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

(60) Provisional application No. 62/795,900, filed on Jan. 23, 2019, provisional application No. 62/673,516, filed on May 18, 2018.

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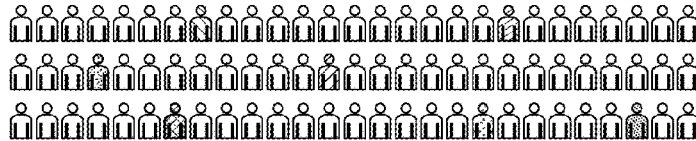
(57) **ABSTRACT**

(22) Filed: **Mar. 17, 2021**

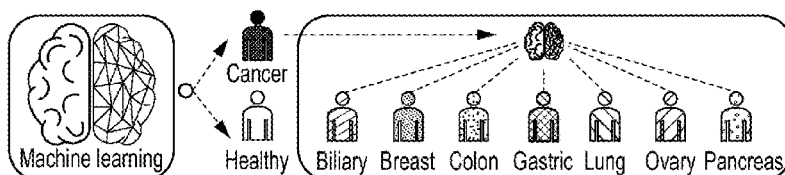
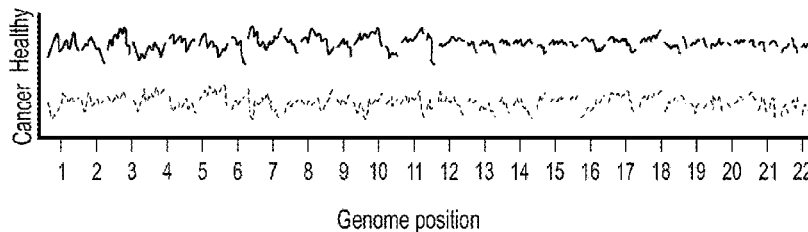
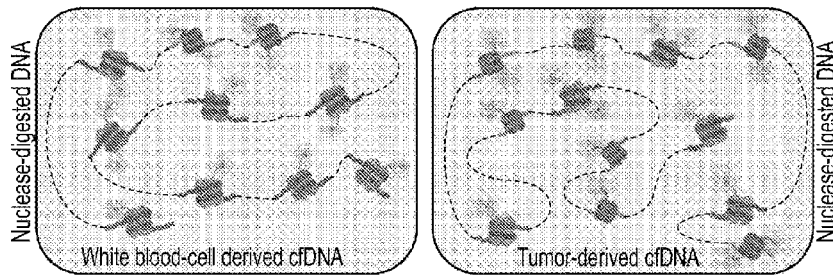
This document relates to methods and materials for assessed, monitored, and/or treated mammals (e.g., humans) having cancer. For example, methods and materials for identifying a mammal as having cancer (e.g., a localized cancer) are provided. For example, methods and materials for assessing, monitoring,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

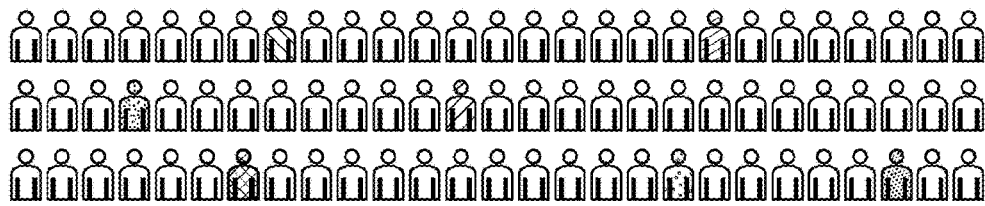
Related U.S. Application Data

(63) Continuation of application No. 16/730,938, filed on Dec. 30, 2019, now Pat. No. 10,982,279, which is a continuation of application No. PCT/US19/32914, filed on May 17, 2019.



Noninvasive cancer screening (DELFI)





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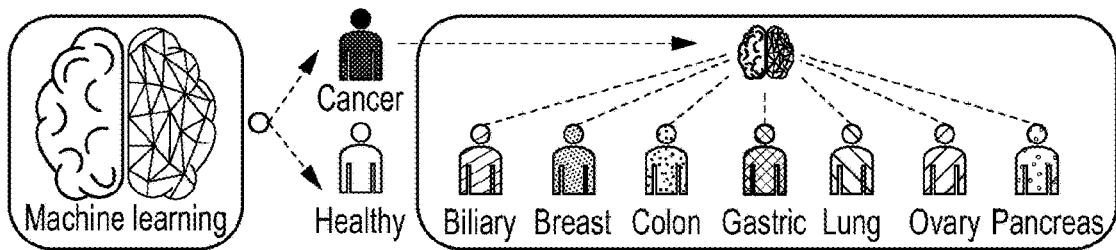
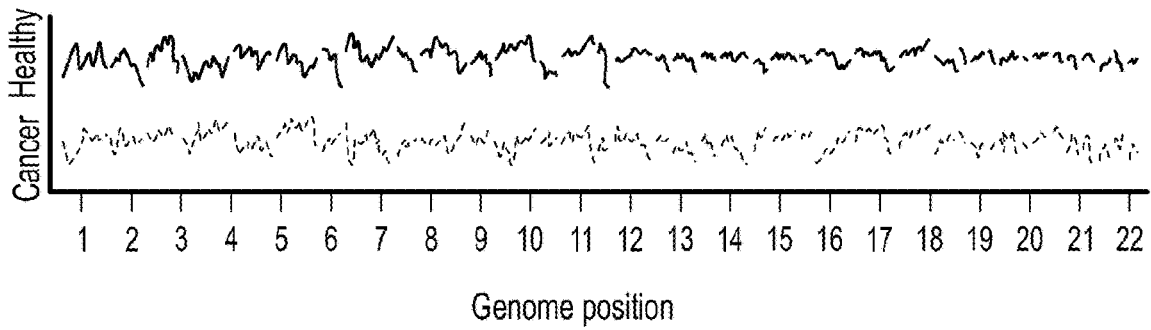
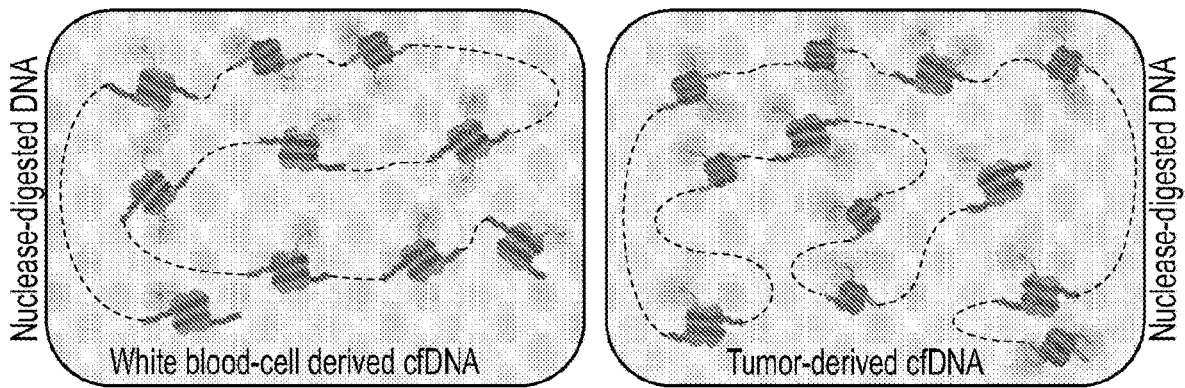


