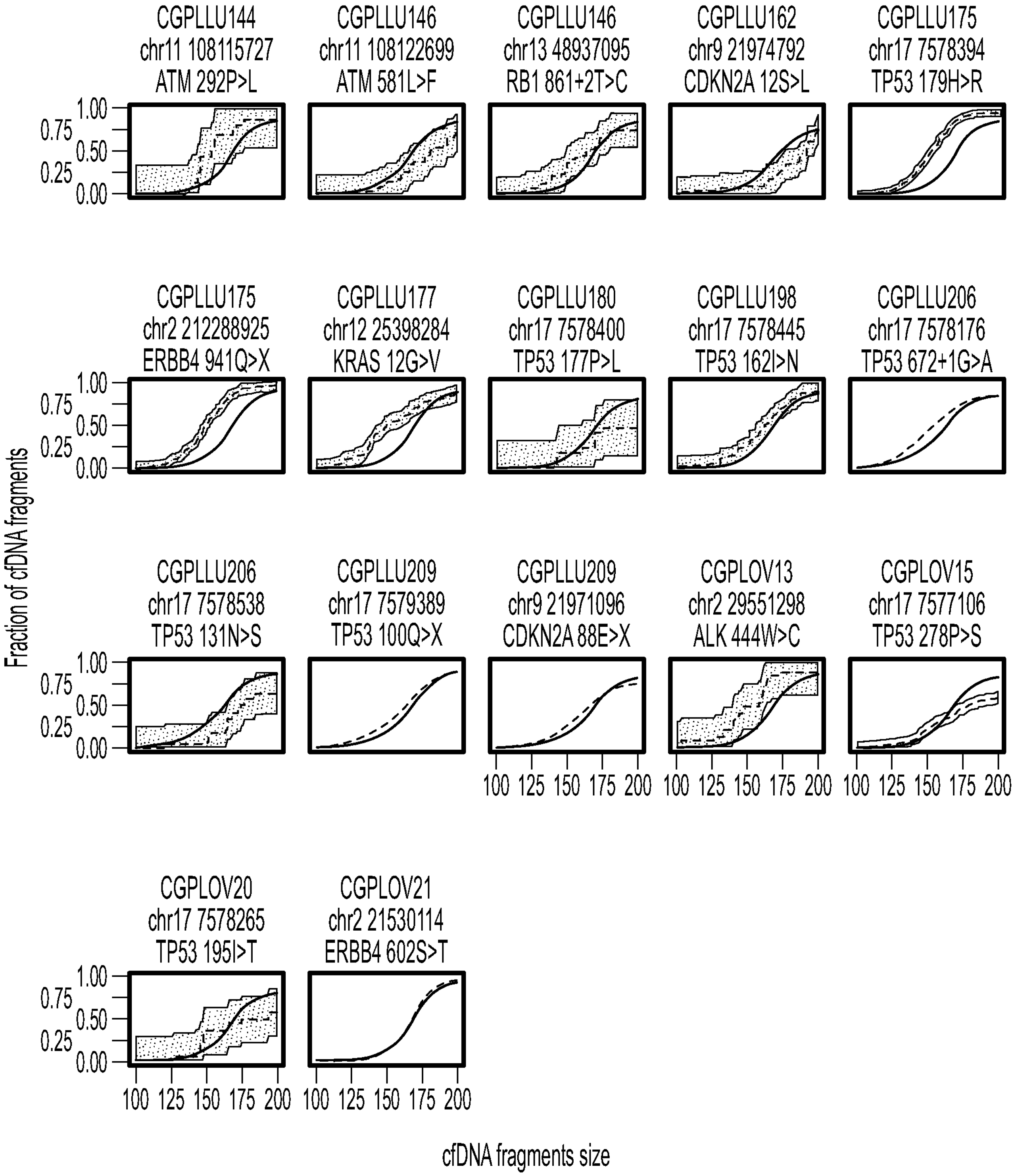

CGPLLU144
chr11 108115727
ATM 292P>L
CGPLLU146
chr11 108122699
ATM 581L>F
CGPLLU146
chr13 48937095
RB1 861+2T>C
CGPLLU162
chr9 21974792
CDKN2A 12S>L
CGPLLU175
chr17 7578394
TP53 179H>R
CGPLLU175
chr2 212288925
ERBB4 941Q>X
CGPLLU177
chr12 25398284
KRAS 12G>V
CGPLLU180
chr17 7578400
TP53 177P>L
CGPLLU198
chr17 7578445
TP53 162I>N
CGPLLU206
chr17 7578176
TP53 672+1G>A
CGPLLU206
chr17 7578538
TP53 131N>S
CGPLLU209
chr17 7579389
TP53 100Q>X
CGPLLU209
chr9 21971096
CDKN2A 88E>X
CGPLOV13
chr2 29551298
ALK 444W>C
CGPLOV15
chr17 7577106
TP53 278P>S
CGPLOV20
chr17 7578265
TP53 195I>T
CGPLOV21
chr2 21530114
ERBB4 602S>T
Fraction of cfDNA fragments
1.00
0.75
0.50
0.25
0.00
100
125
150
175
200
cfDNA fragments size

FIG. 3 (Cont.)

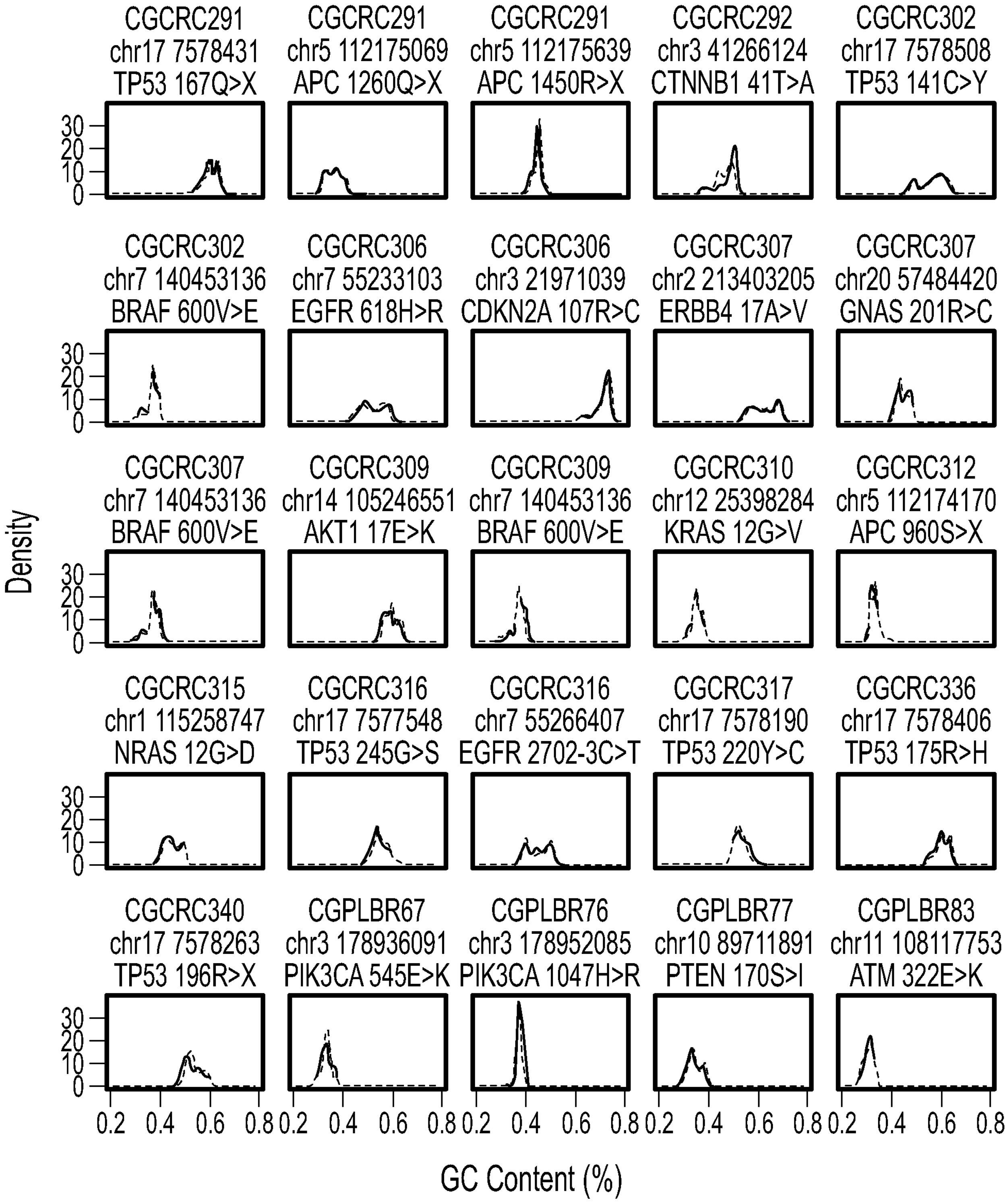

CGCRC291
chr17 7578431
TP53 167Q>X
CGCRC291
chr5 112175069
APC 1260Q>X
CGCRC291
chr5 112175639
APC 1450R>X
CGCRC292
chr3 41266124
CTNNB1 41T>A
CGCRC302
chr17 7578508
TP53 141C>Y
CGCRC302
chr7 140453136
BRAF 600V>E
CGCRC306
chr7 55233103
EGFR 618H>R
CGCRC306
chr3 21971039
CDKN2A 107R>C
CGCRC307
chr2 213403205
ERBB4 17A>V
CGCRC307
chr20 57484420
GNAS 201R>C
CGCRC307
chr7 140453136
BRAF 600V>E
CGCRC309
chr14 105246551
AKT1 17E>K
CGCRC309
chr7 140453136
BRAF 600V>E
CGCRC310
chr12 25398284
KRAS 12G>V
CGCRC312
chr5 112174170
APC 960S>X
CGCRC315
chr1 115258747
NRAS 12G>D
CGCRC316
chr17 7577548
TP53 245G>S
CGCRC316
chr7 55266407
EGFR 2702-3C>T
CGCRC317
chr17 7578190
TP53 220Y>C
CGCRC336
chr17 7578406
TP53 175R>H
CGCRC340
chr17 7578263
TP53 196R>X
CGPLBR67
chr3 178936091
PIK3CA 545E>K
CGPLBR76
chr3 178952085
PIK3CA 1047H>R
CGPLBR77
chr10 89711891
PTEN 170S>I
CGPLBR83
chr11 108117753
ATM 322E>K
Density
30
20
10
0
0.2
0.4
0.6
0.8
GC Content (%)

FIG. 4A

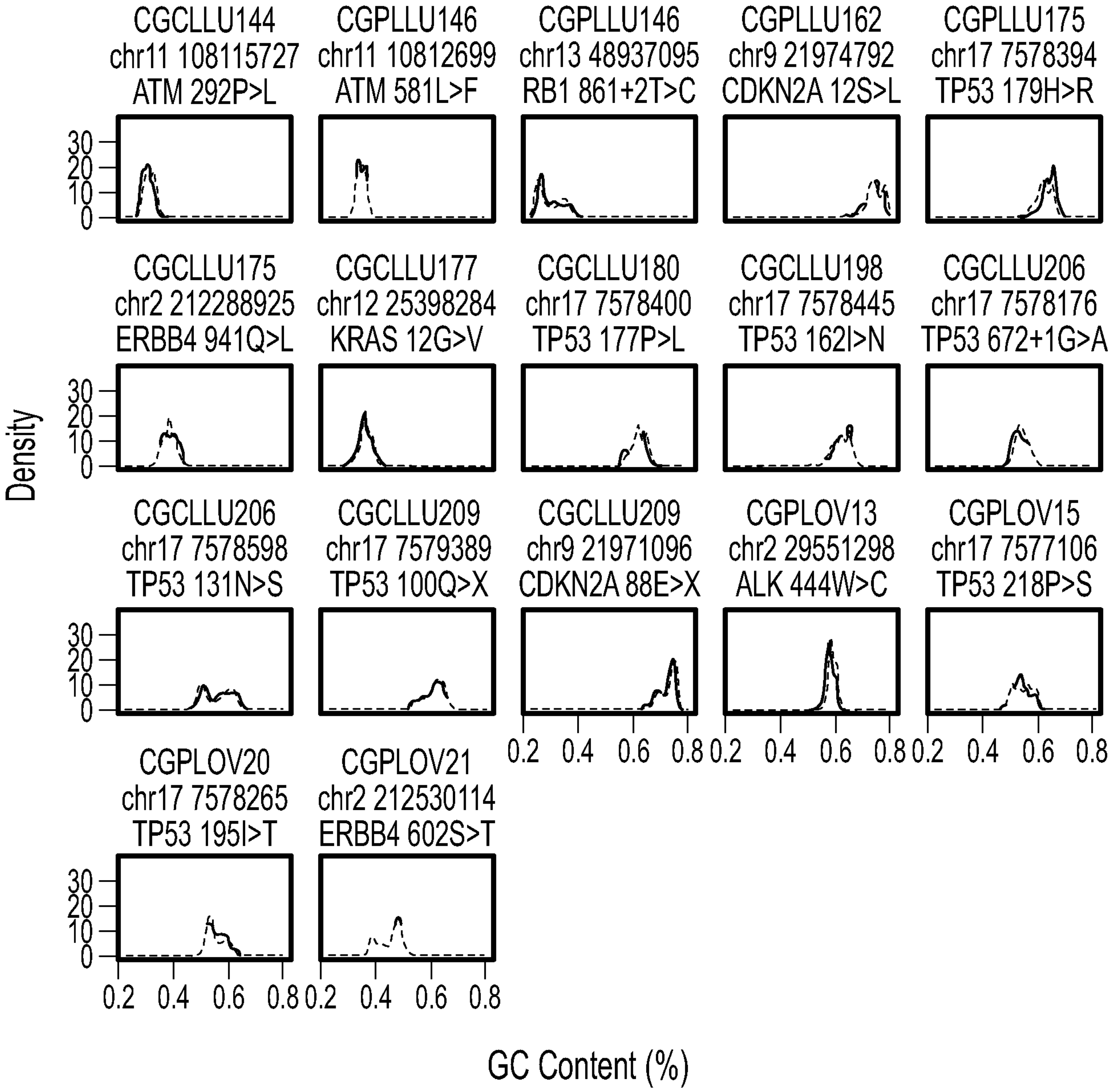

CGCLLU144
chr11 108115727
ATM 292P>L
CGPLLU146
chr11 10812699
ATM 581L>F
CGPLLU146
chr13 48937095
RB1 861+2T>C
CGPLLU162
chr9 21974792
CDKN2A 12S>L
CGPLLU175
chr17 7578394
TP53 179H>R
CGCLLU175
chr2 212288925
ERBB4 941Q>L
CGCLLU177
chr12 25398284
KRAS 12G>V
CGCLLU180
chr17 7578400
TP53 177P>L
CGCLLU198
chr17 7578445
TP53 162I>N
CGCLLU206
chr17 7578176
TP53 672+1G>A
CGCLLU206
chr17 7578598
TP53 131N>S
CGCLLU209
chr17 7579389
TP53 100Q>X
CGCLLU209
chr9 21971096
CDKN2A 88E>X
CGPLOV13
chr2 29551298
ALK 444W>C
CGPLOV15
chr17 7577106
TP53 218P>S
CGPLOV20
chr17 7578265
TP53 195I>T
CGPLOV21
chr2 212530114
ERBB4 602S>T
Density
0
10
20
30
0.2
0.4
0.6
0.8
GC Content (%)

FIG. 4A (Cont.)