FIG. 1

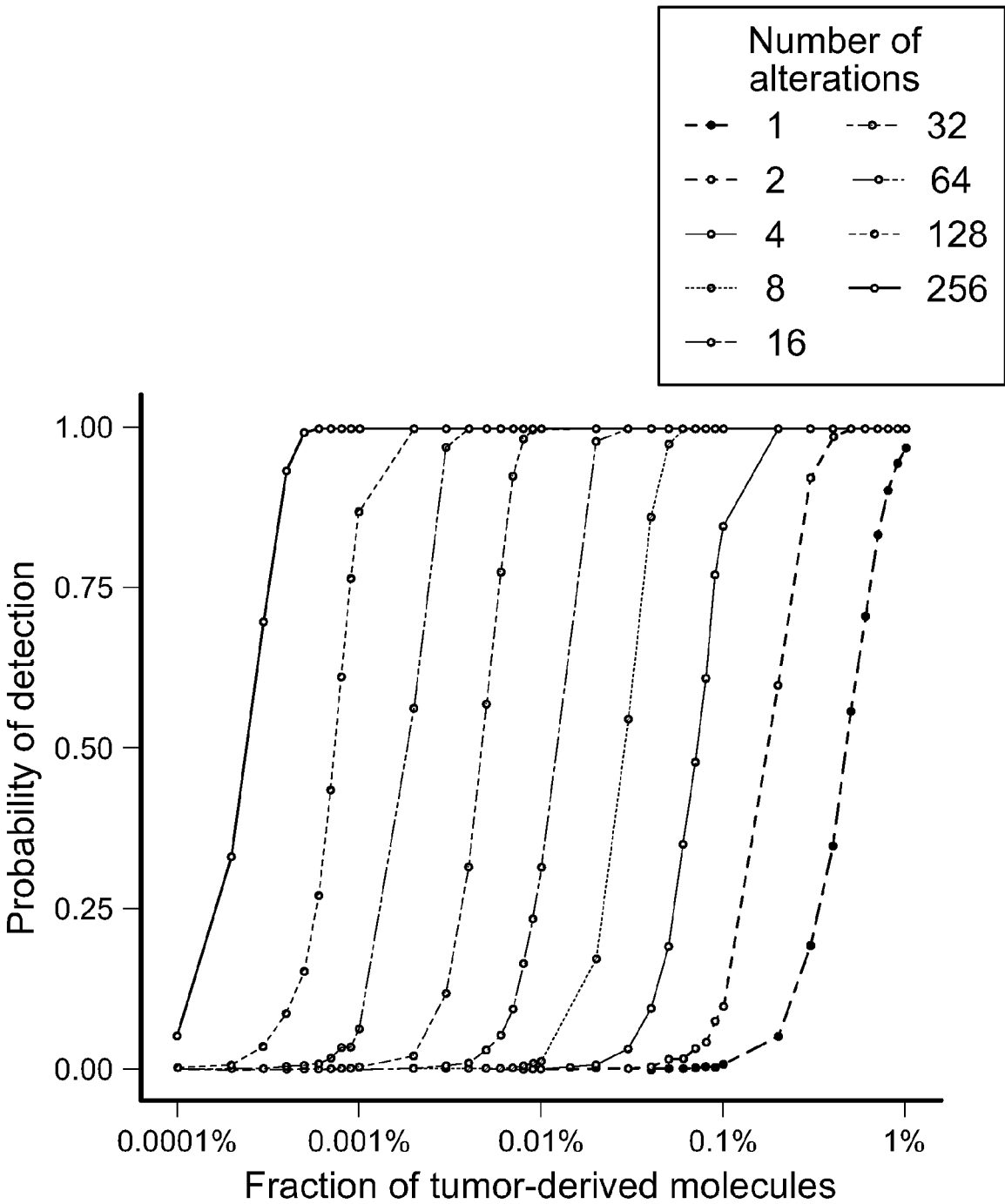


FIG. 2

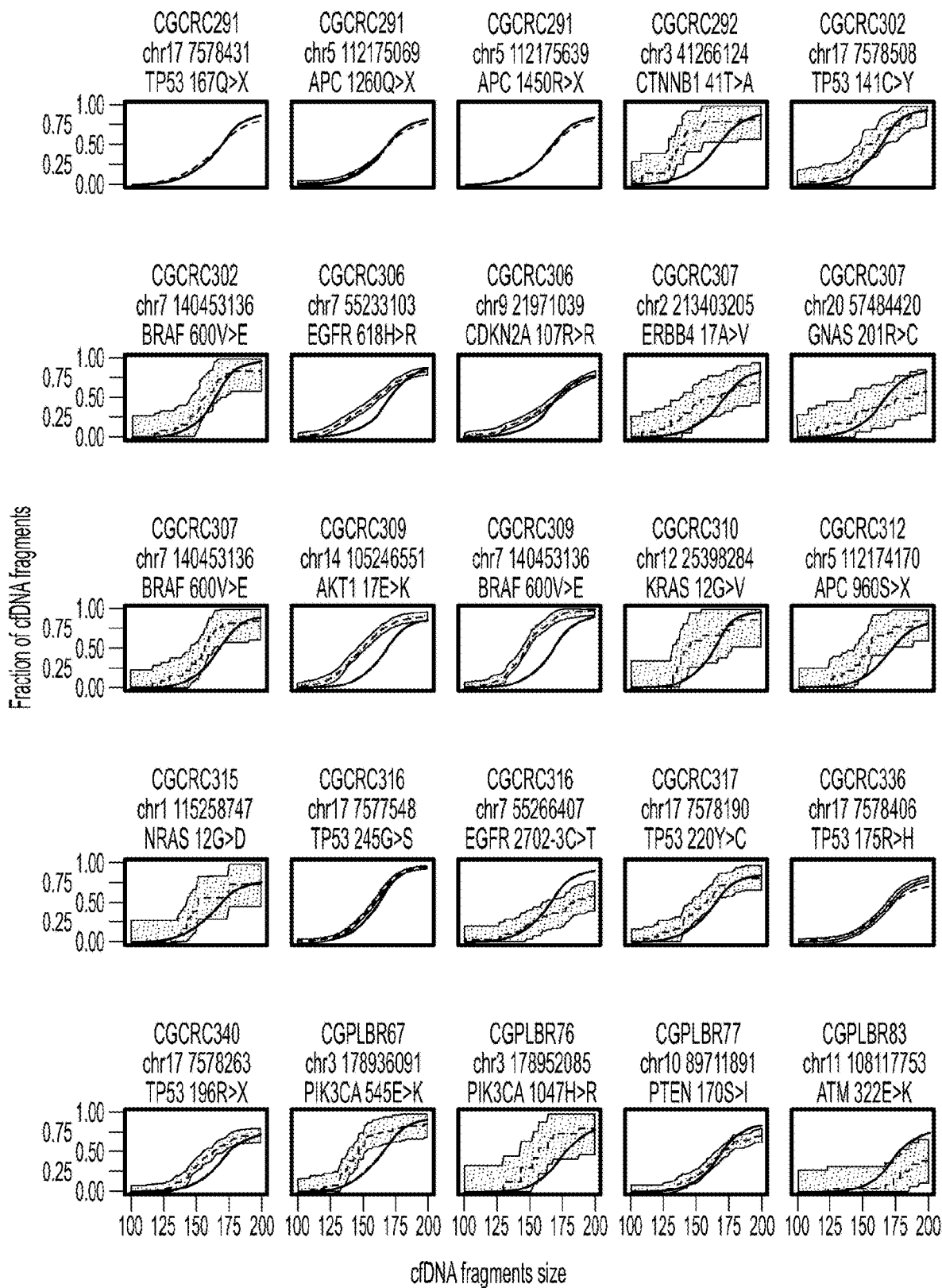


FIG. 3

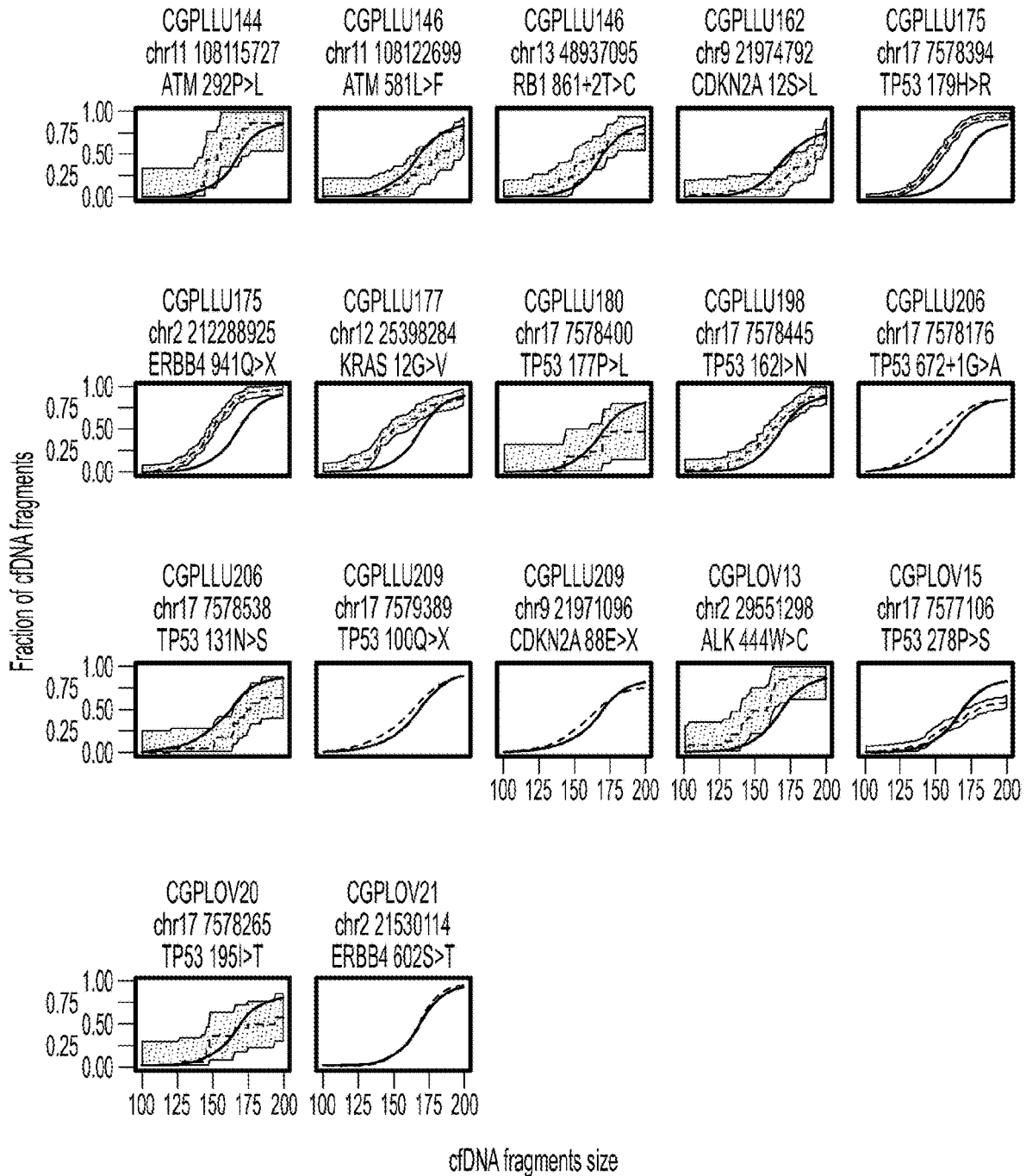


FIG. 3 (Cont.)

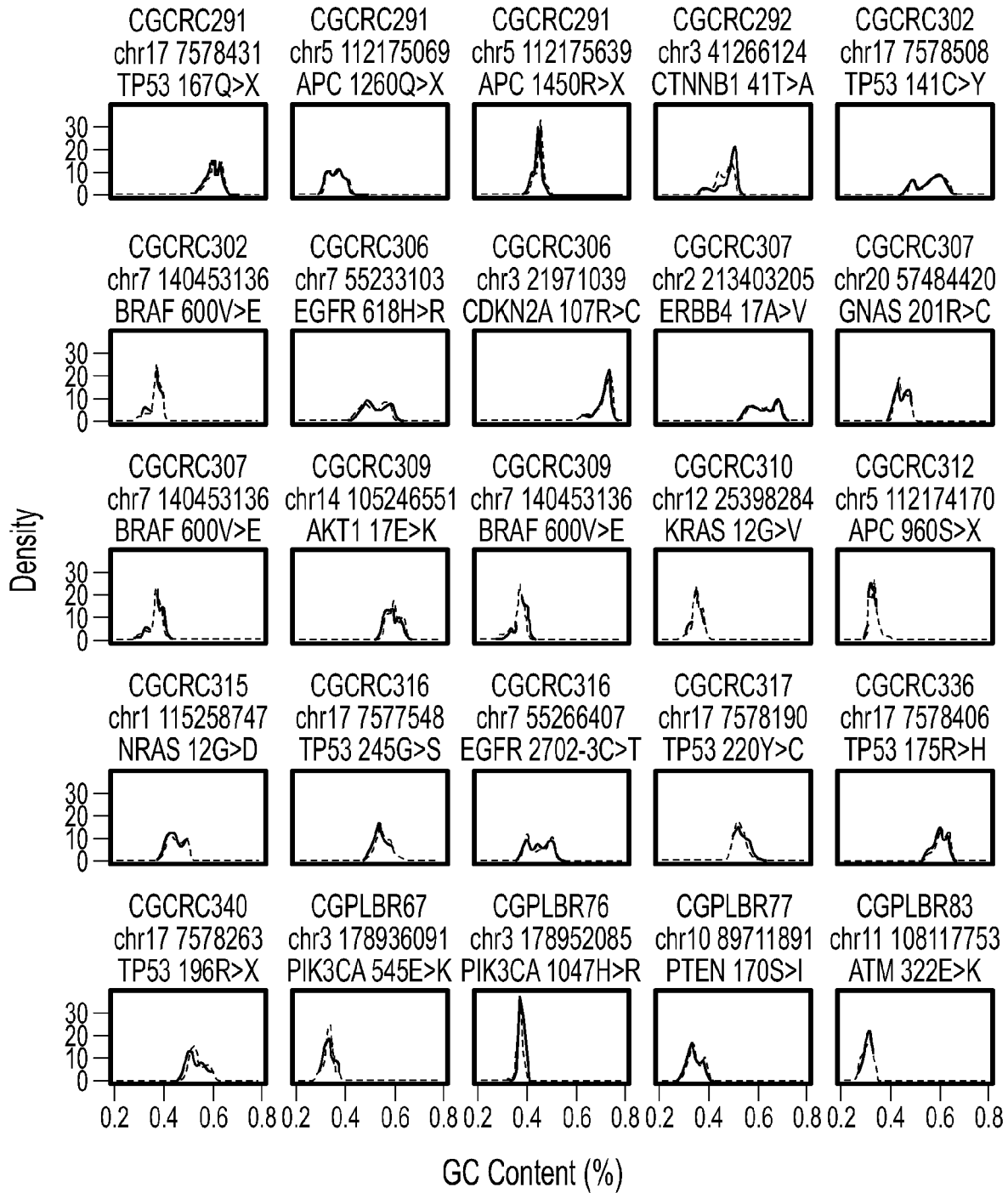


FIG. 4A

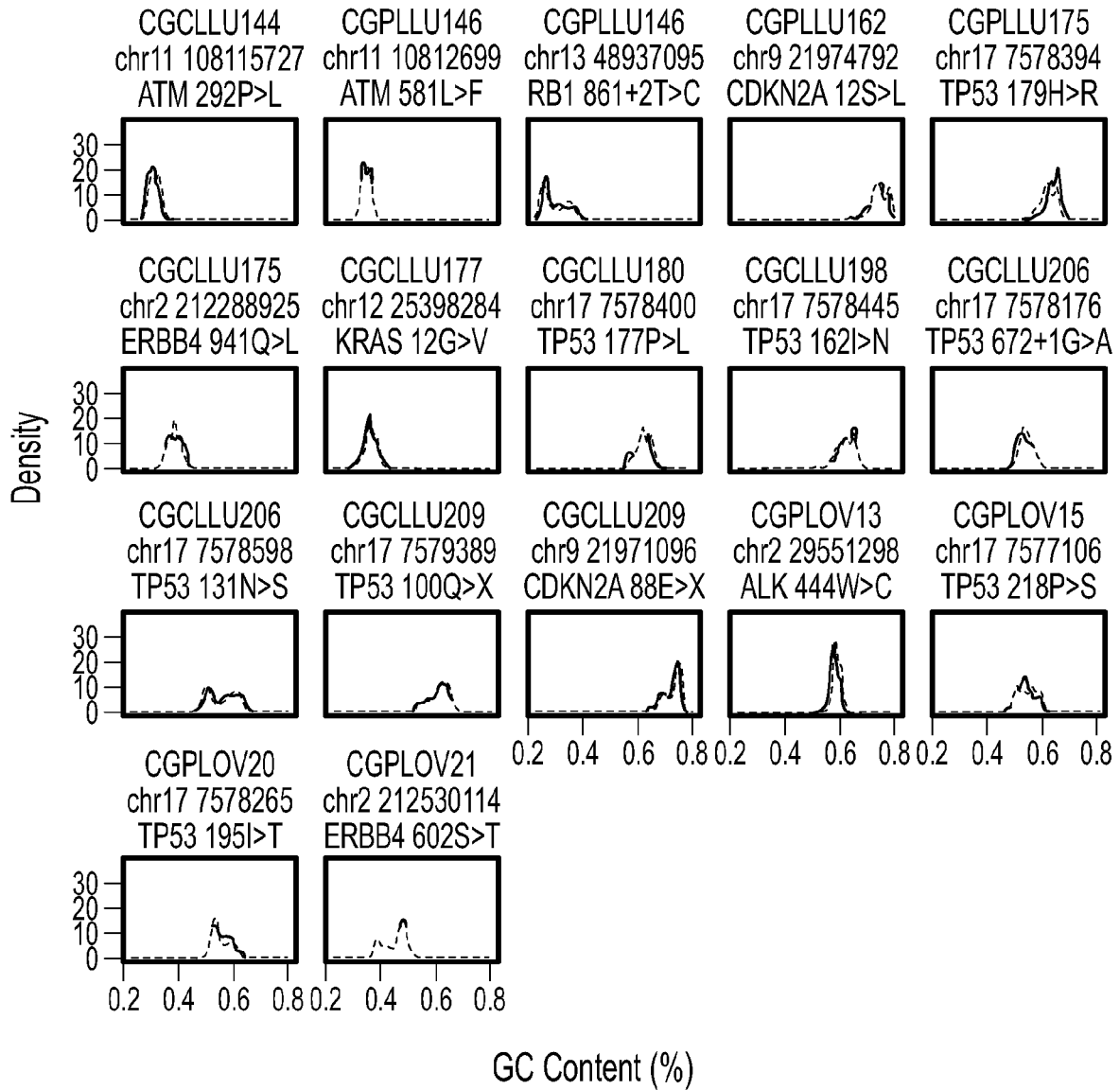


FIG. 4A (Cont.)