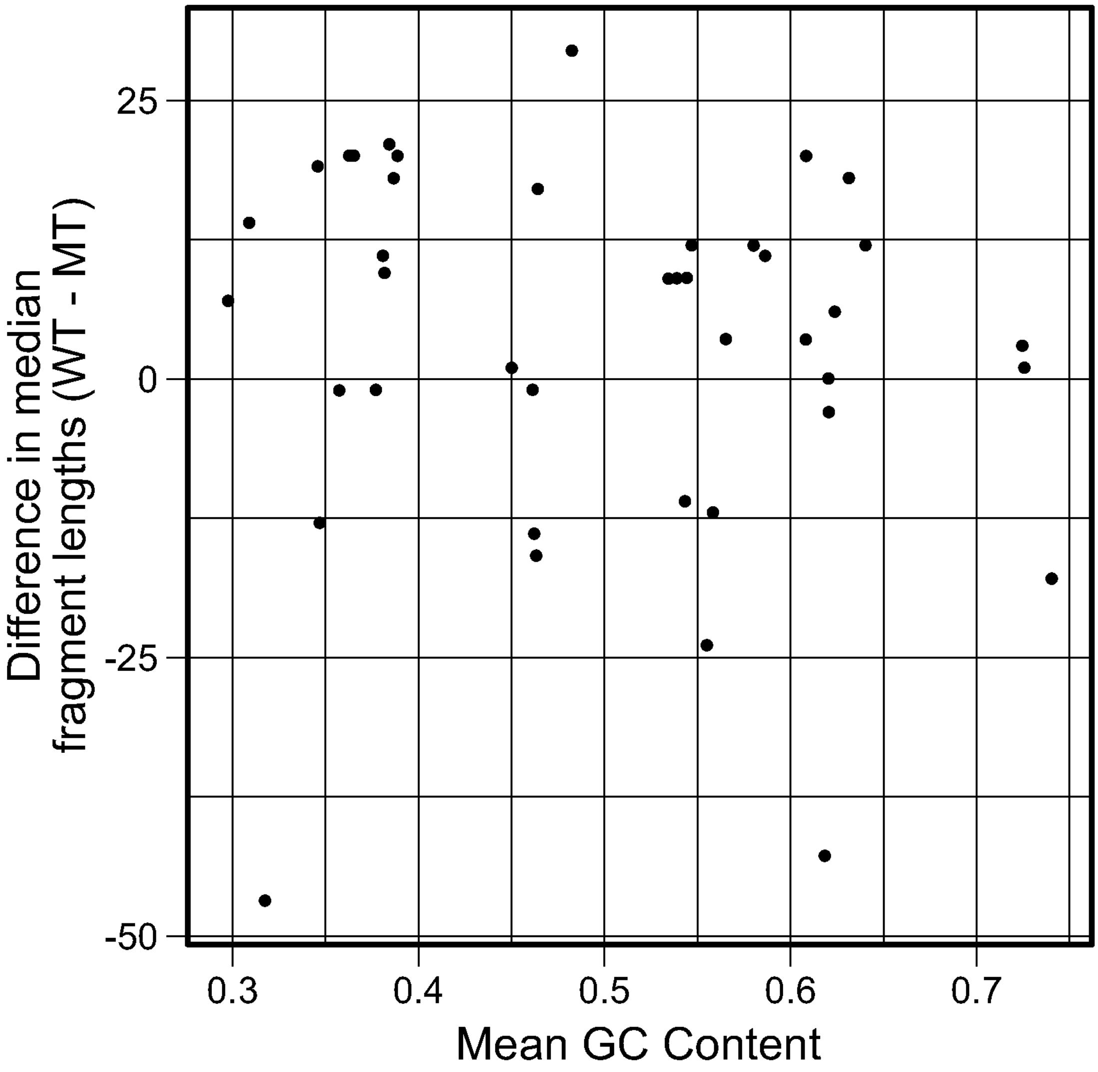

Difference in median fragment lengths (WT - MT)
25
0
-25
-50
0.3
0.4
0.5
0.6
0.7
Mean GC Content

FIG. 4B

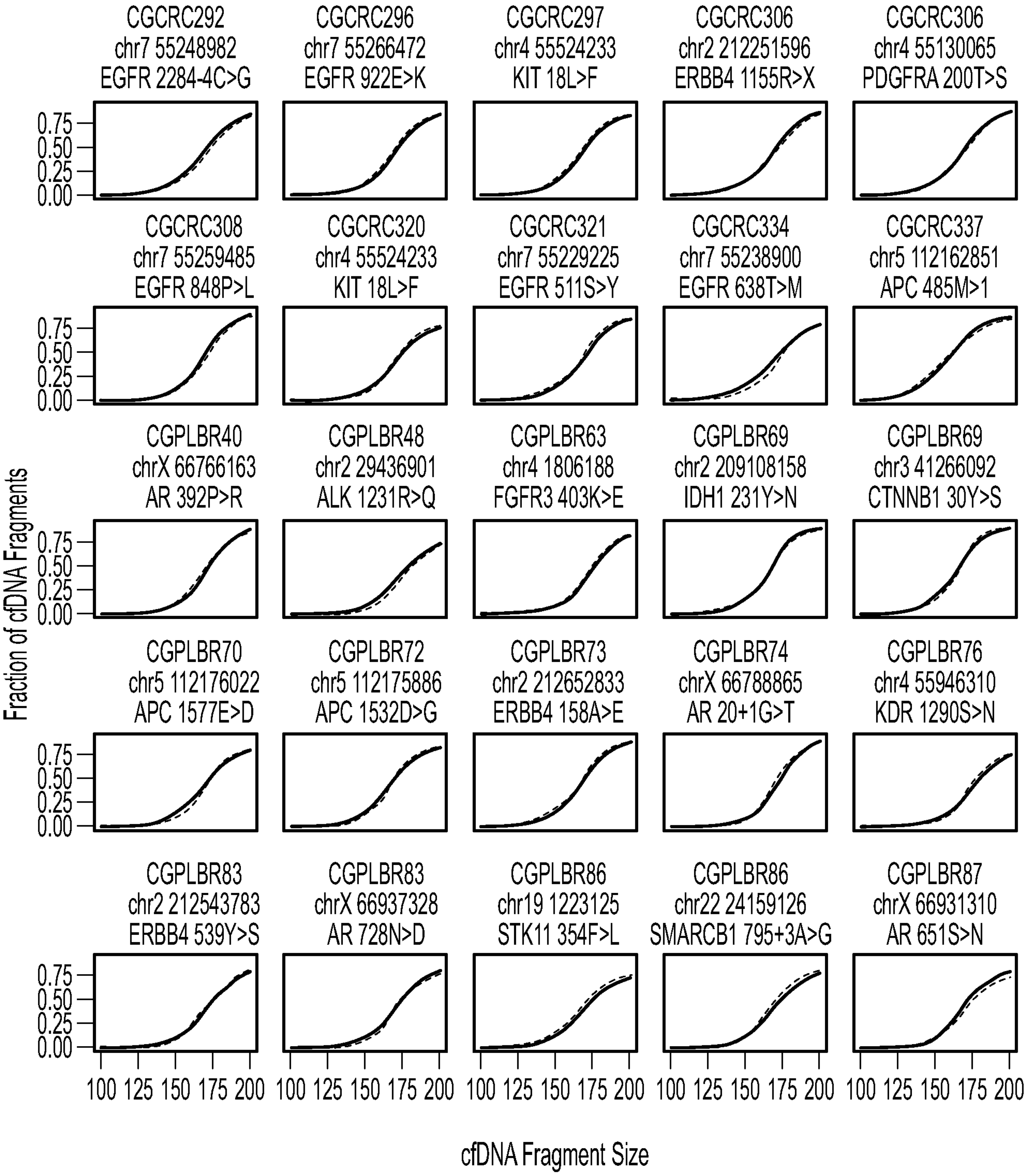

CGCRC292
chr7 55248982
EGFR 2284-4C>G
CGCRC296
chr7 55266472
EGFR 922E>K
CGCRC297
chr4 55524233
KIT 18L>F
CGCRC306
chr2 212251596
ERBB4 1155R>X
CGCRC306
chr4 55130065
PDGFRA 200T>S
CGCRC308
chr7 55259485
EGFR 848P>L
CGCRC320
chr4 55524233
KIT 18L>F
CGCRC321
chr7 55229225
EGFR 511S>Y
CGCRC334
chr7 55238900
EGFR 638T>M
CGCRC337
chr5 112162851
APC 485M>1
CGPLBR40
chrX 66766163
AR 392P>R
CGPLBR48
chr2 29436901
ALK 1231R>Q
CGPLBR63
chr4 1806188
FGFR3 403K>E
CGPLBR69
chr2 209108158
IDH1 231Y>N
CGPLBR69
chr3 41266092
CTNNB1 30Y>S
CGPLBR70
chr5 112176022
APC 1577E>D
CGPLBR72
chr5 112175886
APC 1532D>G
CGPLBR73
chr2 212652833
ERBB4 158A>E
CGPLBR74
chrX 66788865
AR 20+1G>T
CGPLBR76
chr4 55946310
KDR 1290S>N
CGPLBR83
chr2 212543783
ERBB4 539Y>S
CGPLBR83
chrX 66937328
AR 728N>D
CGPLBR86
chr19 1223125
STK11 354F>L
CGPLBR86
chr22 24159126
SMARCB1 795+3A>G
CGPLBR87
chrX 66931310
AR 651S>N
Fraction of cfDNA Fragments
0.75
0.50
0.25
0.00
100 125 150 175 200
cfDNA Fragment Size

FIG. 5

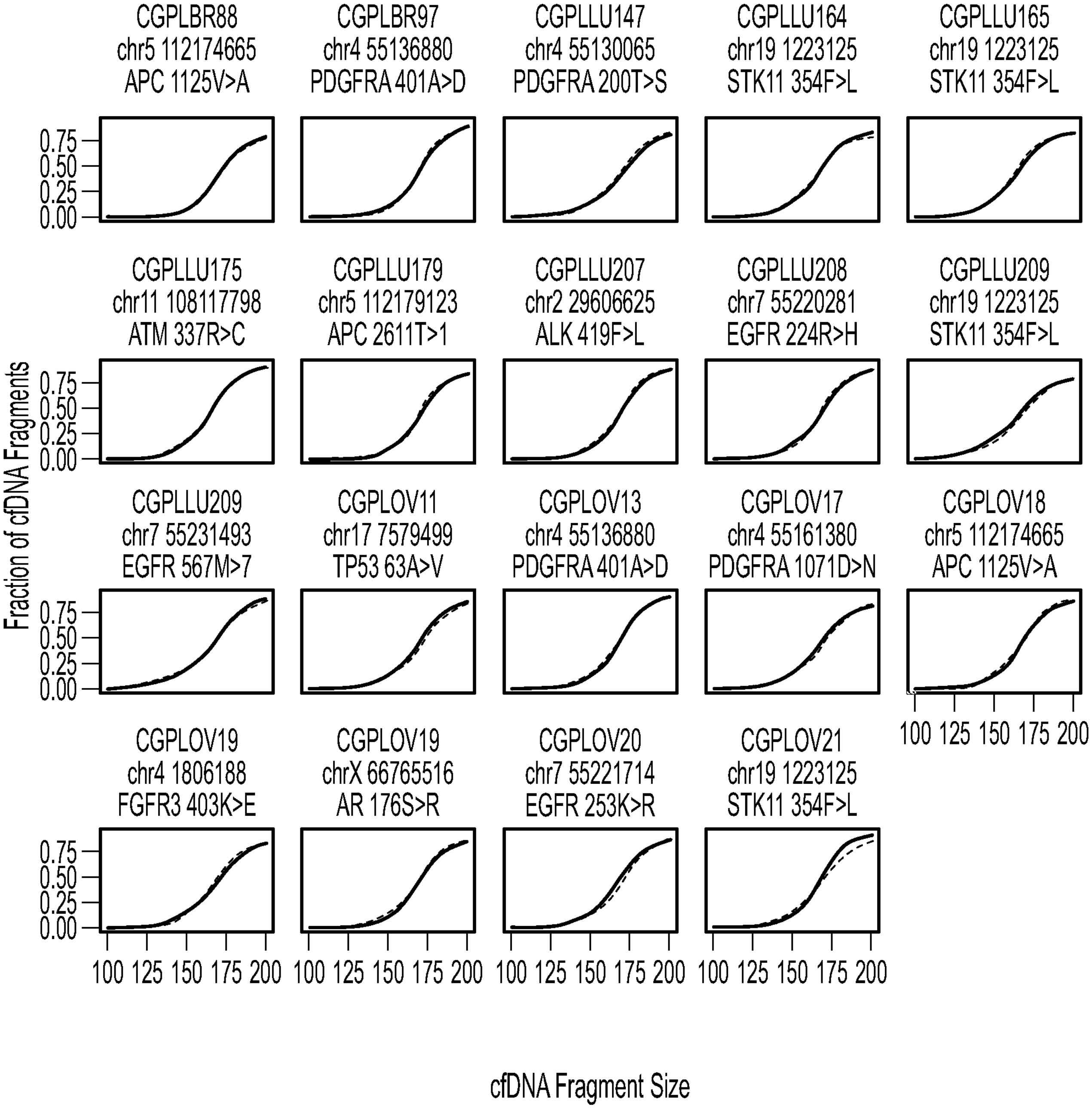

CGPLBR88
chr5 112174665
APC 1125V>A
CGPLBR97
chr4 55136880
PDGFRA 401A>D
CGPLLU147
chr4 55130065
PDGFRA 200T>S
CGPLLU164
chr19 1223125
STK11 354F>L
CGPLLU165
chr19 1223125
STK11 354F>L
CGPLLU175
chr11 108117798
ATM 337R>C
CGPLLU179
chr5 112179123
APC 2611T>1
CGPLLU207
chr2 29606625
ALK 419F>L
CGPLLU208
chr7 55220281
EGFR 224R>H
CGPLLU209
chr19 1223125
STK11 354F>L
CGPLLU209
chr7 55231493
EGFR 567M>7
CGPLOV11
chr17 7579499
TP53 63A>V
CGPLOV13
chr4 55136880
PDGFRA 401A>D
CGPLOV17
chr4 55161380
PDGFRA 1071D>N
CGPLOV18
chr5 112174665
APC 1125V>A
CGPLOV19
chr4 1806188
FGFR3 403K>E
CGPLOV19
chrX 66765516
AR 176S>R
CGPLOV20
chr7 55221714
EGFR 253K>R
CGPLOV21
chr19 1223125
STK11 354F>L
Fraction of cfDNA Fragments
0.00
0.25
0.50
0.75
100
125
150
175
200
cfDNA Fragment Size

FIG. 5(Cont.)