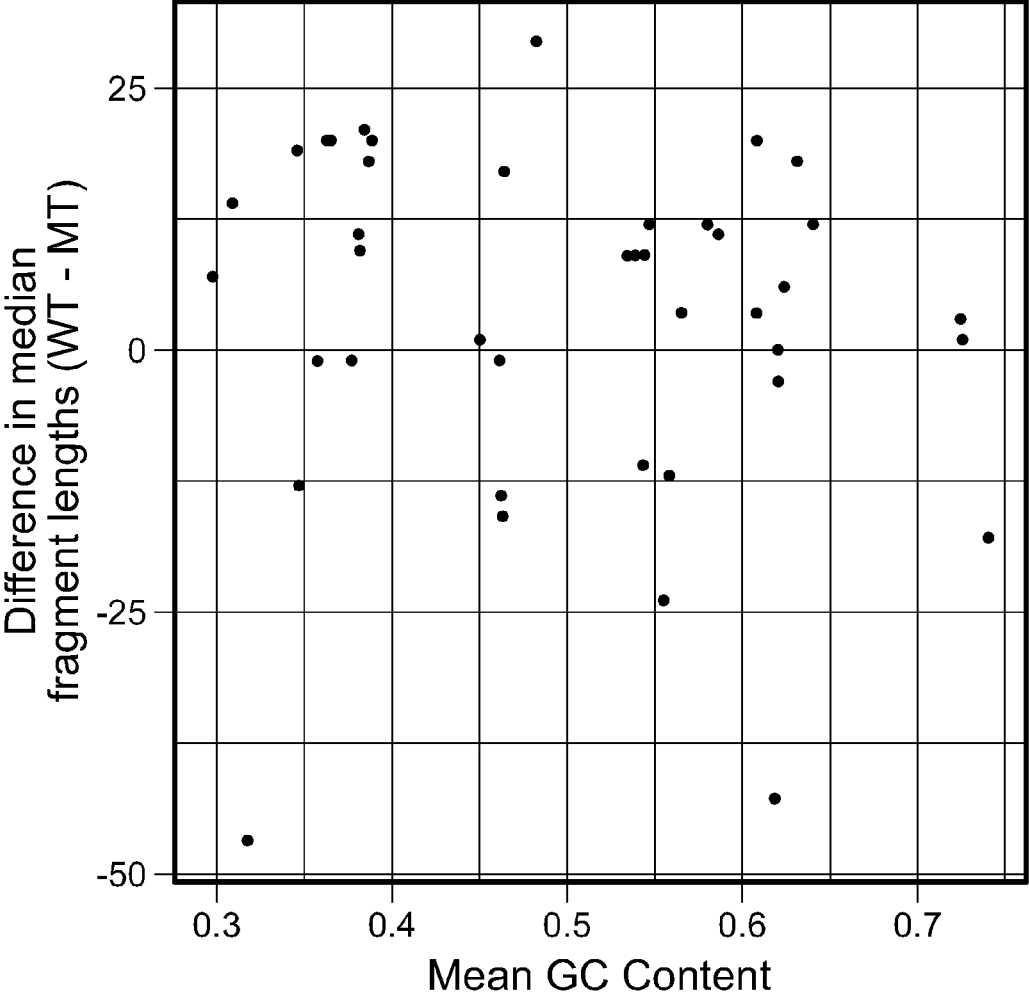


FIG. 4B

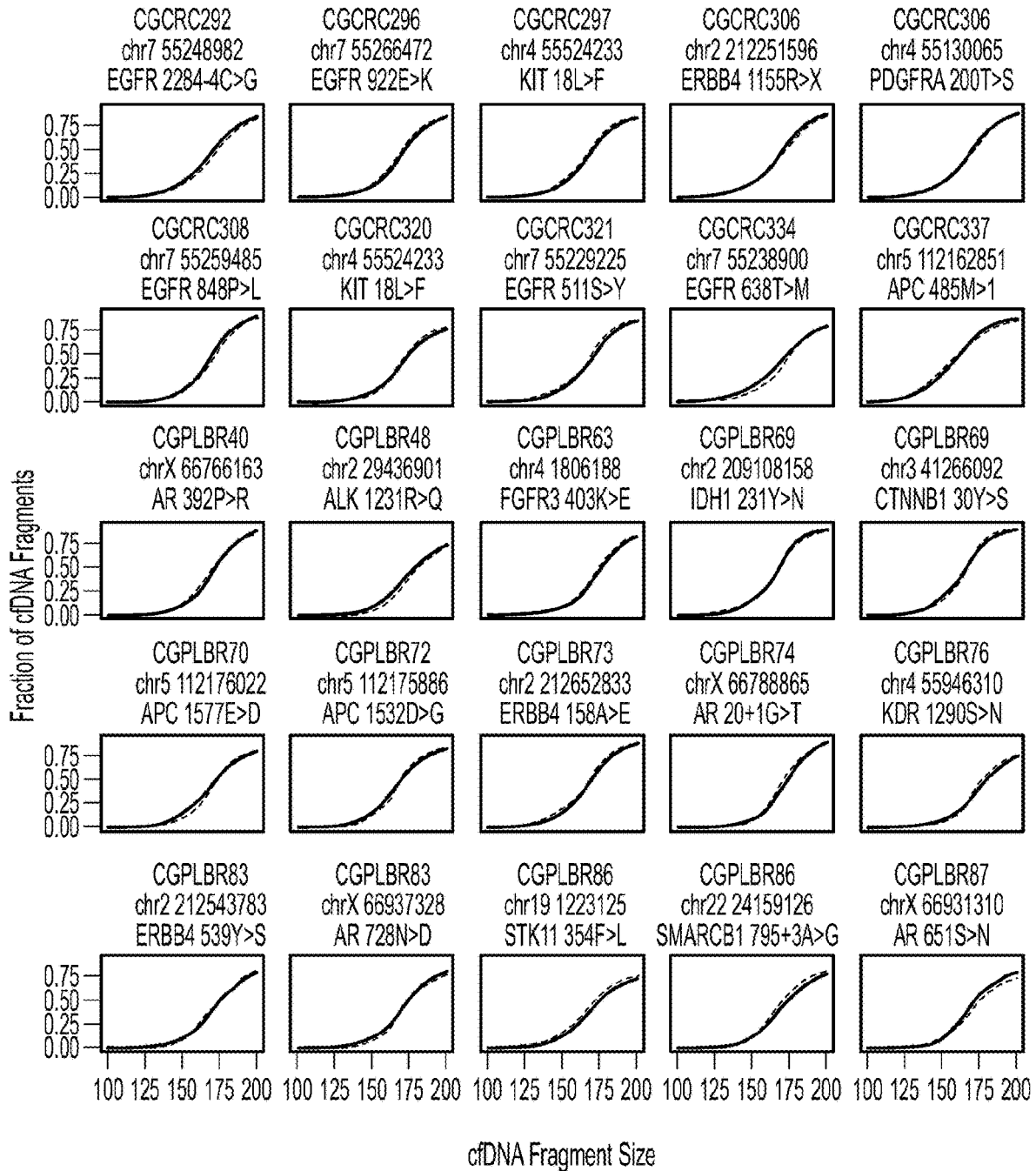


FIG. 5

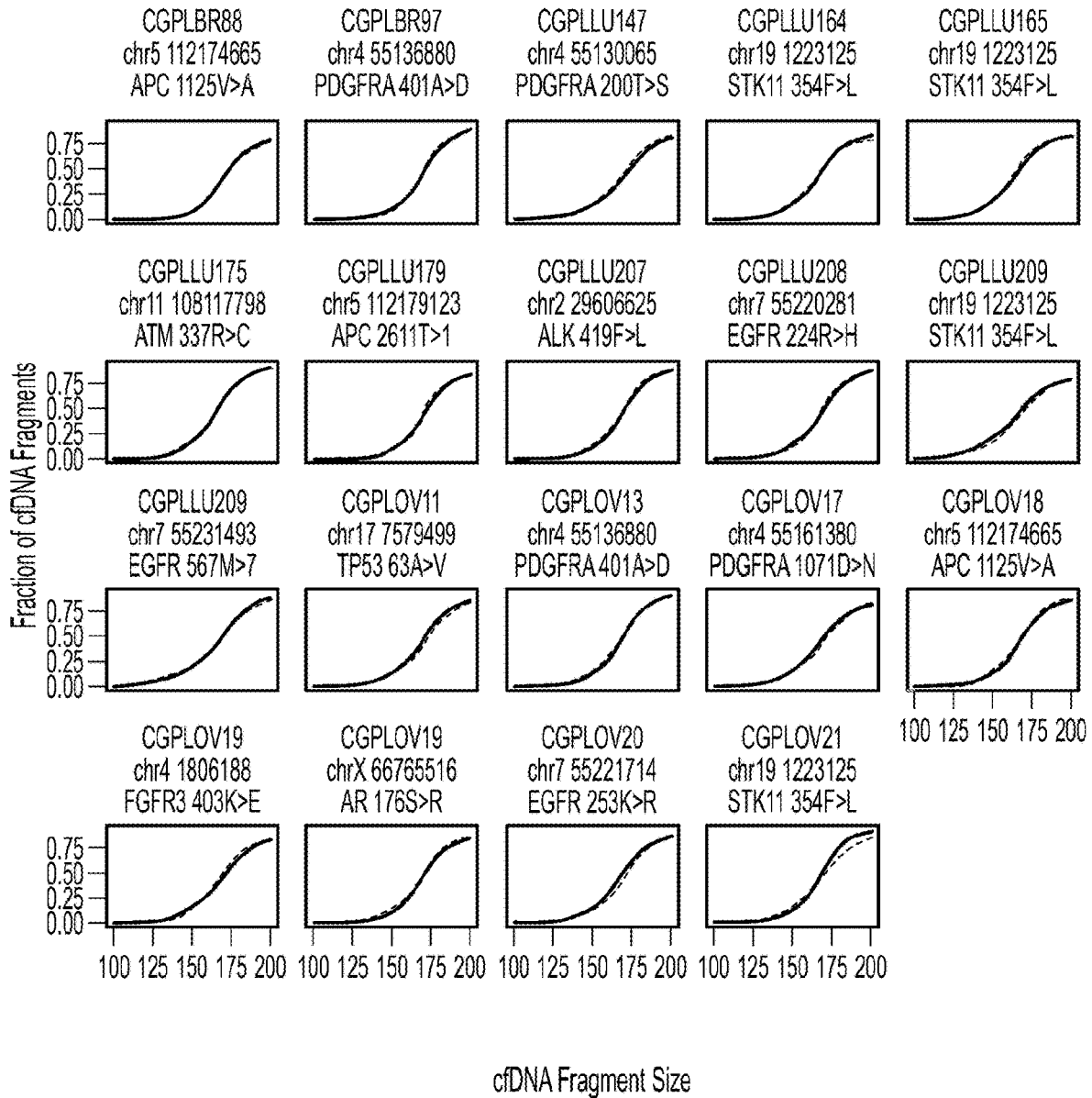


FIG. 5(Cont.)

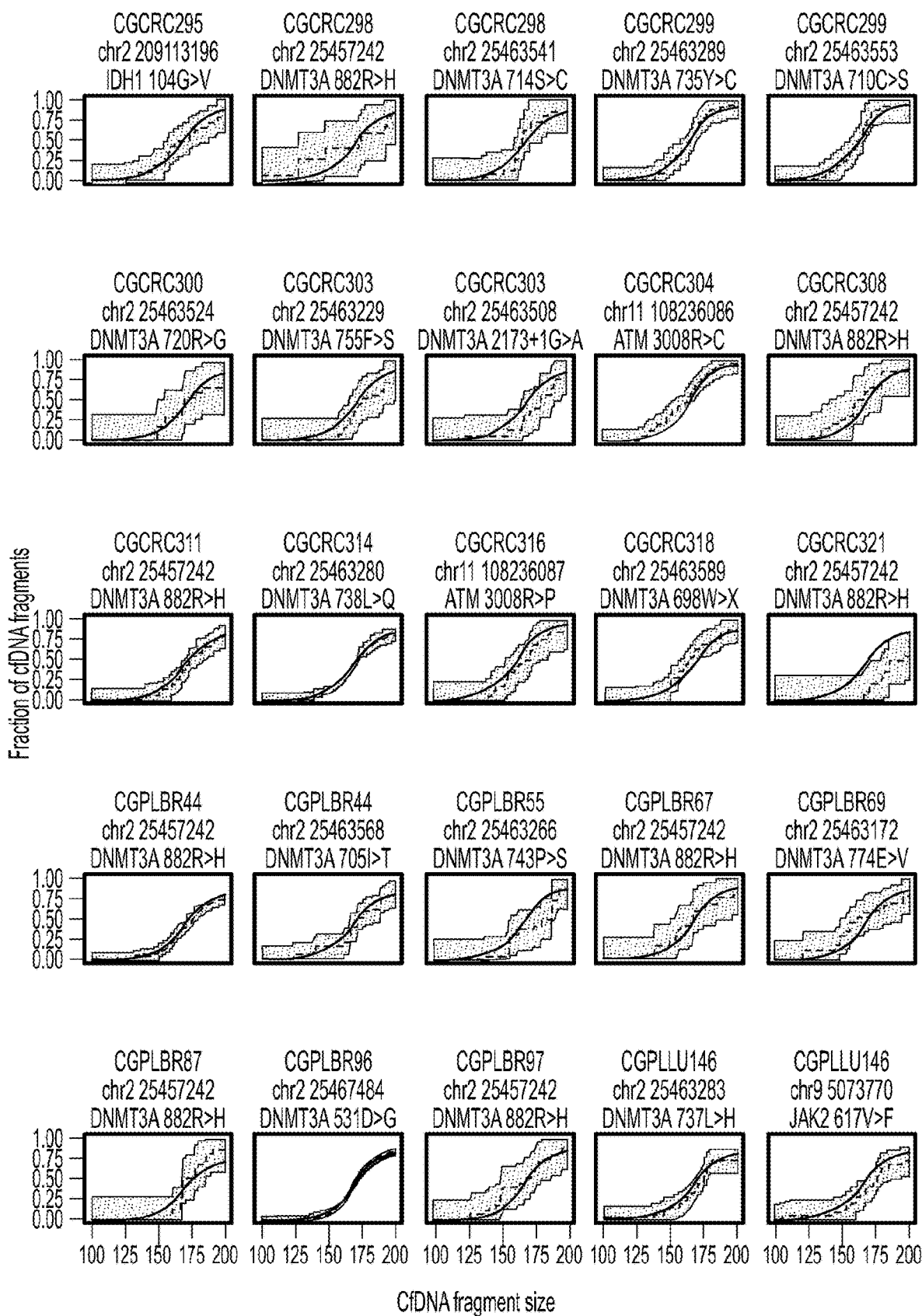


FIG. 6

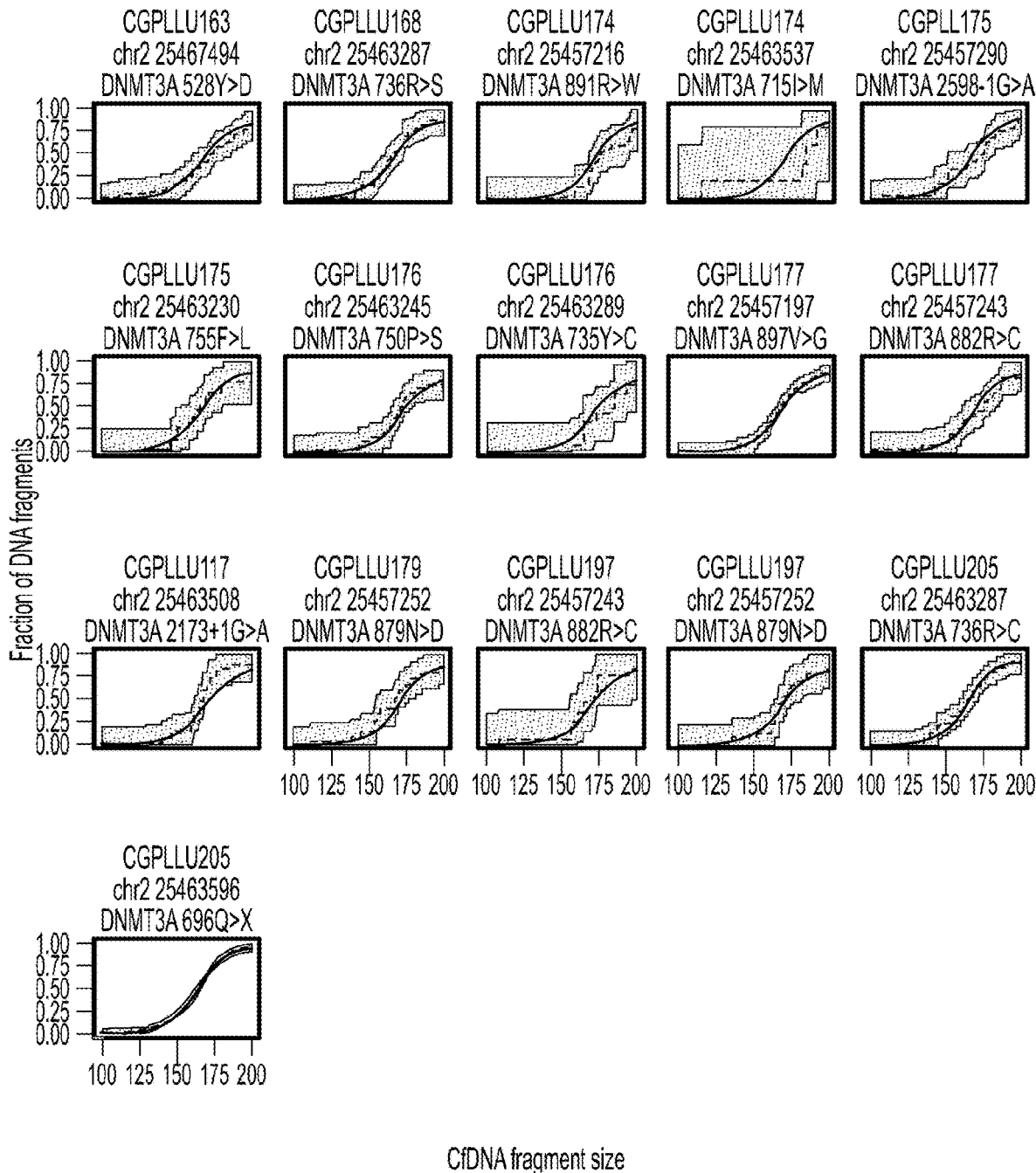


FIG. 6(Cont.)