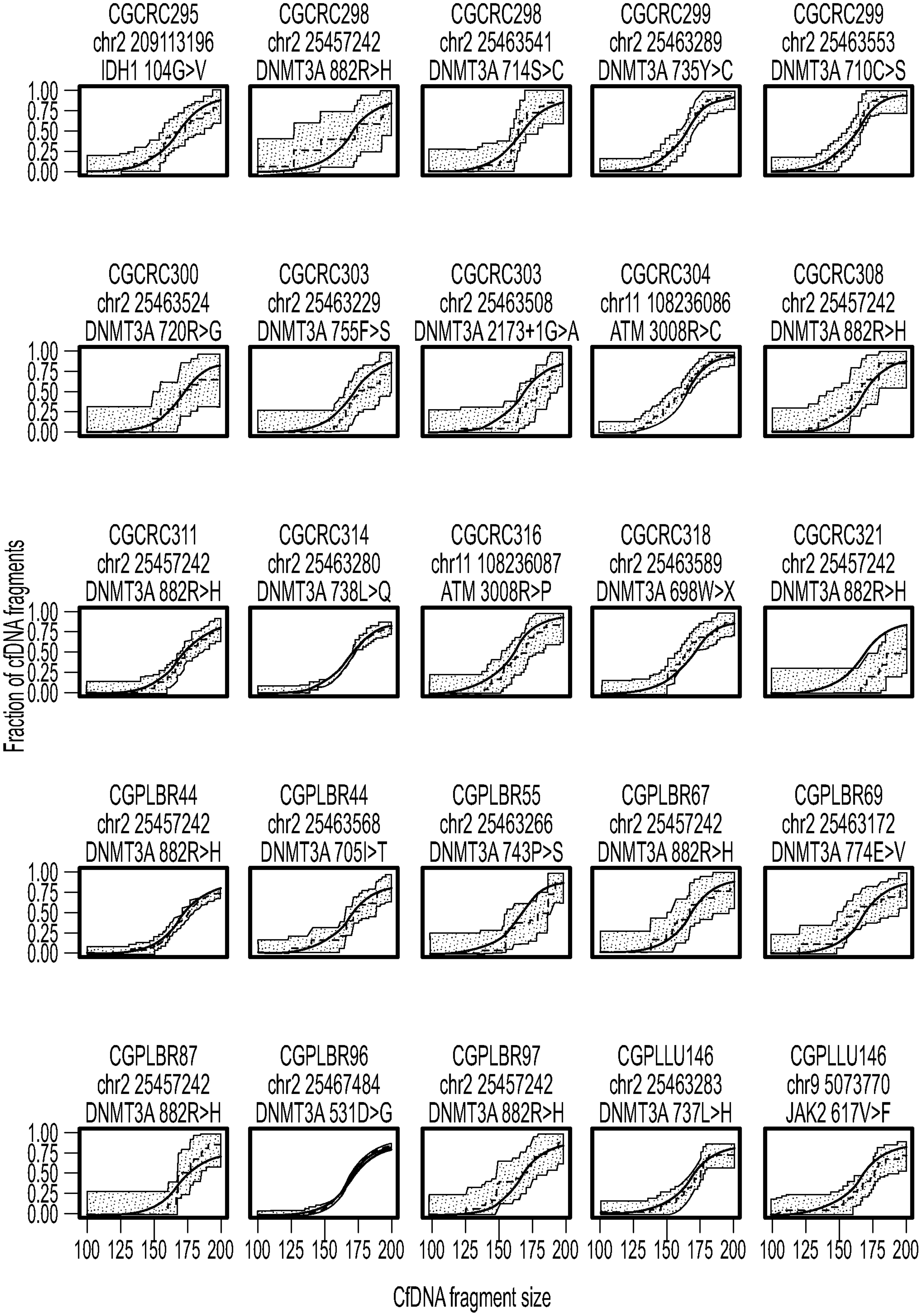

CGCRC295
chr2 209113196
IDH1 104G>V
CGCRC298
chr2 25457242
DNMT3A 882R>H
CGCRC298
chr2 25463541
DNMT3A 714S>C
CGCRC299
chr2 25463289
DNMT3A 735Y>C
CGCRC299
chr2 25463553
DNMT3A 710C>S
CGCRC300
chr2 25463524
DNMT3A 720R>G
CGCRC303
chr2 25463229
DNMT3A 755F>S
CGCRC303
chr2 25463508
DNMT3A 2173+1G>A
CGCRC304
chr11 108236086
ATM 3008R>C
CGCRC308
chr2 25457242
DNMT3A 882R>H
CGCRC311
chr2 25457242
DNMT3A 882R>H
CGCRC314
chr2 25463280
DNMT3A 738L>Q
CGCRC316
chr11 108236087
ATM 3008R>P
CGCRC318
chr2 25463589
DNMT3A 698W>X
CGCRC321
chr2 25457242
DNMT3A 882R>H
CGPLBR44
chr2 25457242
DNMT3A 882R>H
CGPLBR44
chr2 25463568
DNMT3A 705I>T
CGPLBR55
chr2 25463266
DNMT3A 743P>S
CGPLBR67
chr2 25457242
DNMT3A 882R>H
CGPLBR69
chr2 25463172
DNMT3A 774E>V
CGPLBR87
chr2 25457242
DNMT3A 882R>H
CGPLBR96
chr2 25467484
DNMT3A 531D>G
CGPLBR97
chr2 25457242
DNMT3A 882R>H
CGPLLU146
chr2 25463283
DNMT3A 737L>H
CGPLLU146
chr9 5073770
JAK2 617V>F
1.00
0.75
0.50
0.25
0.00
Fraction of cfDNA fragments
100 125 150 175 200
CfDNA fragment size

FIG. 6

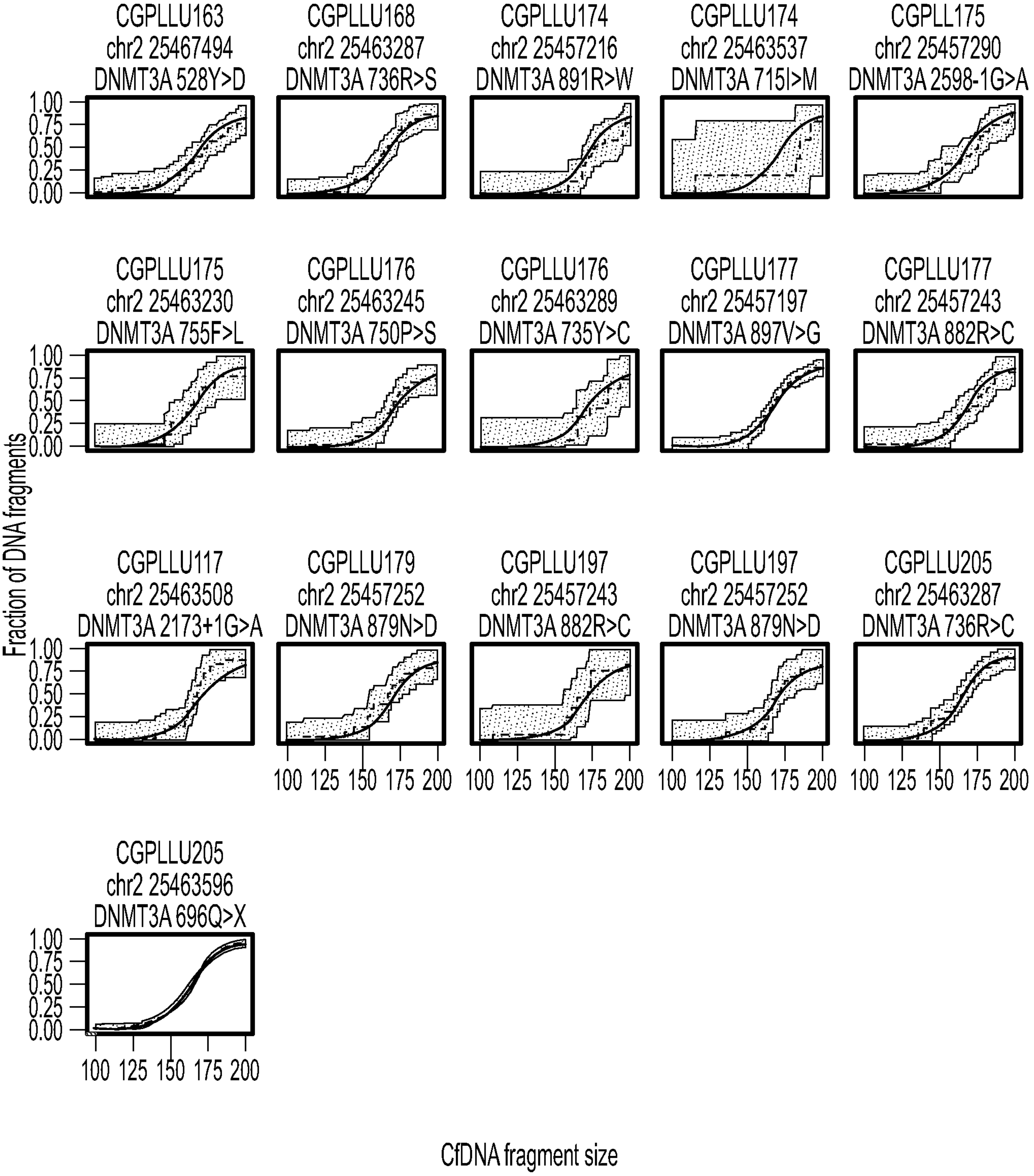

CGPLLU163
chr2 25467494
DNMT3A 528Y>D
CGPLLU168
chr2 25463287
DNMT3A 736R>S
CGPLLU174
chr2 25457216
DNMT3A 891R>W
CGPLLU174
chr2 25463537
DNMT3A 715I>M
CGPLL175
chr2 25457290
DNMT3A 2598-1G>A
CGPLLU175
chr2 25463230
DNMT3A 755F>L
CGPLLU176
chr2 25463245
DNMT3A 750P>S
CGPLLU176
chr2 25463289
DNMT3A 735Y>C
CGPLLU177
chr2 25457197
DNMT3A 897V>G
CGPLLU177
chr2 25457243
DNMT3A 882R>C
CGPLLU117
chr2 25463508
DNMT3A 2173+1G>A
CGPLLU179
chr2 25457252
DNMT3A 879N>D
CGPLLU197
chr2 25457243
DNMT3A 882R>C
CGPLLU197
chr2 25457252
DNMT3A 879N>D
CGPLLU205
chr2 25463287
DNMT3A 736R>C
CGPLLU205
chr2 25463596
DNMT3A 696Q>X
Fraction of DNA fragments
1.00
0.75
0.50
0.25
0.00
100
125
150
175
200
CfDNA fragment size

FIG. 6(Cont.)

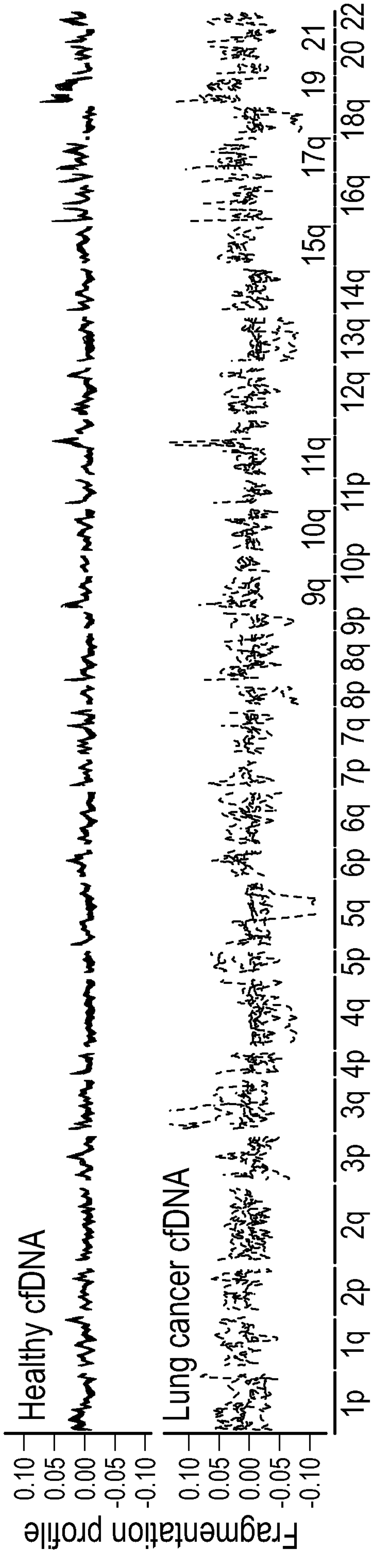

Fragmentation profile
0.10
0.05
0.00
-0.05
-0.10
Healthy cfDNA
Lung cancer cfDNA
1p
1q
2p
2q
3p
3q
4p
4q
5p
5q
6p
6q
7p
7q
8p
8q
9p
9q
10p
10q
11p
11q
12q
13q
14q
15q
16q
17q
18q
19
20
21
22

FIG. 7A

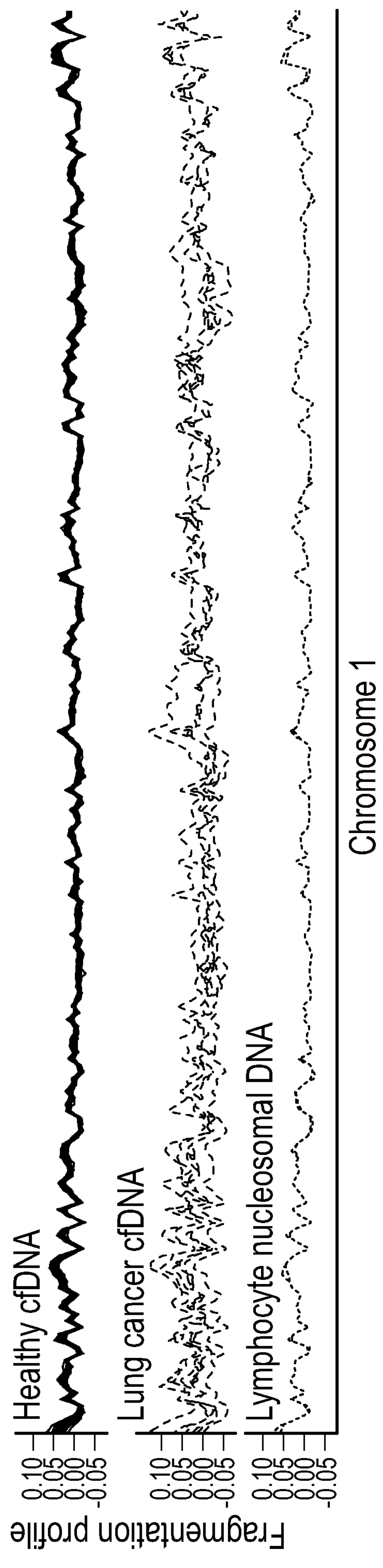

Fragmentation profile
0.10
0.05
0.00
-0.05
Healthy cfDNA
Lung cancer cfDNA
Lymphocyte nucleosomal DNA
1p
1q
2p
2q
3p
3q
4p
4q
5p
5q
6p
6q
7p
7q
8p
8q
9p
9q
10p
10q
11p
11q
12q
13q
14q
15q
16q
17q
18q
19
20
21
22
Chromosome 1