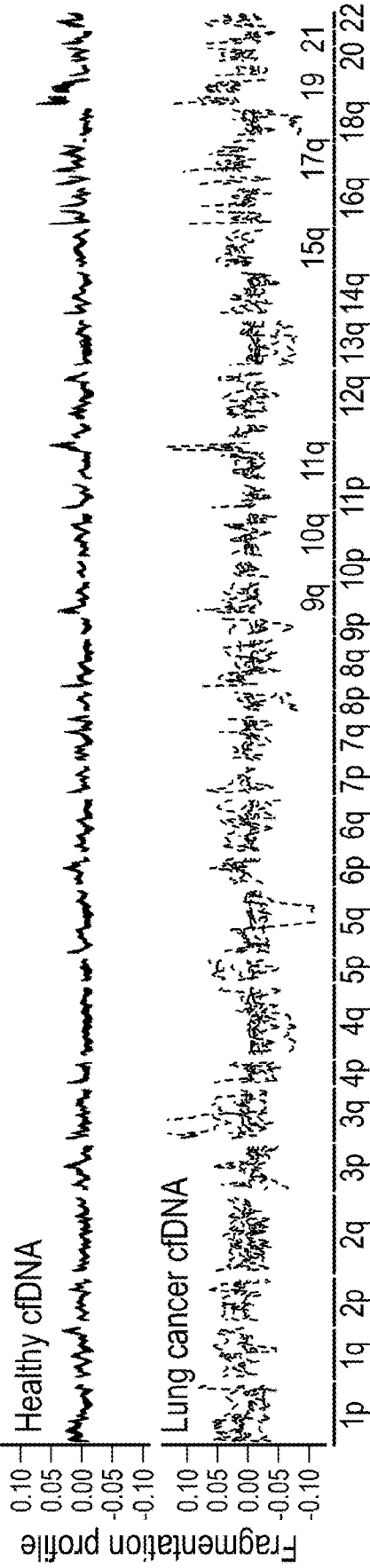
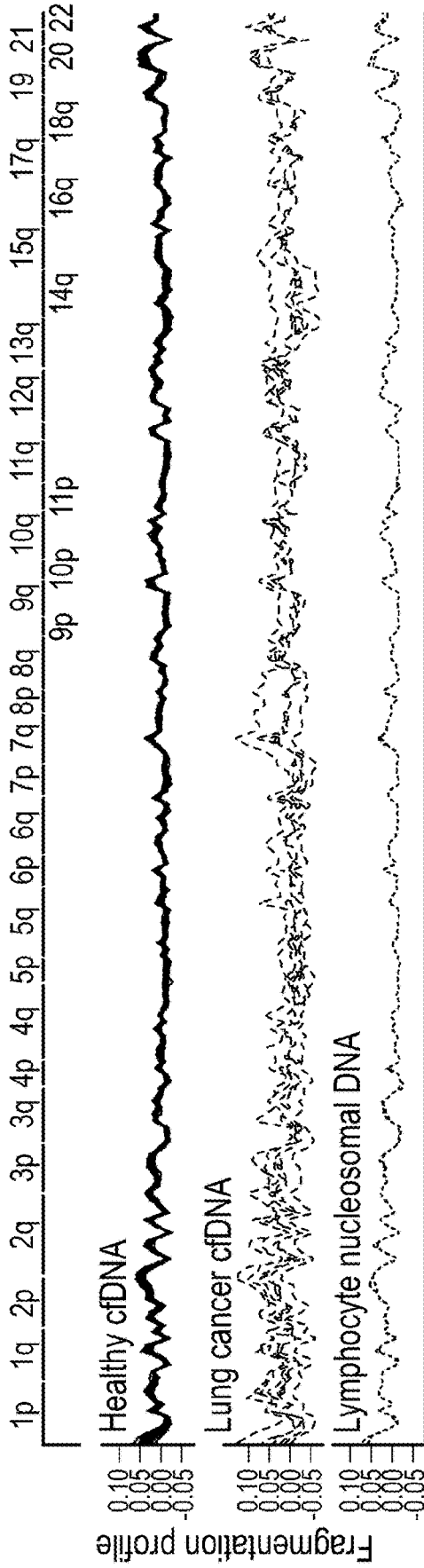
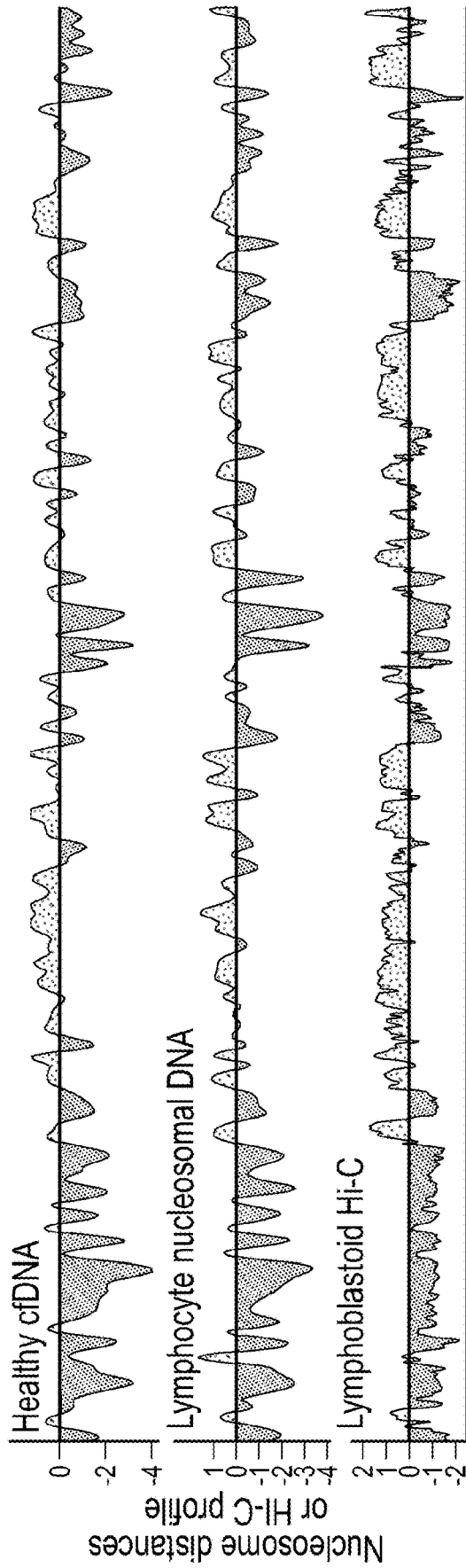


FIG. 7A



Chromosome 1

FIG. 7B



Chromosome 1

FIG. 7C

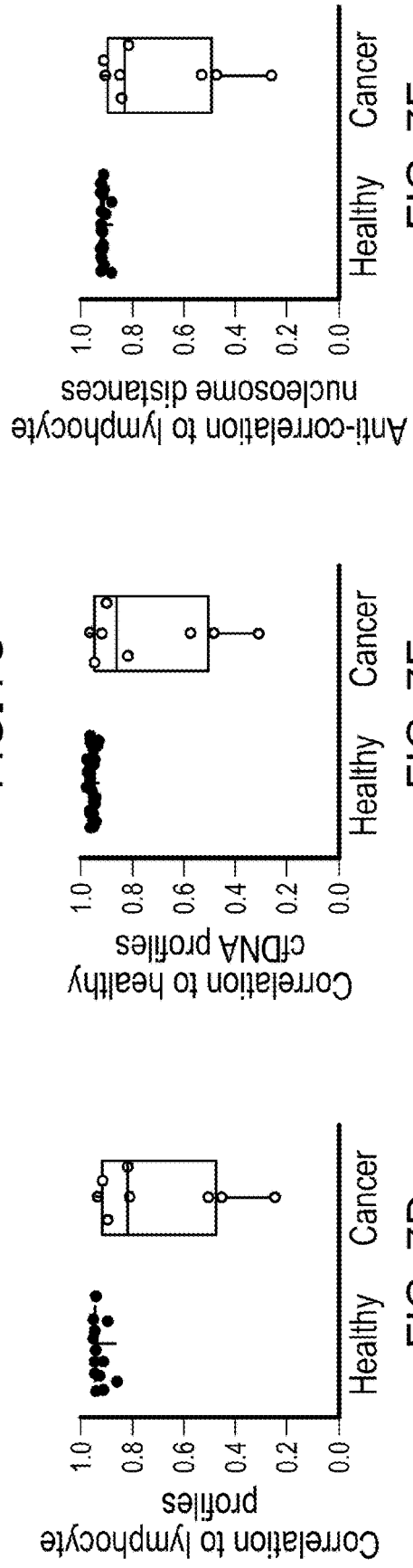


FIG. 7D

FIG. 7E

FIG. 7F

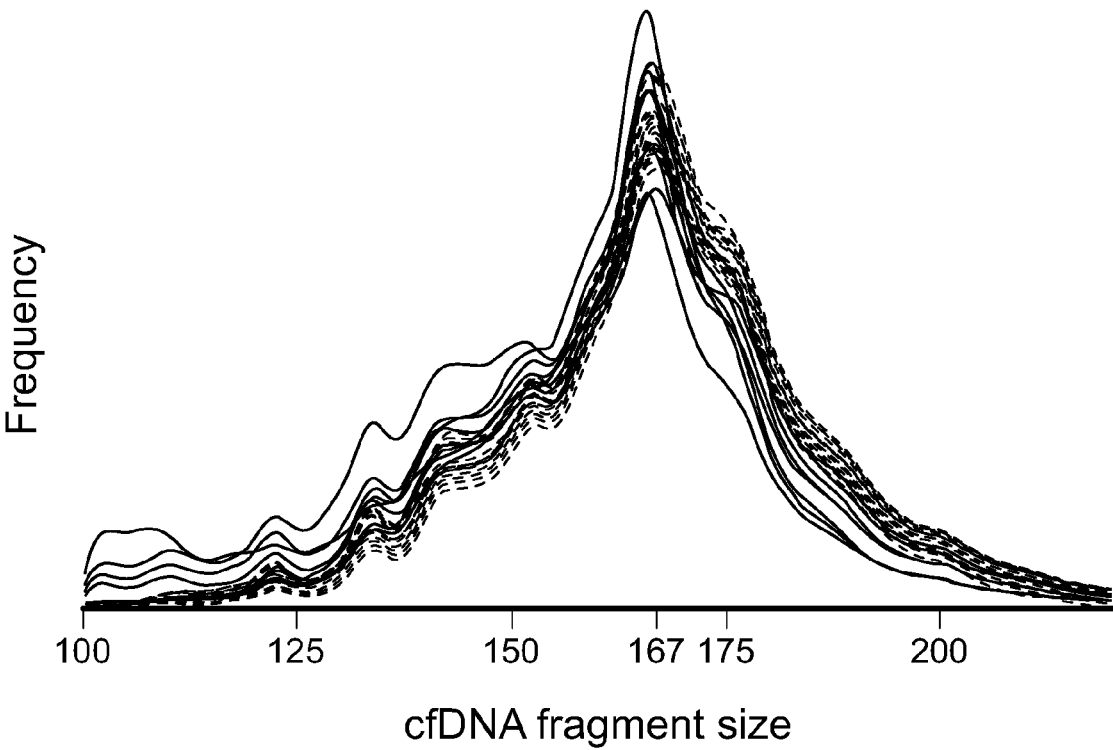


FIG. 8

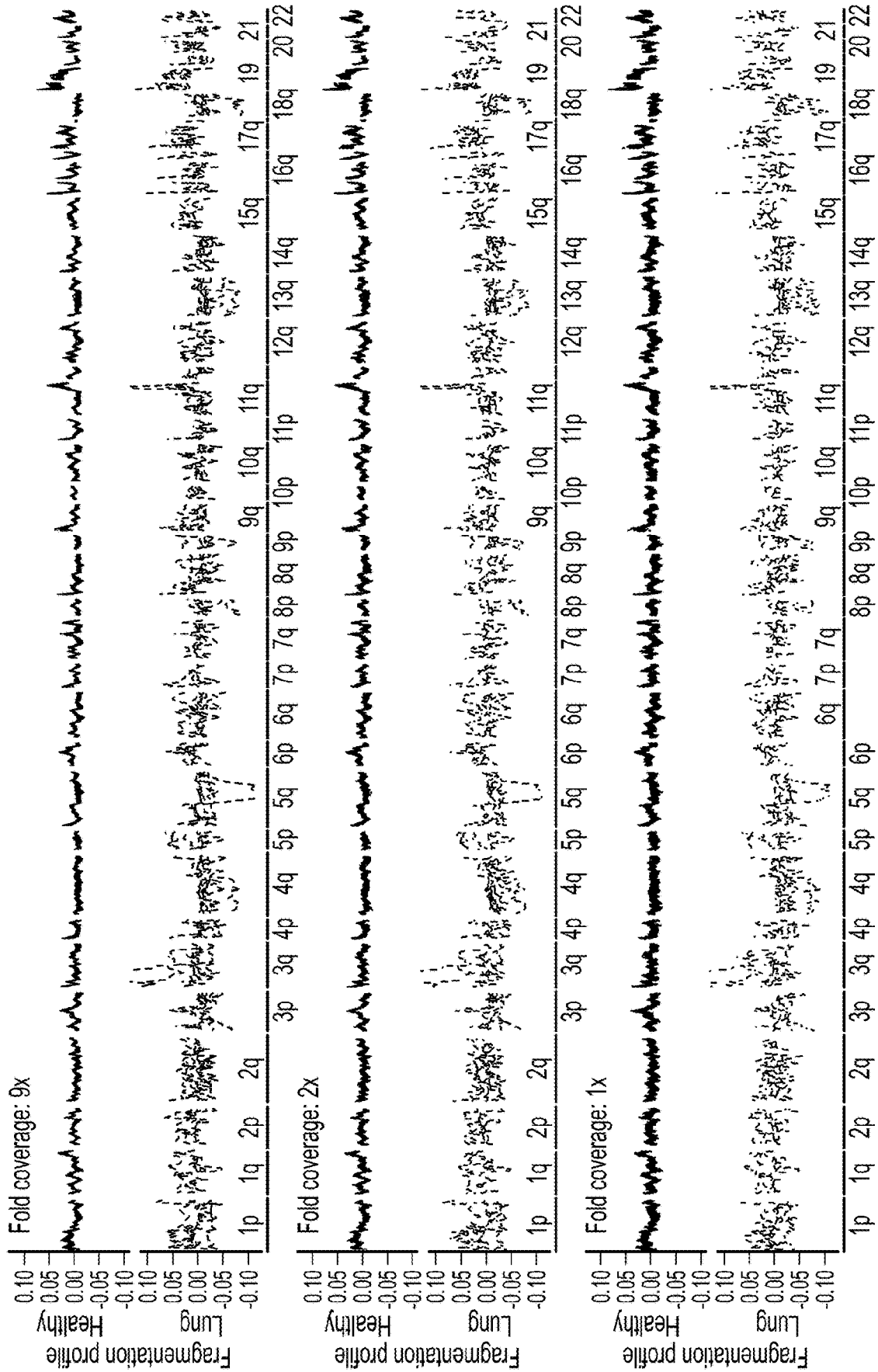


FIG. 9A

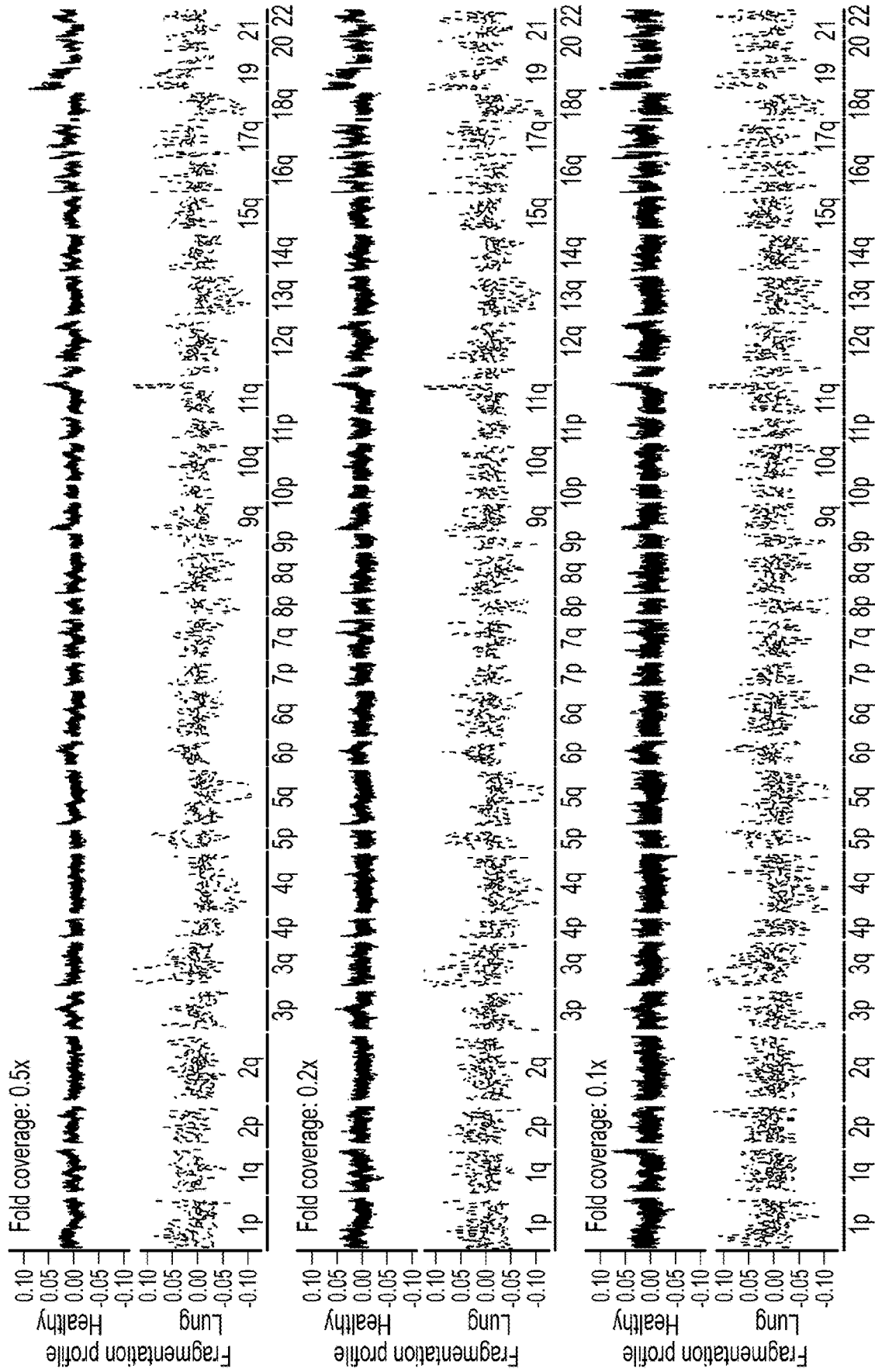


FIG. 9A (Cont.)