FIG. 7B

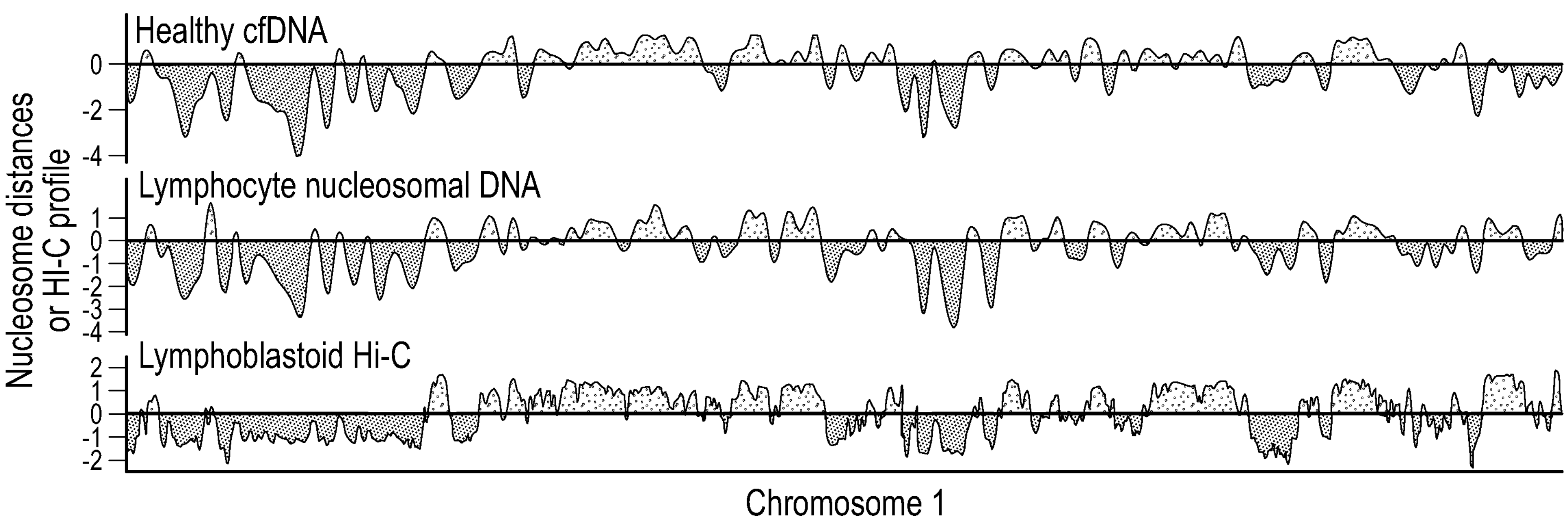


FIG. 7C

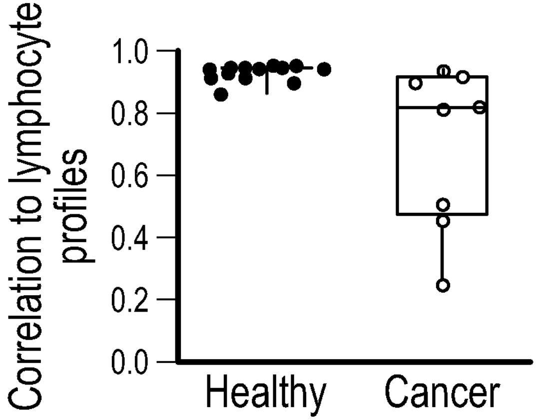


FIG. 7D

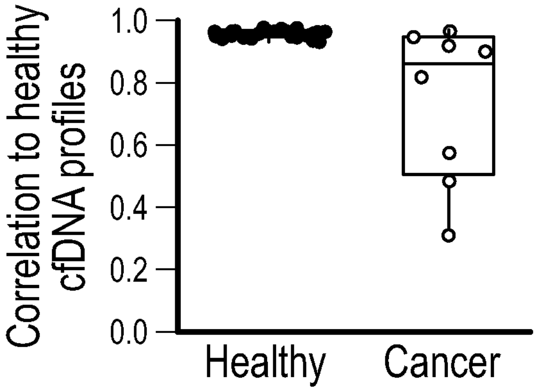


FIG. 7E

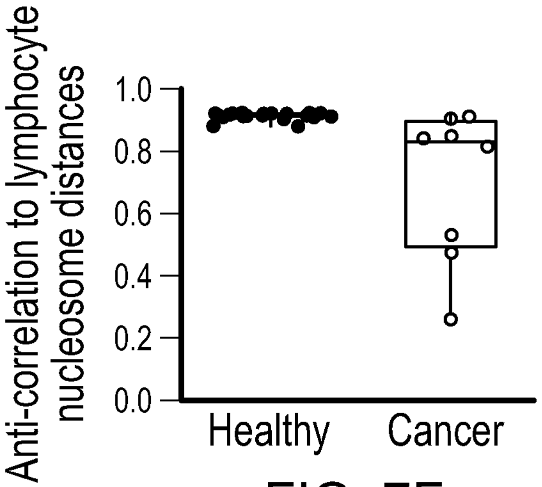


FIG. 7F

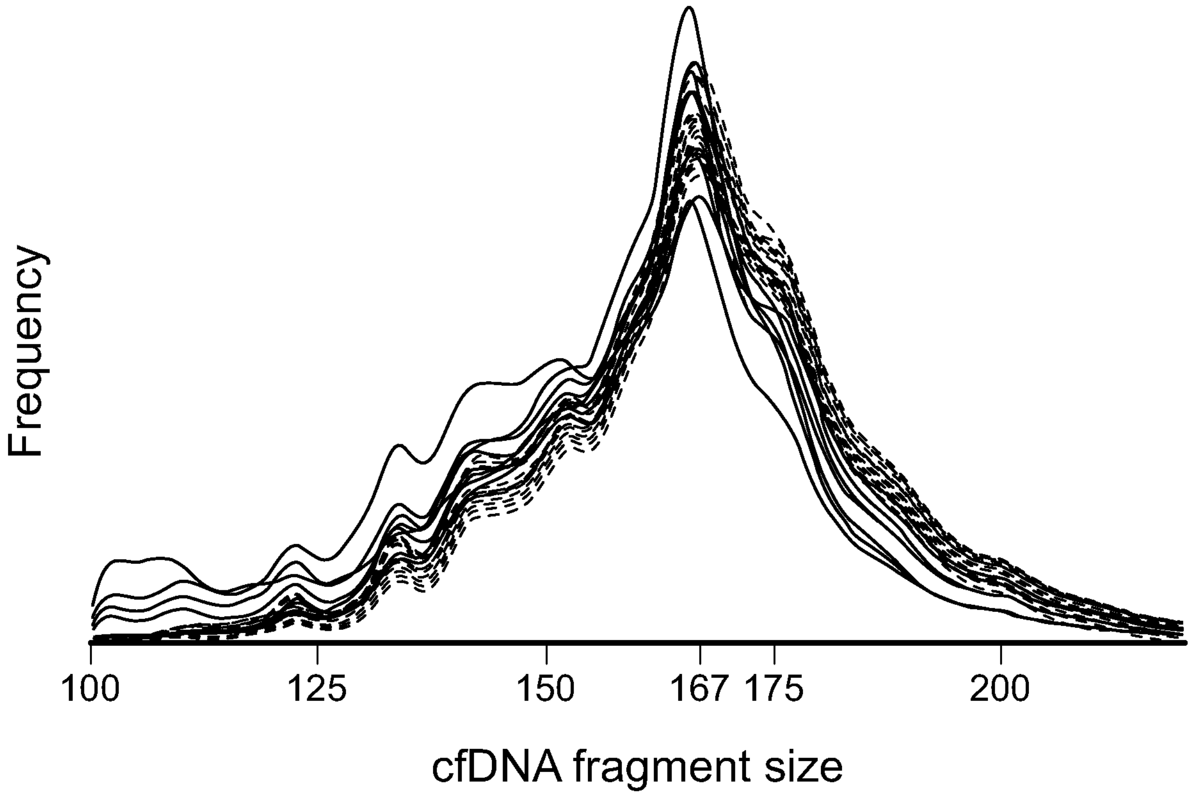


FIG. 8

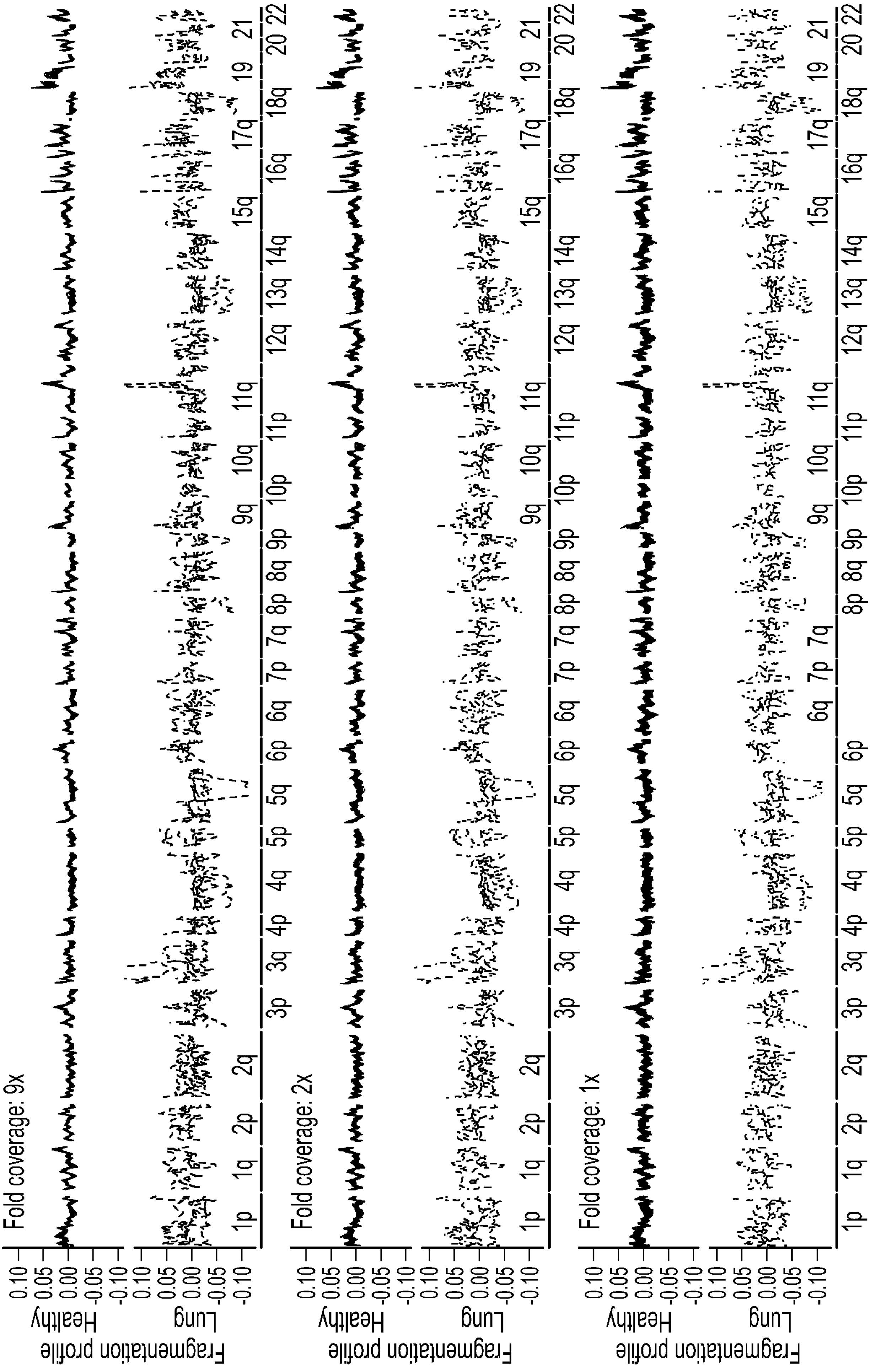

Fold coverage: 9x
Fold coverage: 2x
Fold coverage: 1x
Fragmentation profile
Healthy
Lung
0.10
0.05
0.00
-0.05
-0.10
1p
1q
2p
2q
3p
3q
4p
4q
5p
5q
6p
6q
7p
7q
8p
8q
9p
9q
10p
10q
11p
11q
12q
13q
14q
15q
16q
17q
18q
19
20
21
22

FIG. 9A

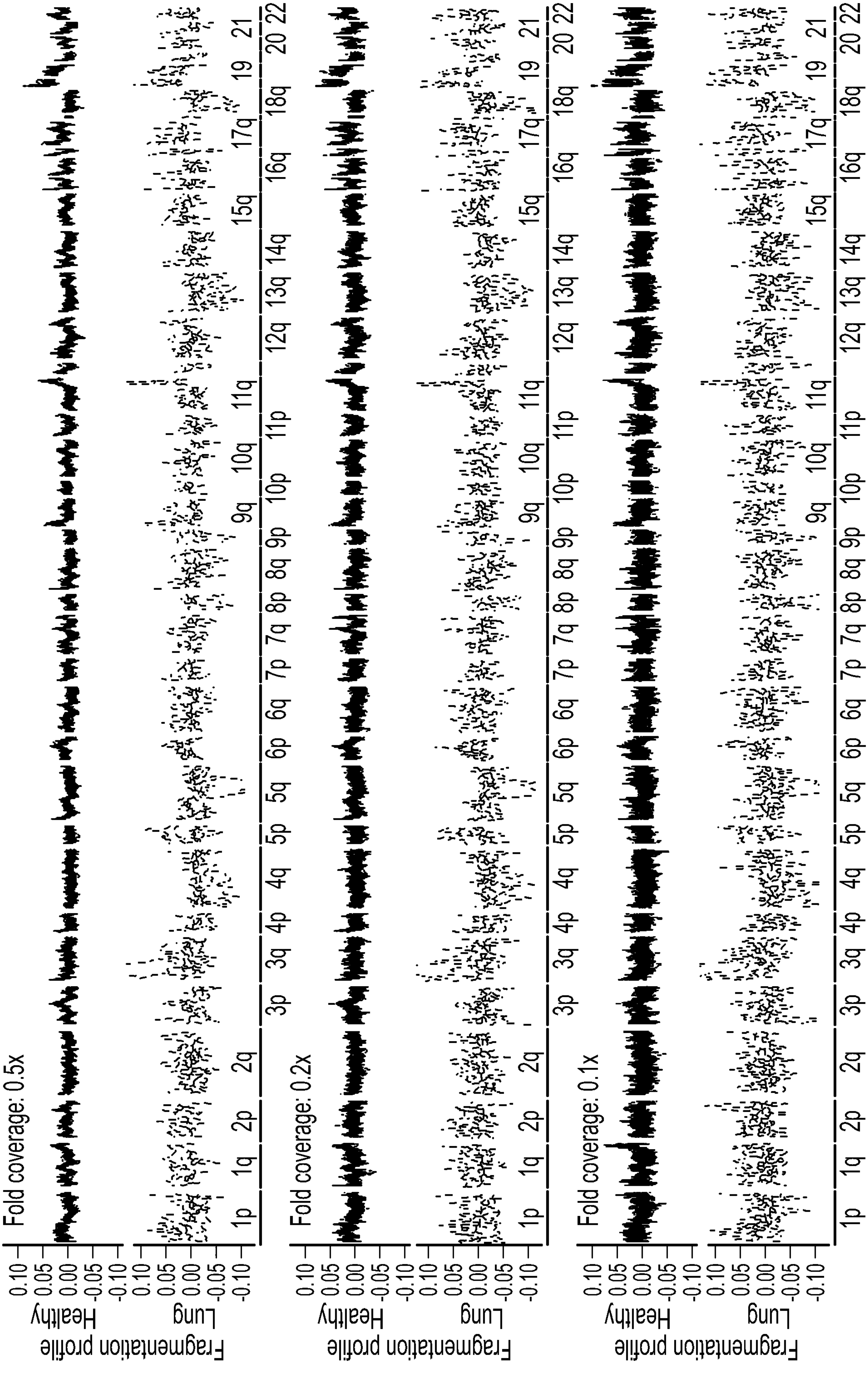

Fold coverage: 0.5x
Fold coverage: 0.2x
Fold coverage: 0.1x
Fragmentation profile
Healthy
Lung
0.10
0.05
0.00
-0.05
-0.10
1p
1q
2p
2q
3p
3q
4p
4q
5p
5q
6p
6q
7p
7q
8p
8q
9p
9q
10p
10q
11p
11q
12q
13q
14q
15q
16q
17q
18q
19
20
21
22

FIG. 9A (Cont.)

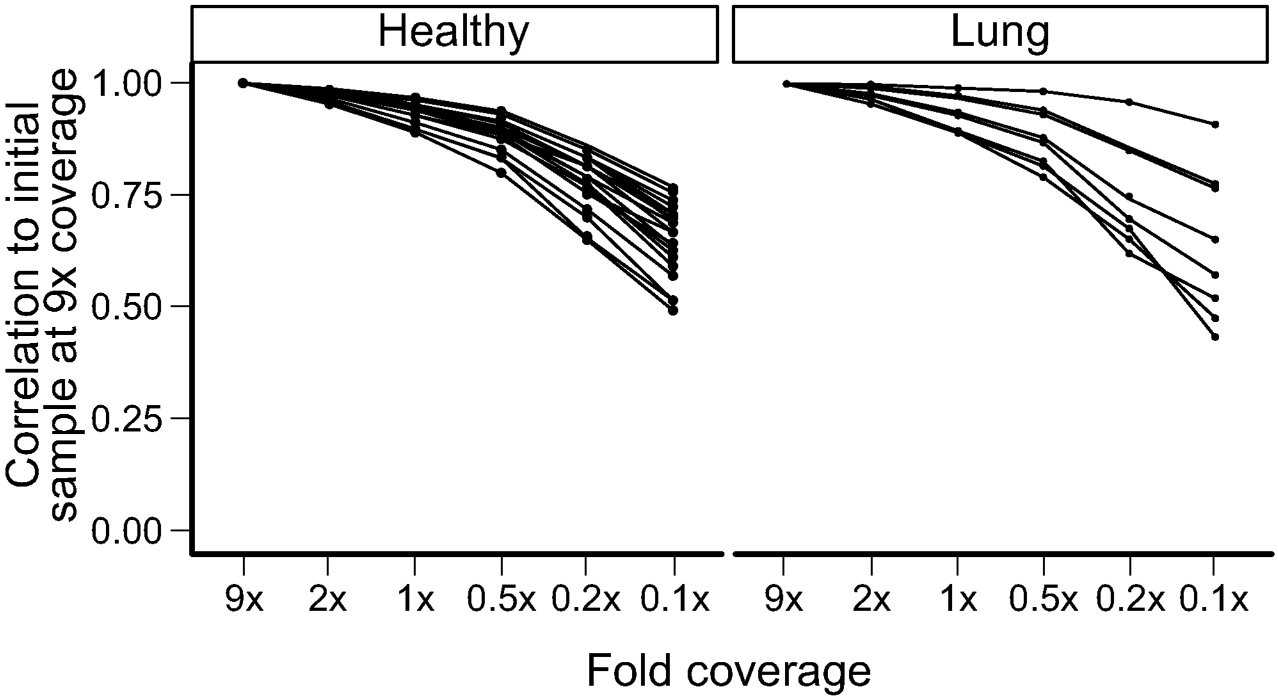
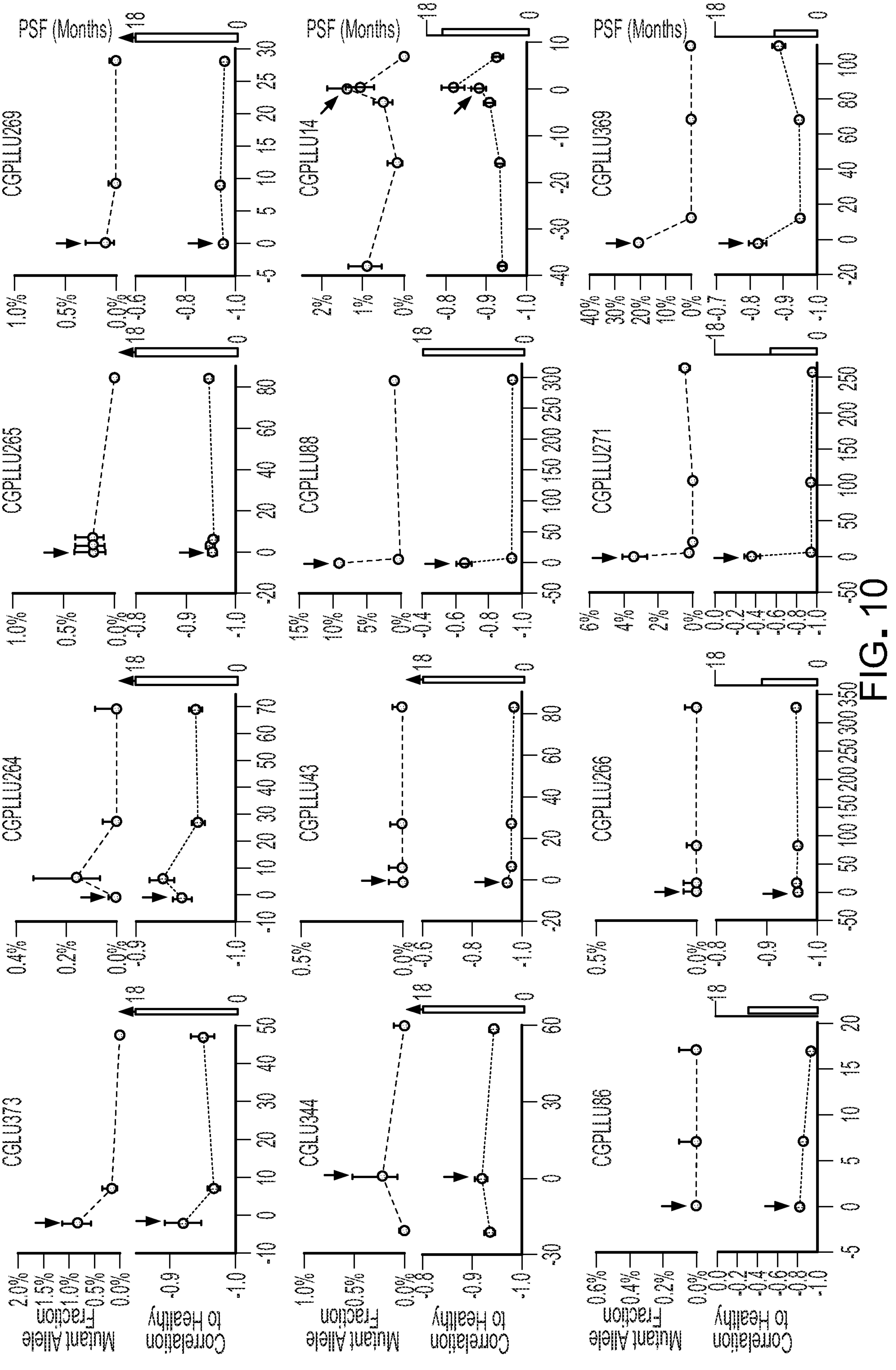

Healthy
Lung
Correlation to initial sample at 9x coverage
1.00
0.75
0.50
0.25
0.00
9x
2x
1x
0.5x
0.2x
0.1x
Fold coverage

FIG. 9B



CGLU373
CGPLLU264
CGPLLU265
CGPLLU269
CGLU344
CGPLLU43
CGPLLU88
CGPLLU14
CGPLLU86
CGPLLU266
CGPLLU271
CGPLLU369
PSF (Months)
Mutant Allele Fraction
Correlation to Healthy
18
0
2.0%
1.5%
1.0%
0.5%
0.0%
0.4%
0.2%
1.0%
2%
1%
0%
15%
10%
5%
6%
4%
40%
30%
20%
10%
0.6%
-0.9
-1.0
-0.8
-0.6
-0.4
-0.7
-0.2
0.0
-10
0
10
20
30
40
50
60
70
80
-30
-5
-20
-50
100
150
200
250
300
350
15
25
-40

FIG. 10

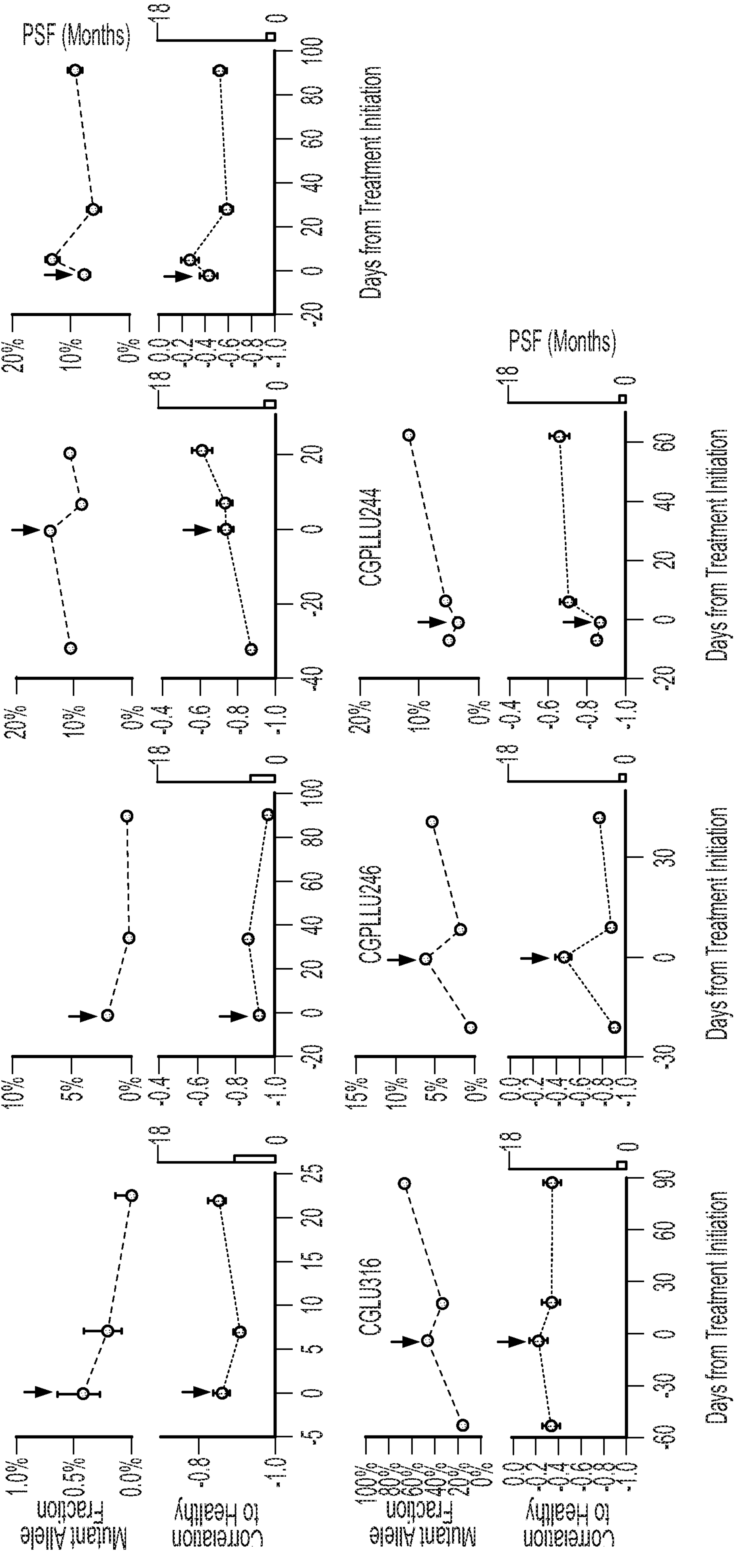

CGPLLU89
CGPLLU267
CGPLLU245
CGPLLU13
CGLU316
CGPLLU246
CGPLLU244
Mutant Allele Fraction
Correlation to Healthy
1.0%
0.5%
0.0%
10%
5%
0%
20%
15%
100%
80%
60%
40%
-0.8
-1.0
-0.4
-0.6
0.0
-0.2
PSF (Months)
18
0
Days from Treatment Initiation
-5
0
5
10
15
20
25
-20
40
60
80
100
-40
-30
30
-60
90

FIG. 10(Cont.)

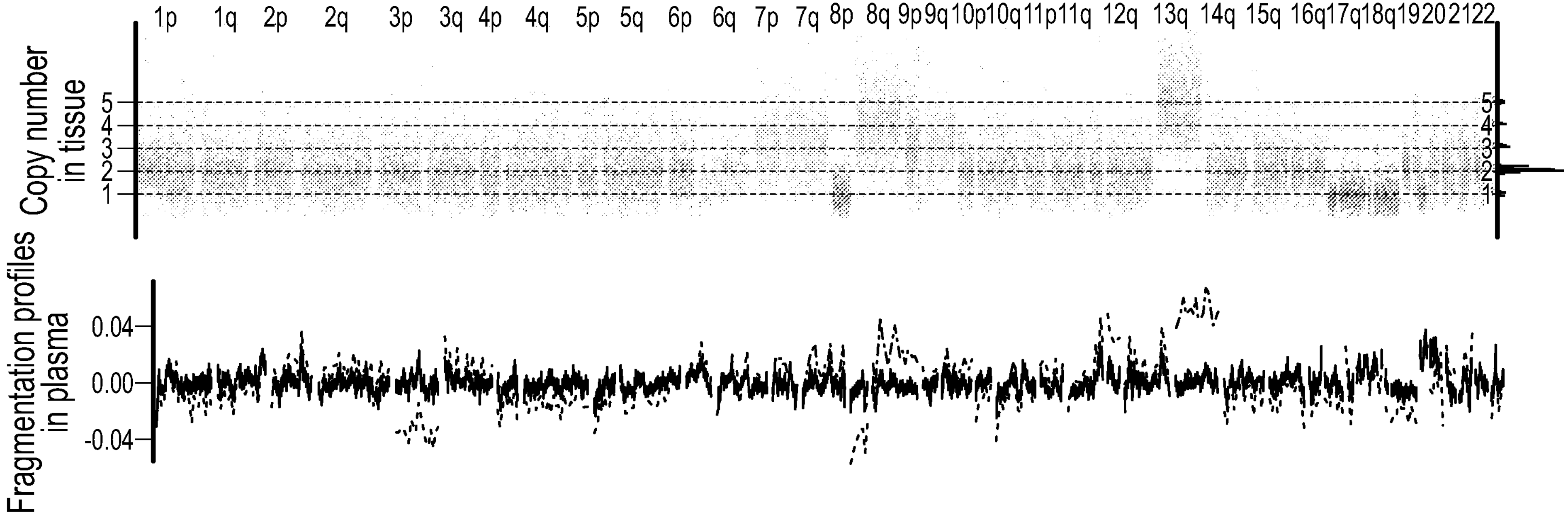

1p
1q
2p
2q
3p
3q
4p
4q
5p
5q
6p
6q
7p
7q
8p
8q
9p
9q
10p
10q
11p
11q
12q
13q
14q
15q
16q
17q
18q
19
20
21
22
Copy number in tissue
5
4
3
2
1
Fragmentation profiles in plasma
0.04
0.00
-0.04

FIG. 11A

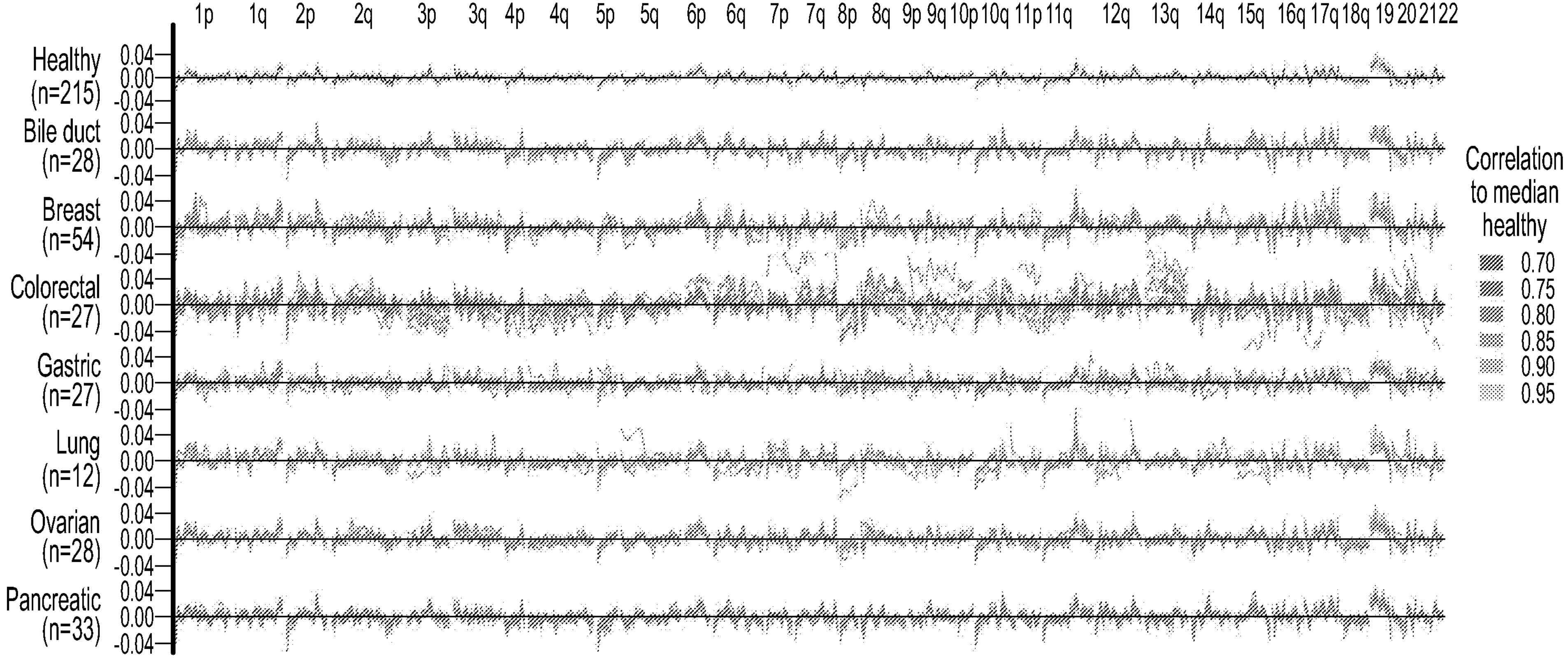


FIG. 11B

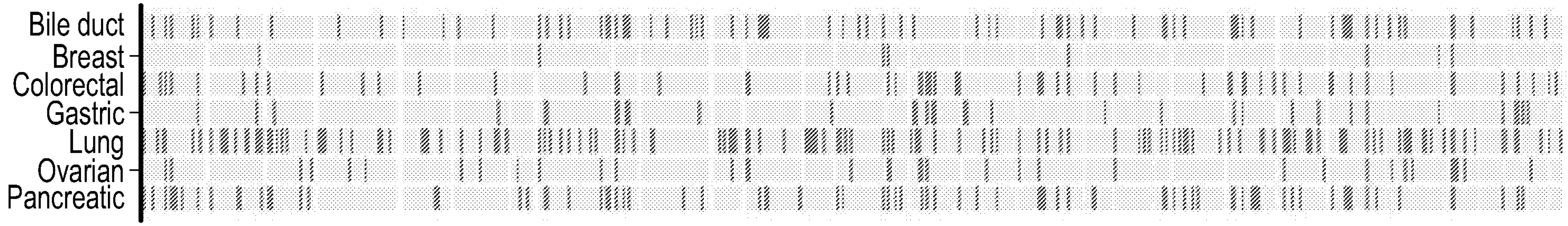


FIG. 11C

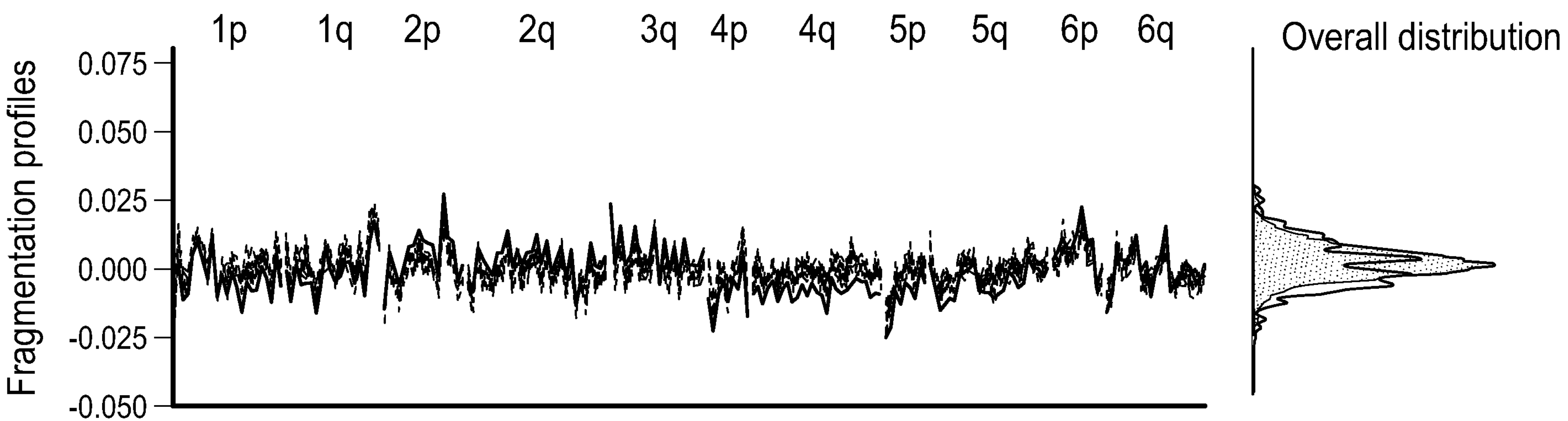


FIG. 12A

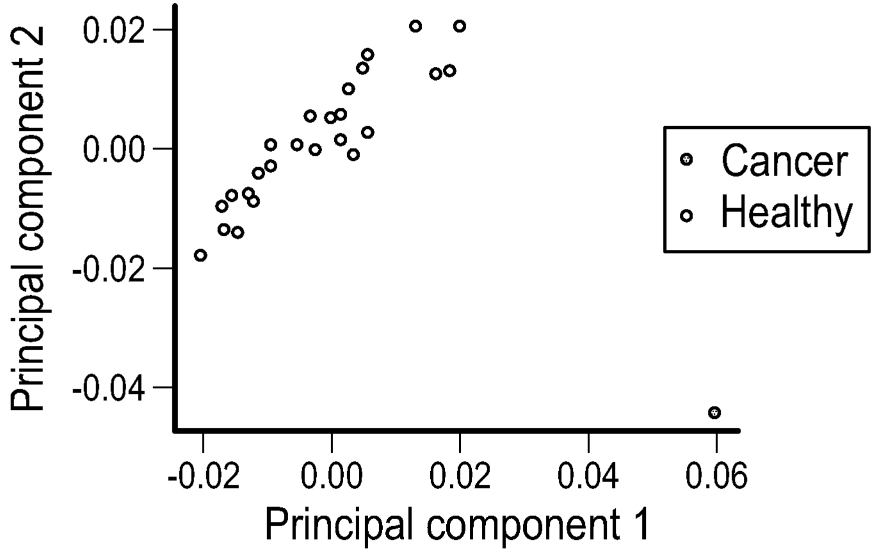


FIG. 12B

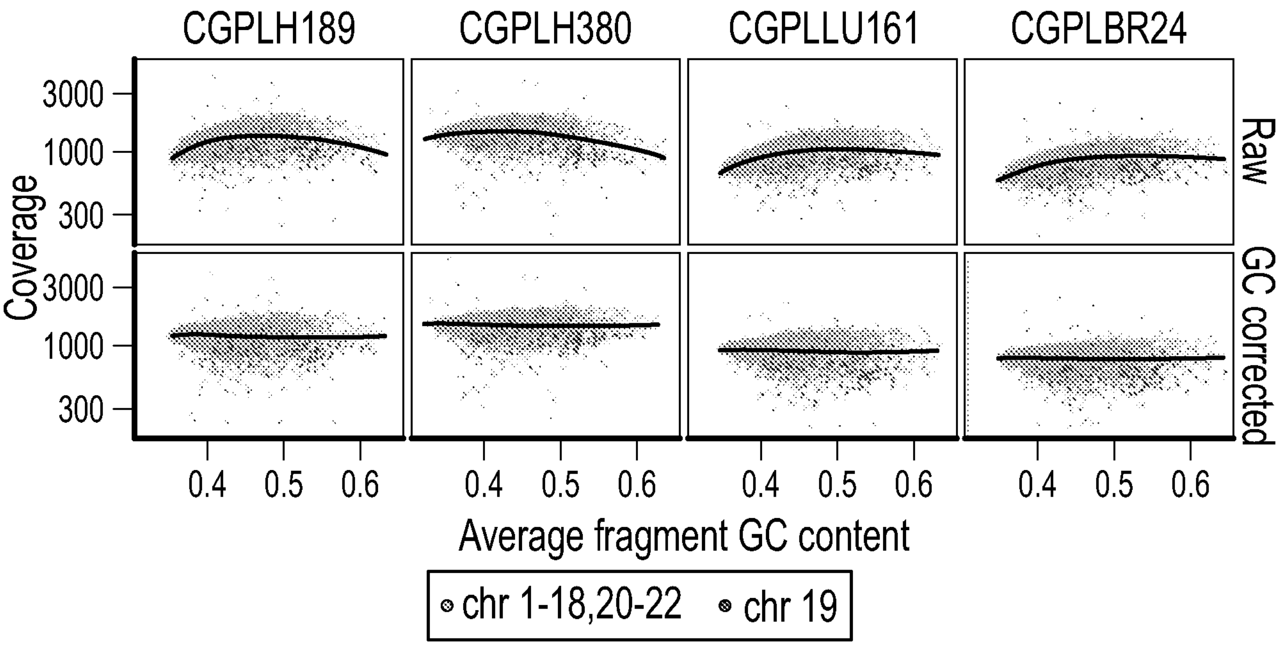


FIG. 13A

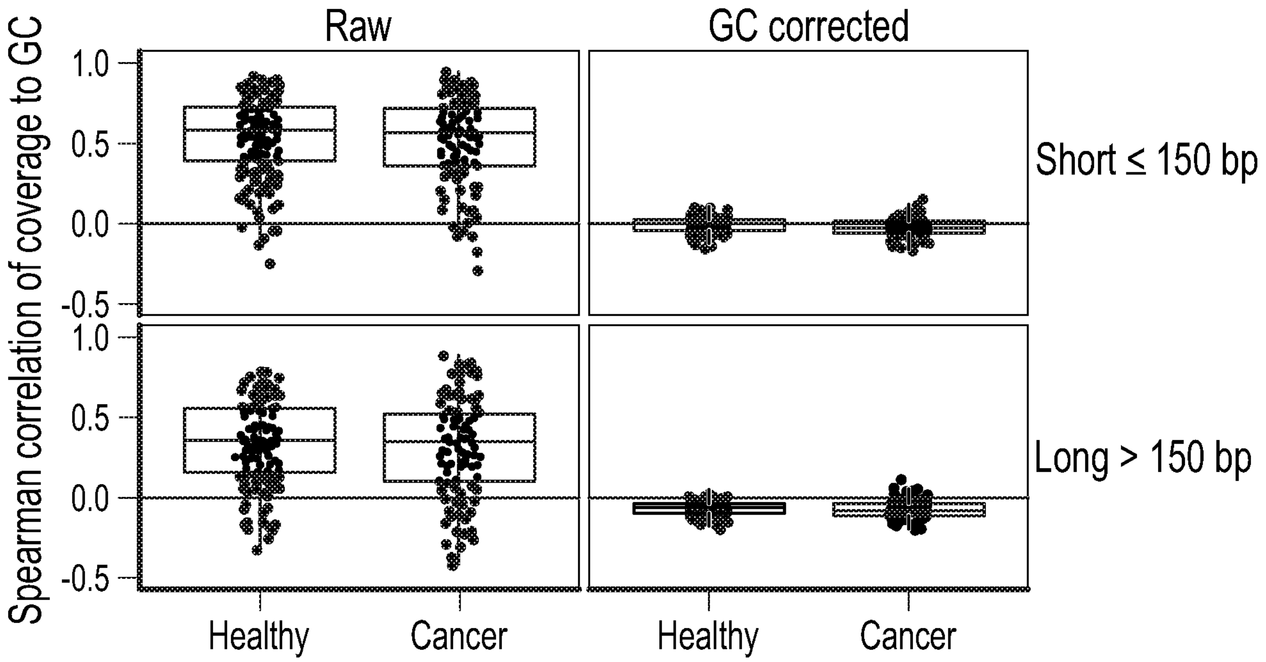


FIG. 13B

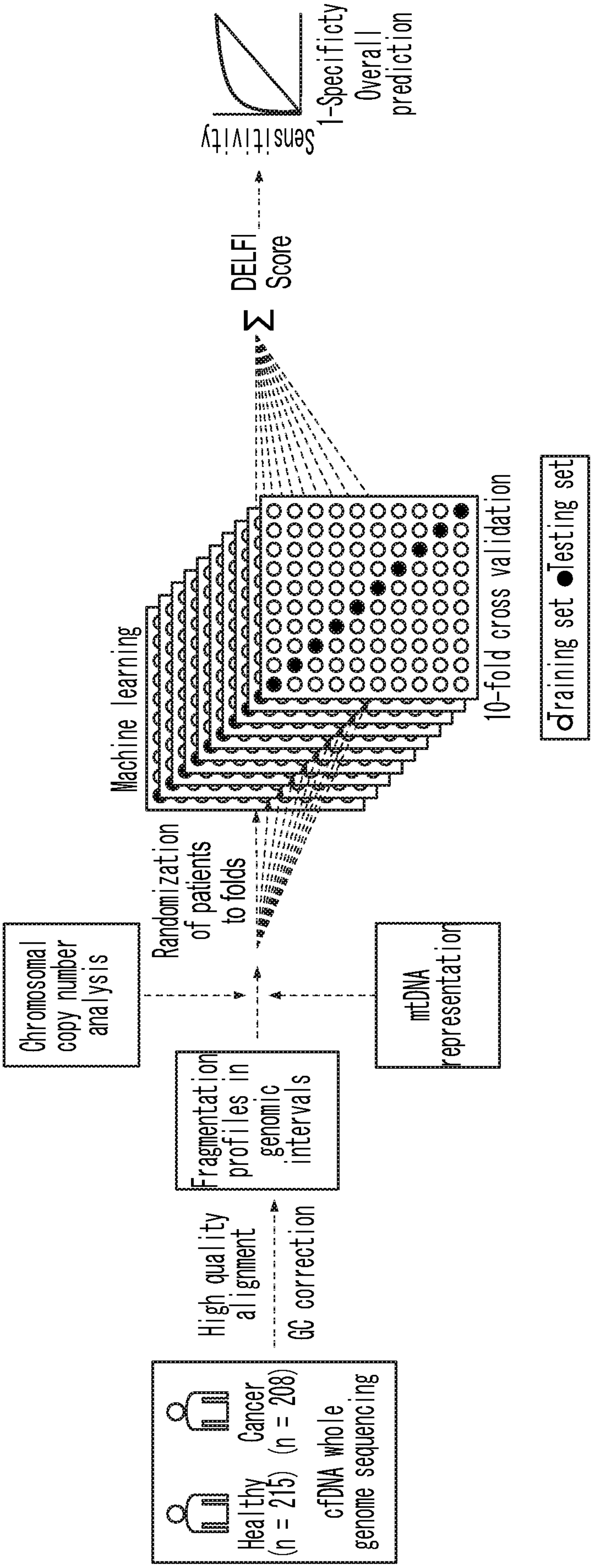

Healthy
(n = 215)
Cancer
(n = 208)
cfDNA whole
genome sequencing
High quality
alignment
GC correction
Fragmentation
profiles in
genomic
intervals
Chromosomal
copy number
analysis
mtDNA
representation
Randomization
of patients
to folds
Machine learning
10-fold cross validation
○Training set ●Testing set
Σ
DELFI
Score
Sensitivity
1-Specificty
Overall
prediction

FIG. 14

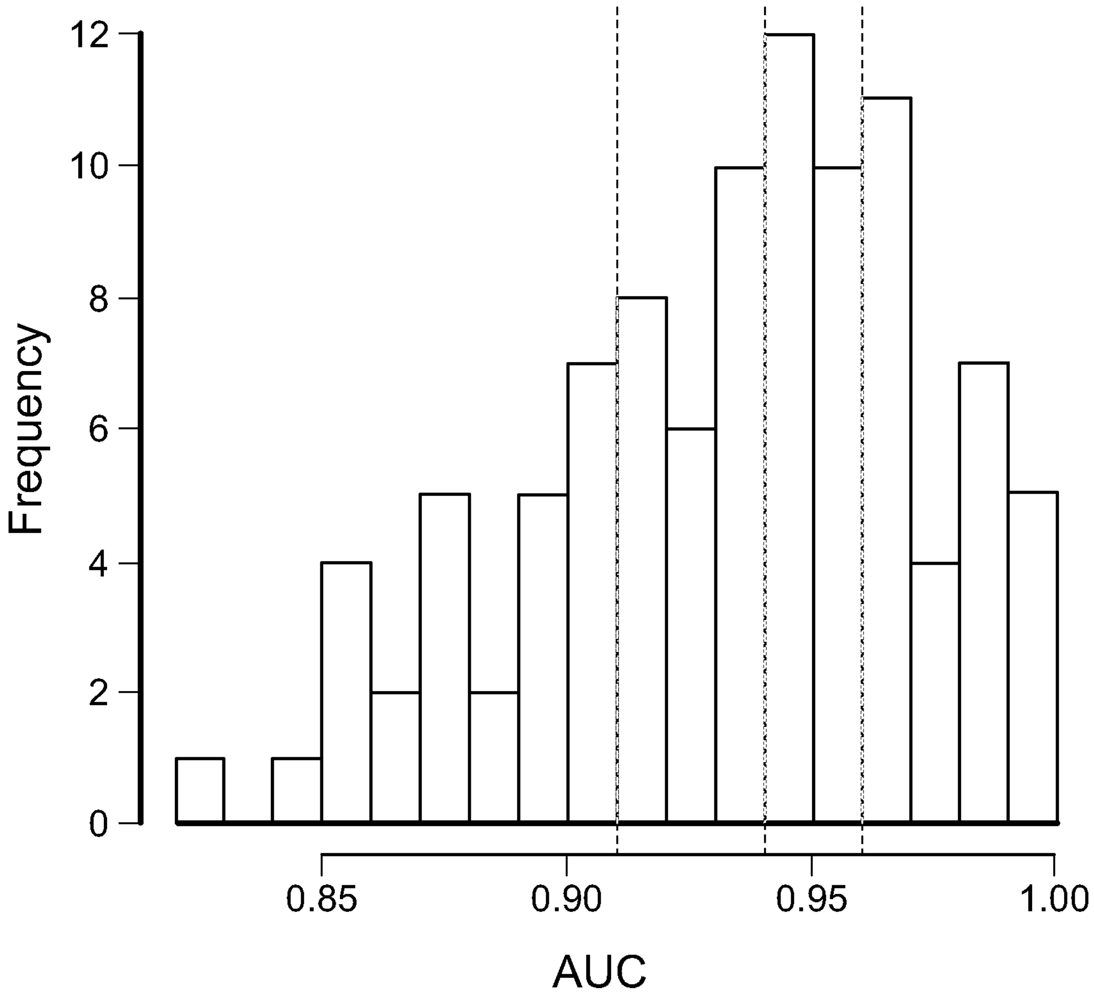


FIG. 15

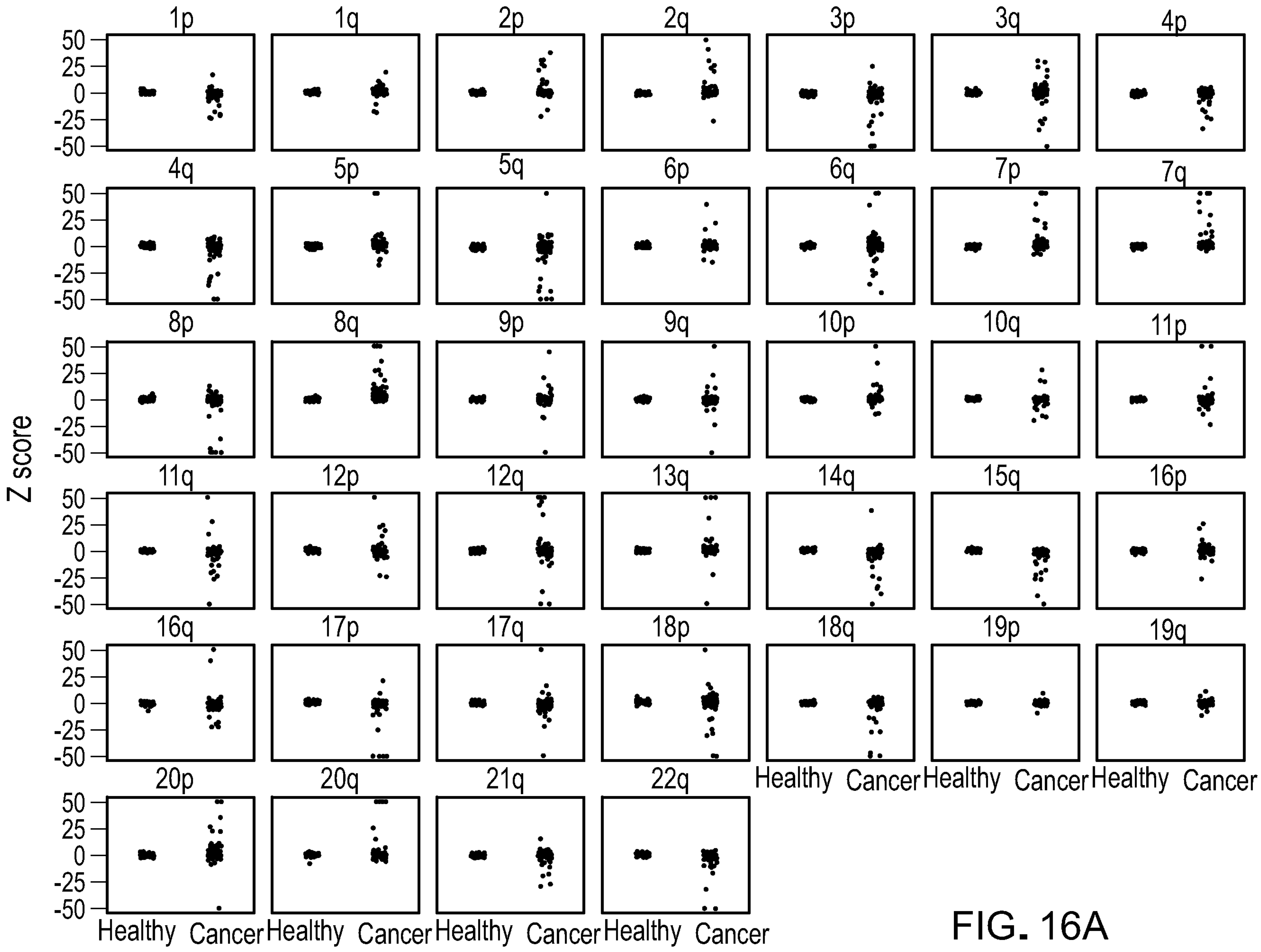

Z score
1p
1q
2p
2q
3p
3q
4p
4q
5p
5q
6p
6q
7p
7q
8p
8q
9p
9q
10p
10q
11p
11q
12p
12q
13q
14q
15q
16p
16q
17p
17q
18p
18q
19p
19q
20p
20q
21q
22q
50
25
0
-25
-50
Healthy
Cancer

FIG. 16A

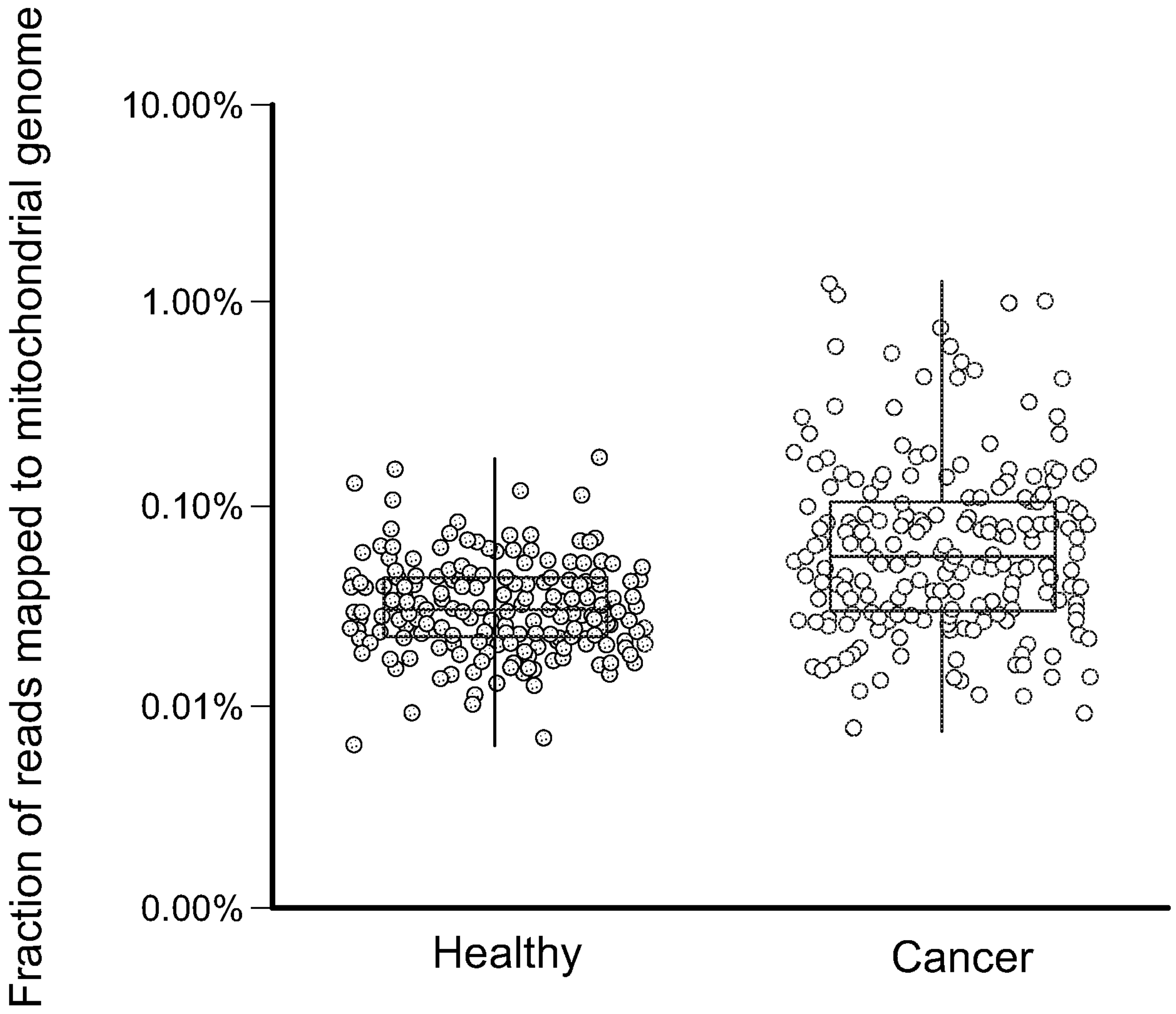

Fraction of reads mapped to mitochondrial genome
10.00%
1.00%
0.10%
0.01%
0.00%
Healthy
Cancer

FIG. 16B

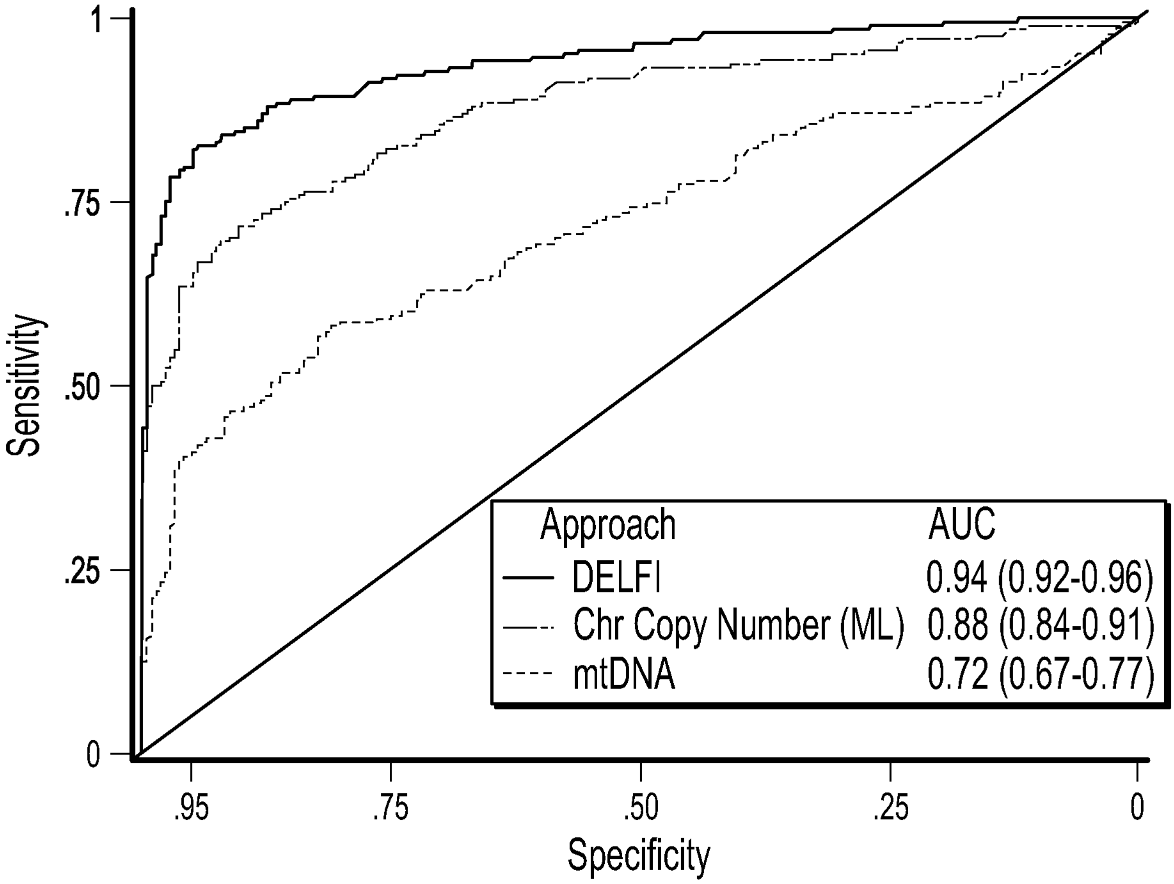

Sensitivity
1
.75
.50
.25
0
.95
.75
.50
.25
0
Specificity
Approach
AUC
DELFI
0.94 (0.92-0.96)
Chr Copy Number (ML)
0.88 (0.84-0.91)
mtDNA
0.72 (0.67-0.77)

FIG. 17A

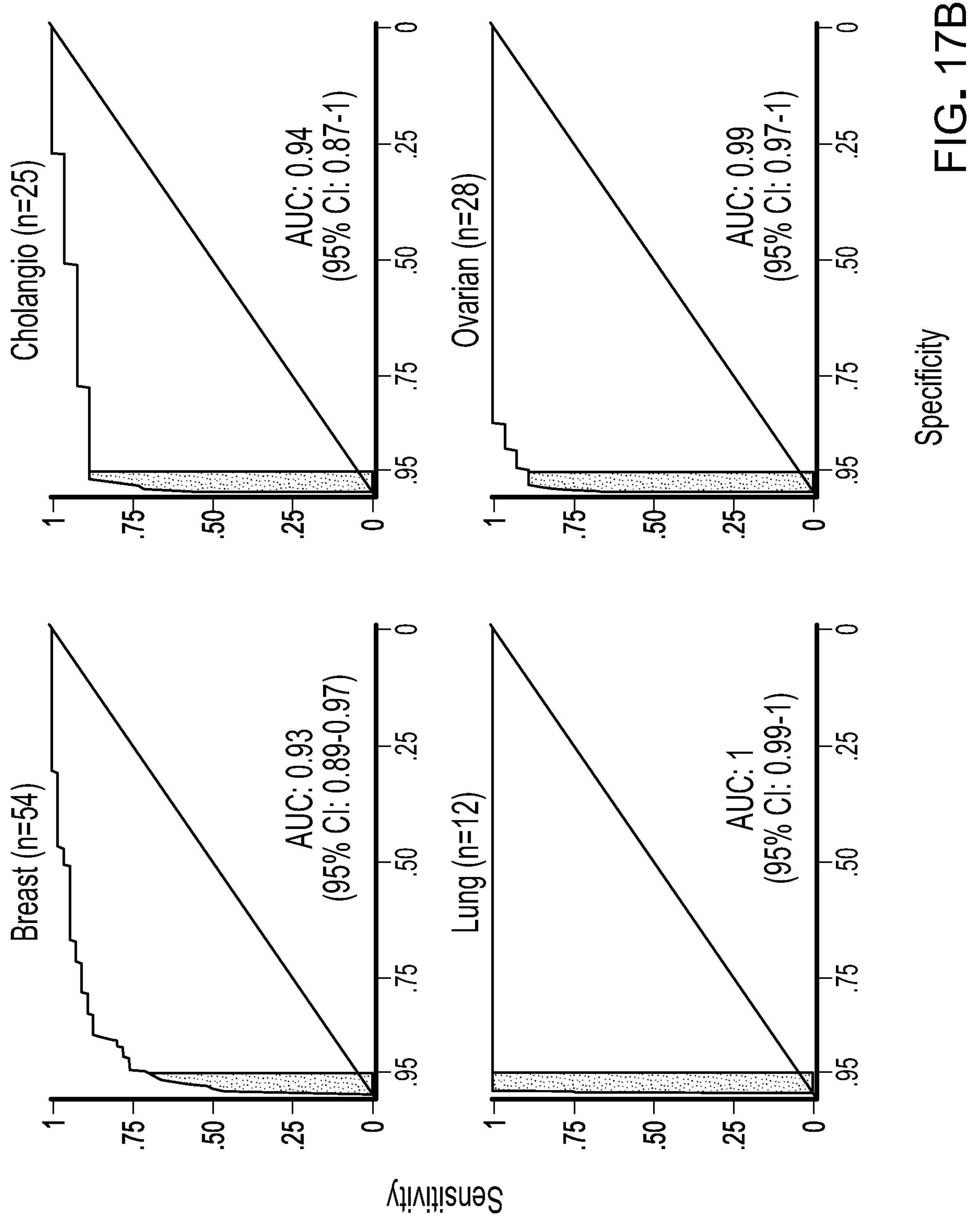

Breast (n=54)
AUC: 0.93
(95% CI: 0.89-0.97)
Cholangio (n=25)
AUC: 0.94
(95% CI: 0.87-1)
Lung (n=12)
AUC: 1
(95% CI: 0.99-1)
Ovarian (n=28)
AUC: 0.99
(95% CI: 0.97-1)
Sensitivity
Specificity
1
.75
.50
.25
0
.95
.75
.50
.25
0

FIG. 17B

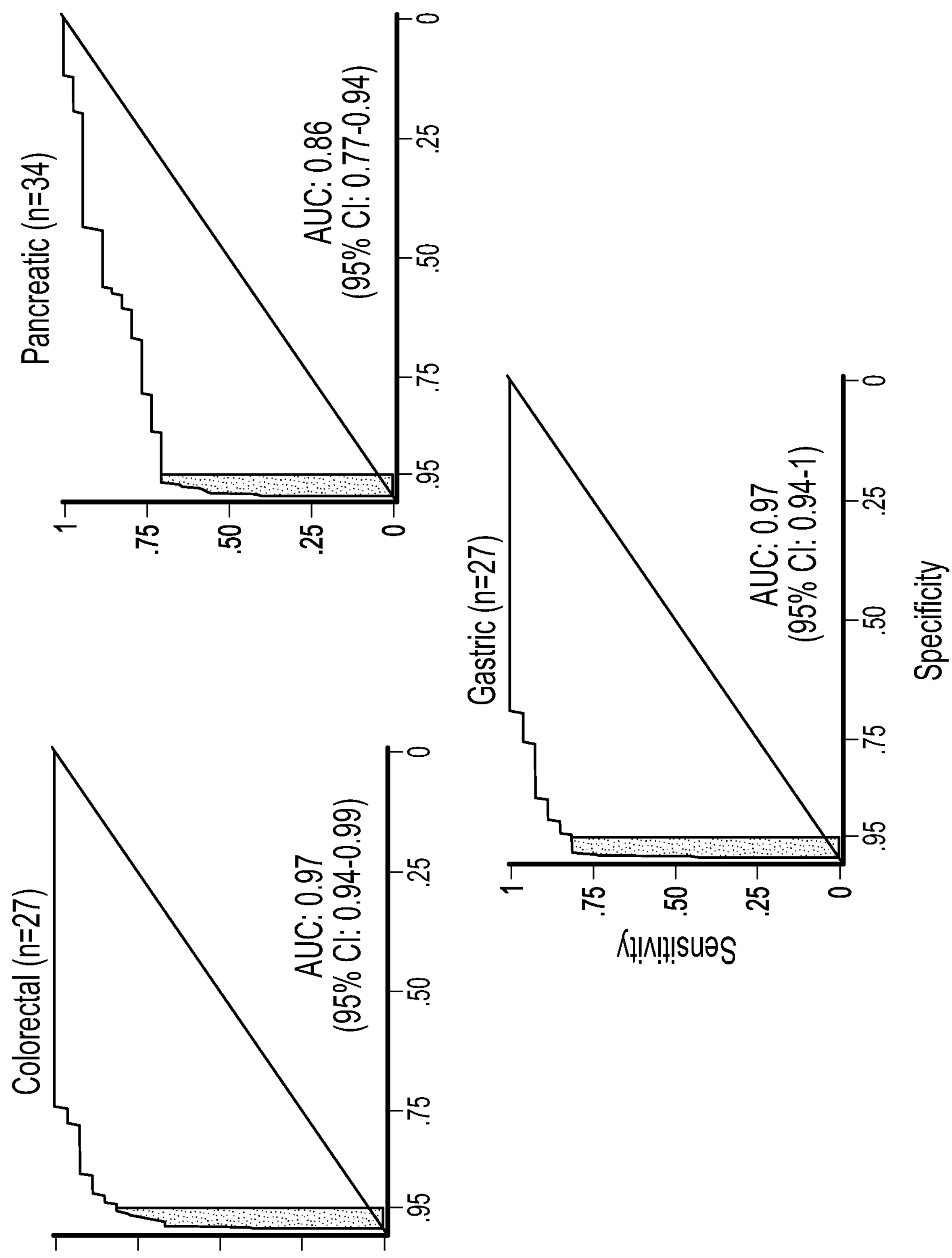

Colorectal (n=27)
AUC: 0.97
(95% CI: 0.94-0.99)
Pancreatic (n=34)
AUC: 0.86
(95% CI: 0.77-0.94)
Gastric (n=27)
AUC: 0.97
(95% CI: 0.94-1)
Sensitivity
1
.75
.50
.25
0
Specificity
.95
.75
.50
.25
0

FIG. 17B (Cont.)

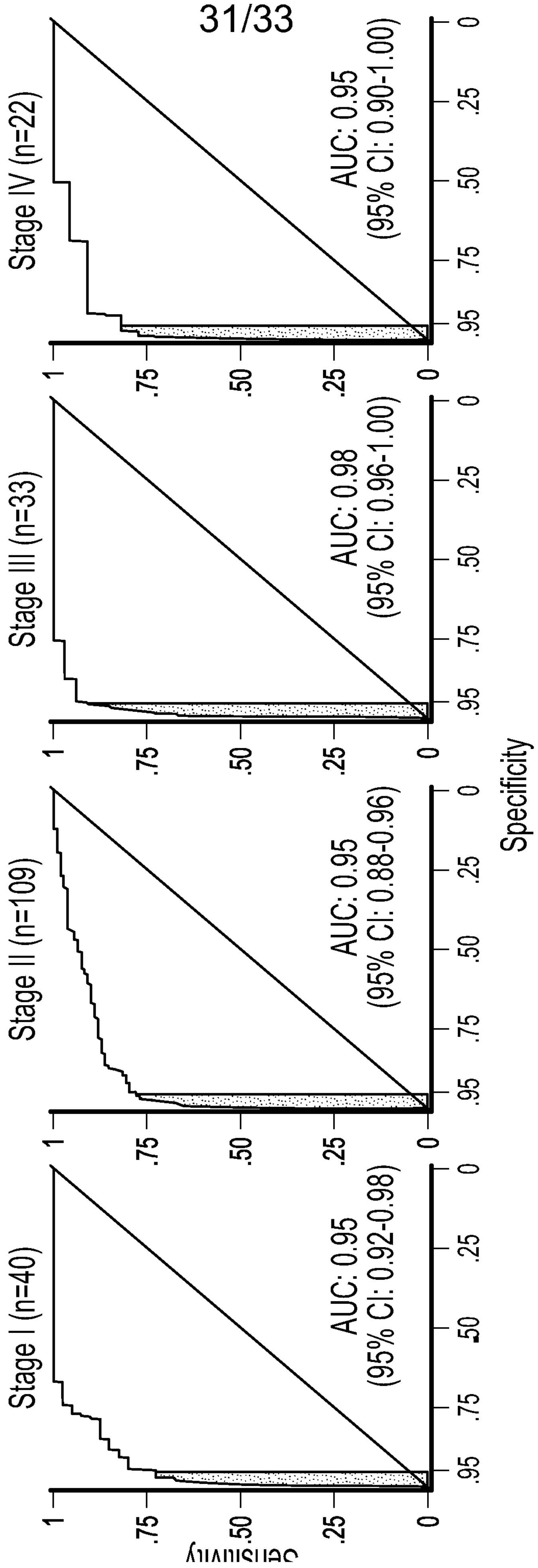

Stage I (n=40)
AUC: 0.95
(95% CI: 0.92-0.98)
Stage II (n=109)
AUC: 0.95
(95% CI: 0.88-0.96)
Stage III (n=33)
AUC: 0.98
(95% CI: 0.96-1.00)
Stage IV (n=22)
AUC: 0.95
(95% CI: 0.90-1.00)
Sensitivity
1
.75
.50
.25
0
Specificity
.95
.75
.50
.25
0

FIG. 18

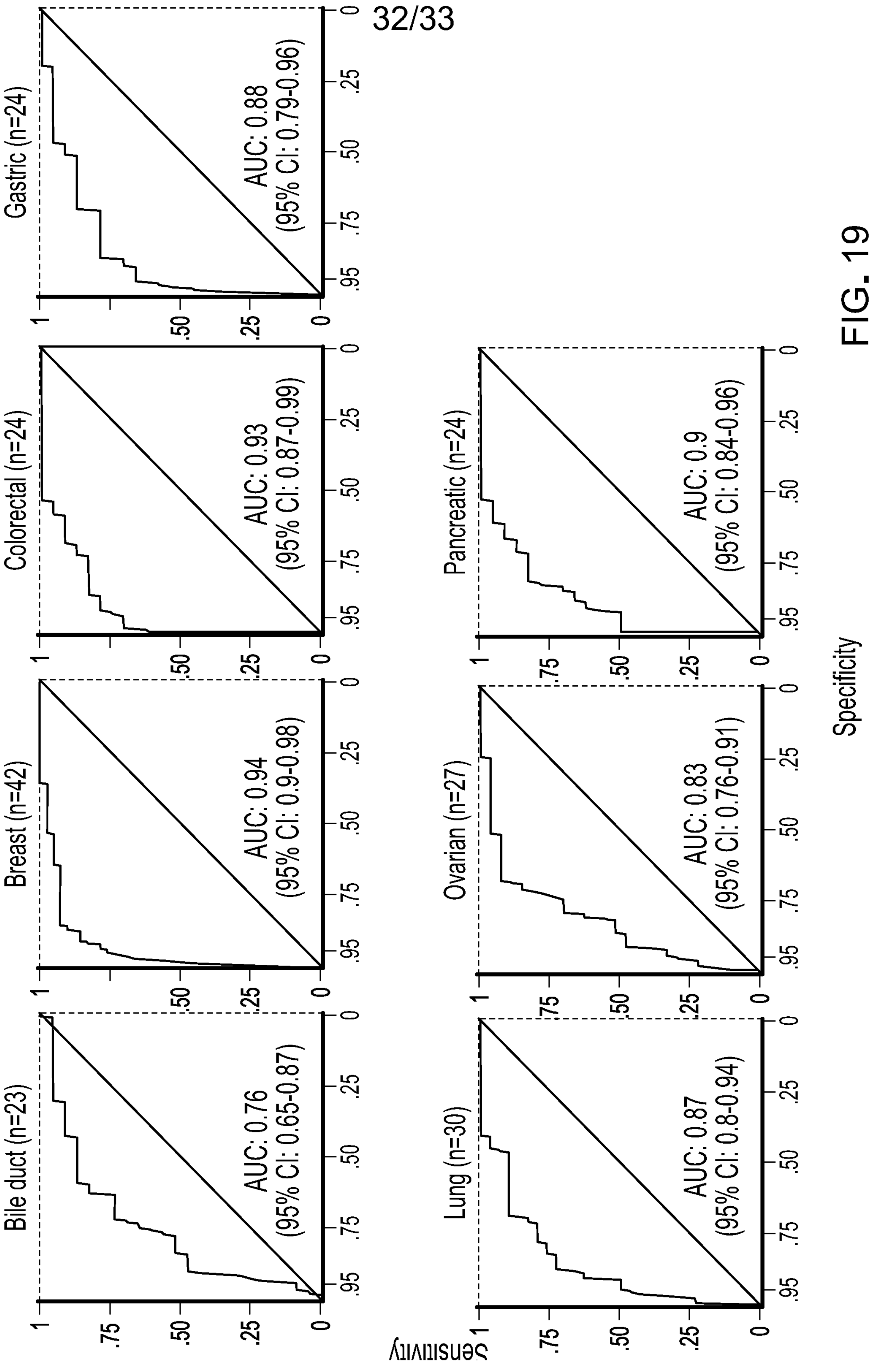

Gastric (n=24)
AUC: 0.88
(95% CI: 0.79-0.96)
Colorectal (n=24)
AUC: 0.93
(95% CI: 0.87-0.99)
Breast (n=42)
AUC: 0.94
(95% CI: 0.9-0.98)
Bile duct (n=23)
AUC: 0.76
(95% CI: 0.65-0.87)
Pancreatic (n=24)
AUC: 0.9
(95% CI: 0.84-0.96)
Ovarian (n=27)
AUC: 0.83
(95% CI: 0.76-0.91)
Lung (n=30)
AUC: 0.87
(95% CI: 0.8-0.94)
Sensitivity
Specificity
1
.75
.50
.25
0
.95
.75
.50
.25
0

FIG. 19

	Detection Approach*	Patients Analyzed	Patients Detected	Fraction of Patients Detected	95% CI
	DELFI	126	103	82%	74%-88%
	Mutations	126	83	66%	57%-74%
	DELFI and Mutations	126	115	91%	85%-96%
Stage	I	32	27	84%	67%-95%
	II	52	48	92%	81%-98%
	III	25	23	92%	74%-99%
	IV	16	16	100%	79%-100%

*Cancer Detuction Using DELFI, Sequence Mutations, and the Combination of DELFI and Mutations was performed at Specificities of 98%, >99%, and 98%, respectively. Per Stage Sensitivities are Included for all Cases Except for one Patient with Stage X.

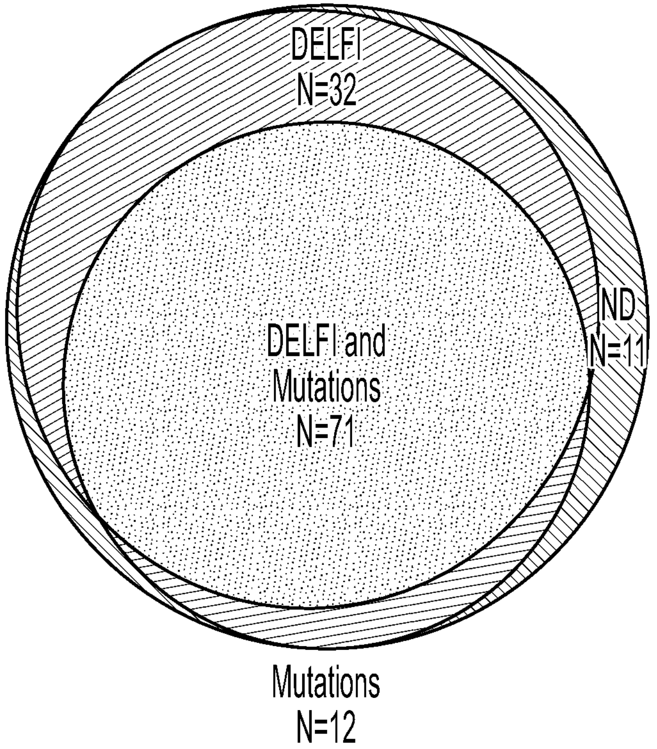


FIG. 20