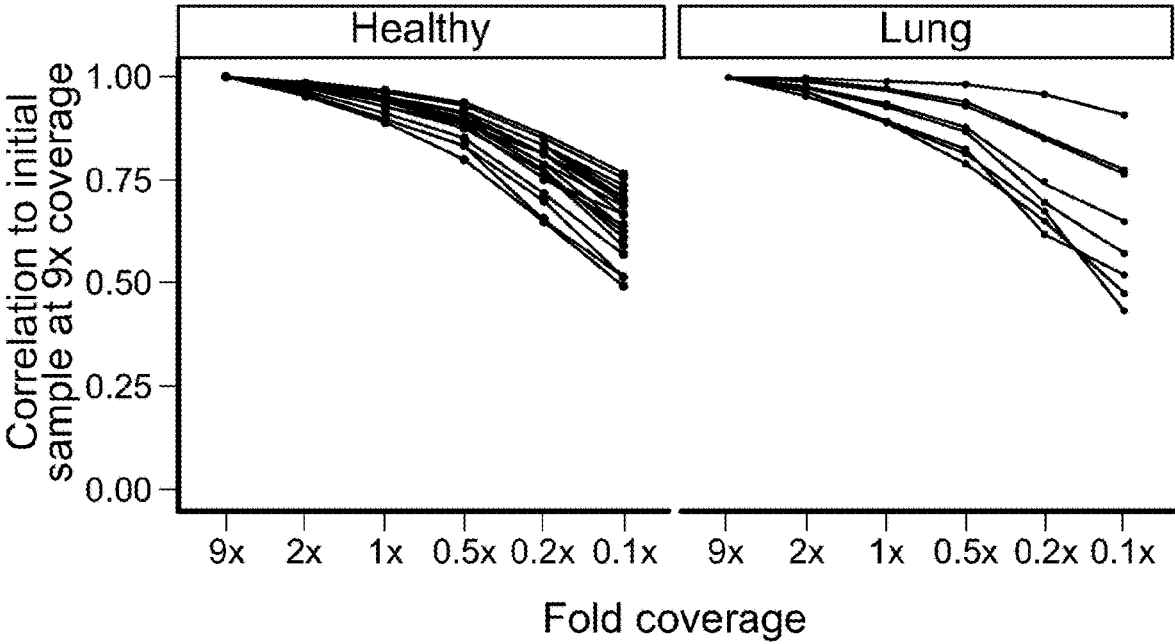


FIG. 9B

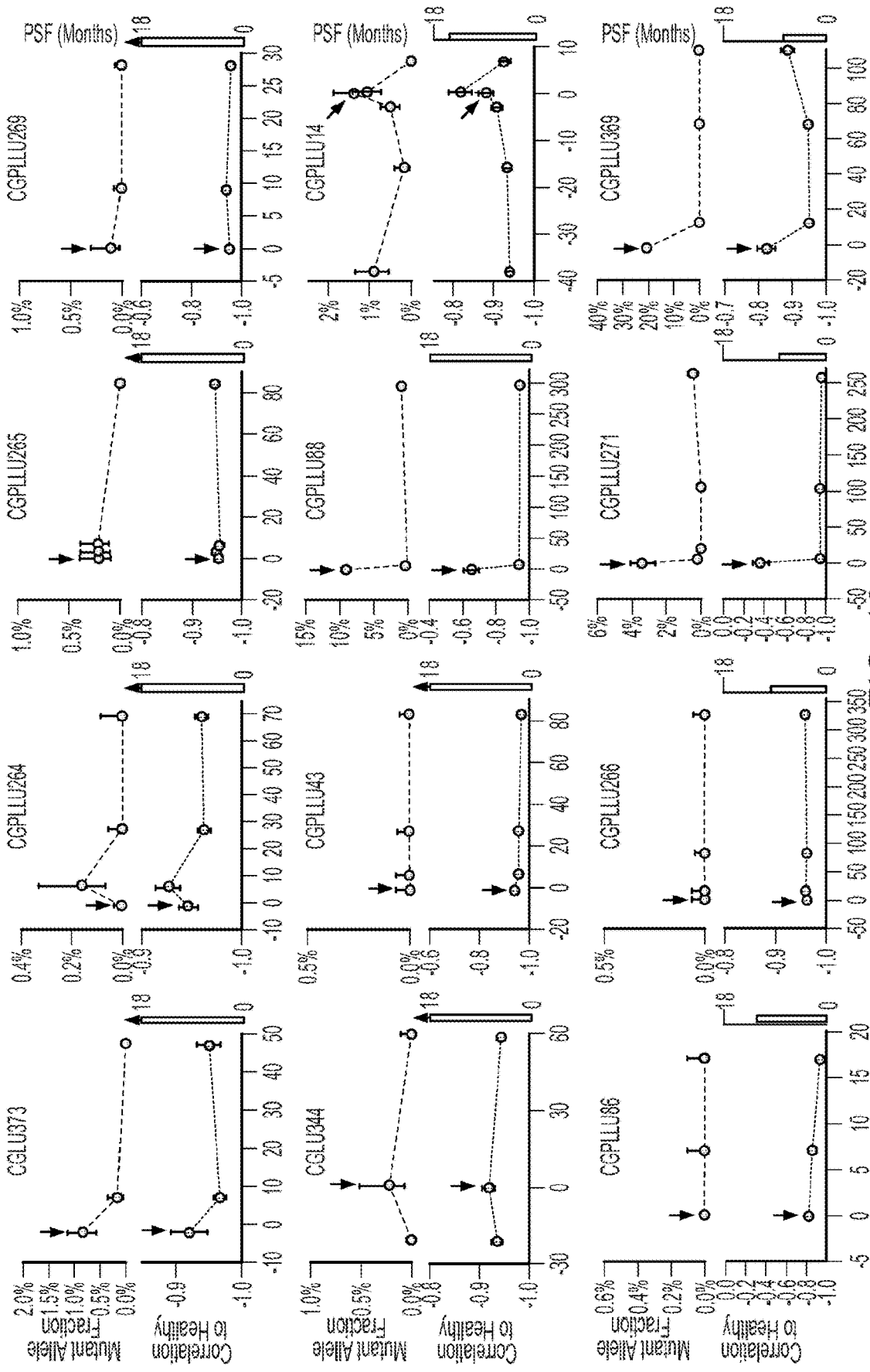


FIG. 10

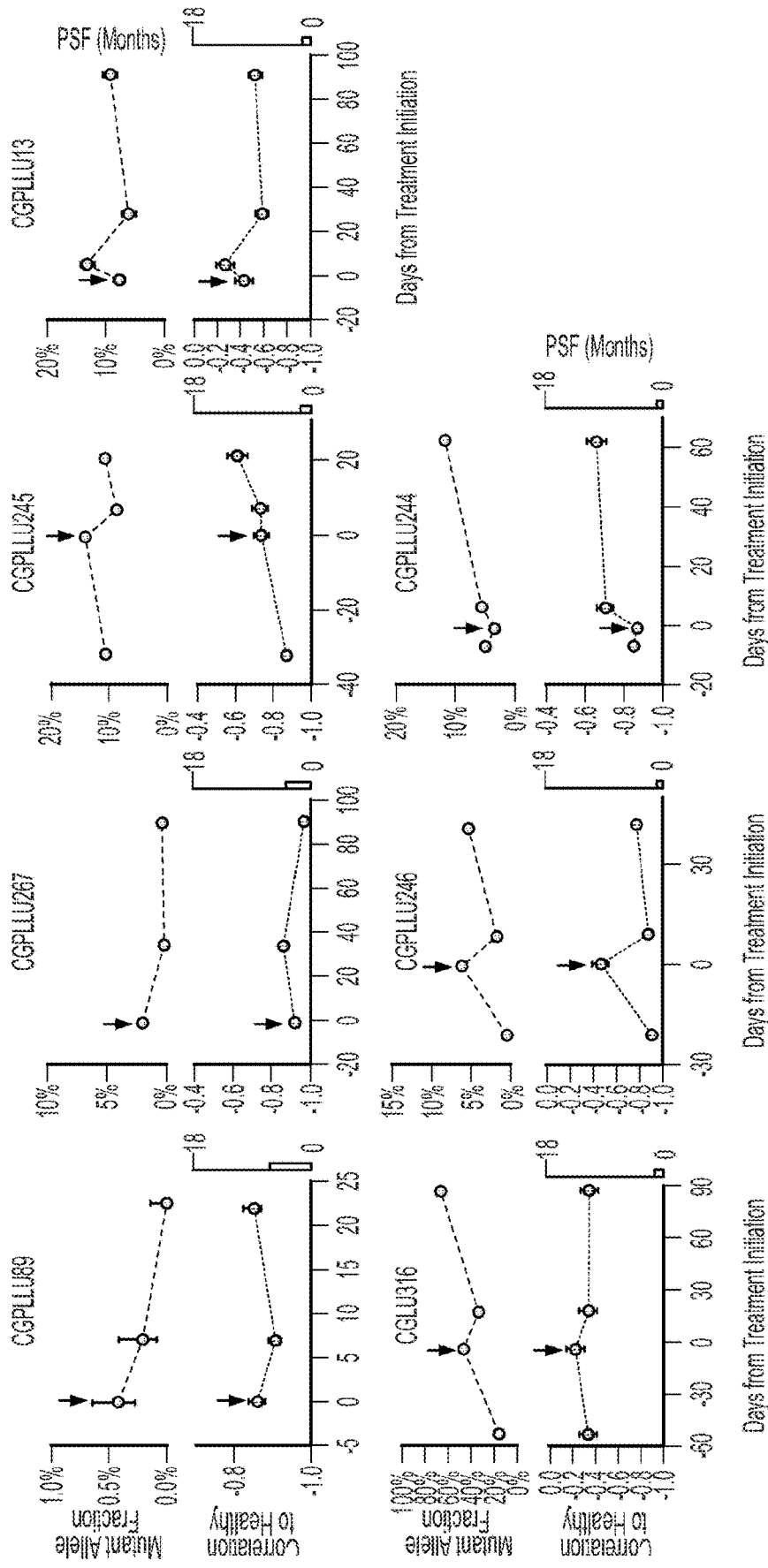


FIG. 10(Cont.)

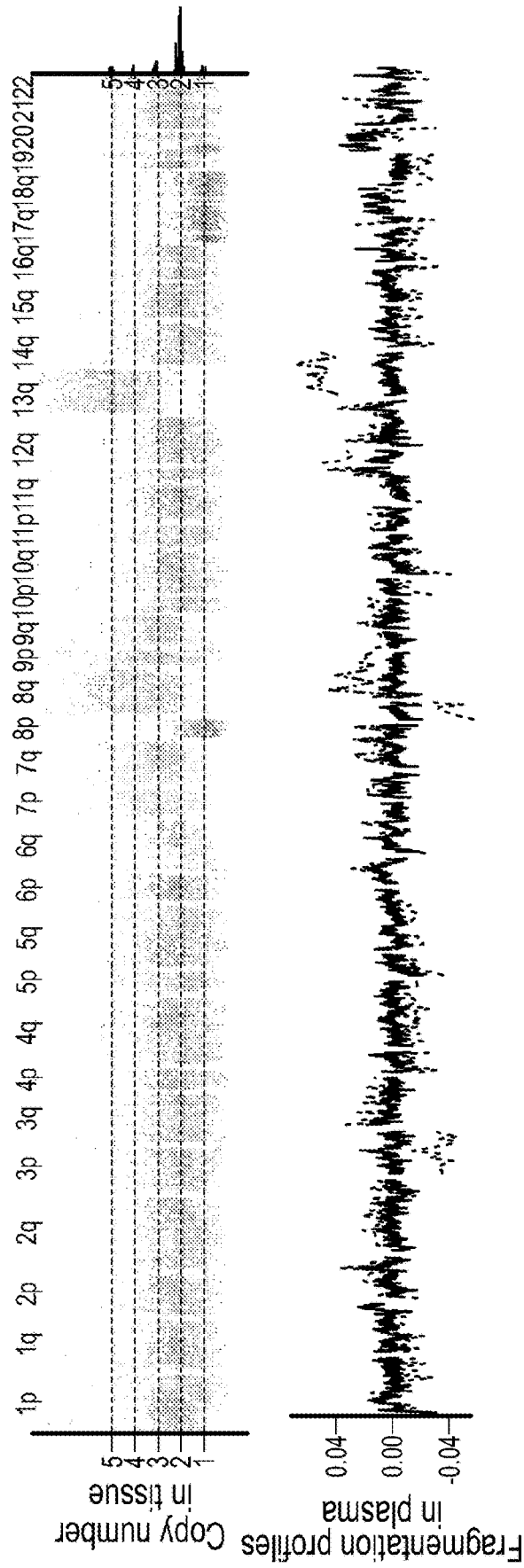


FIG. 11A

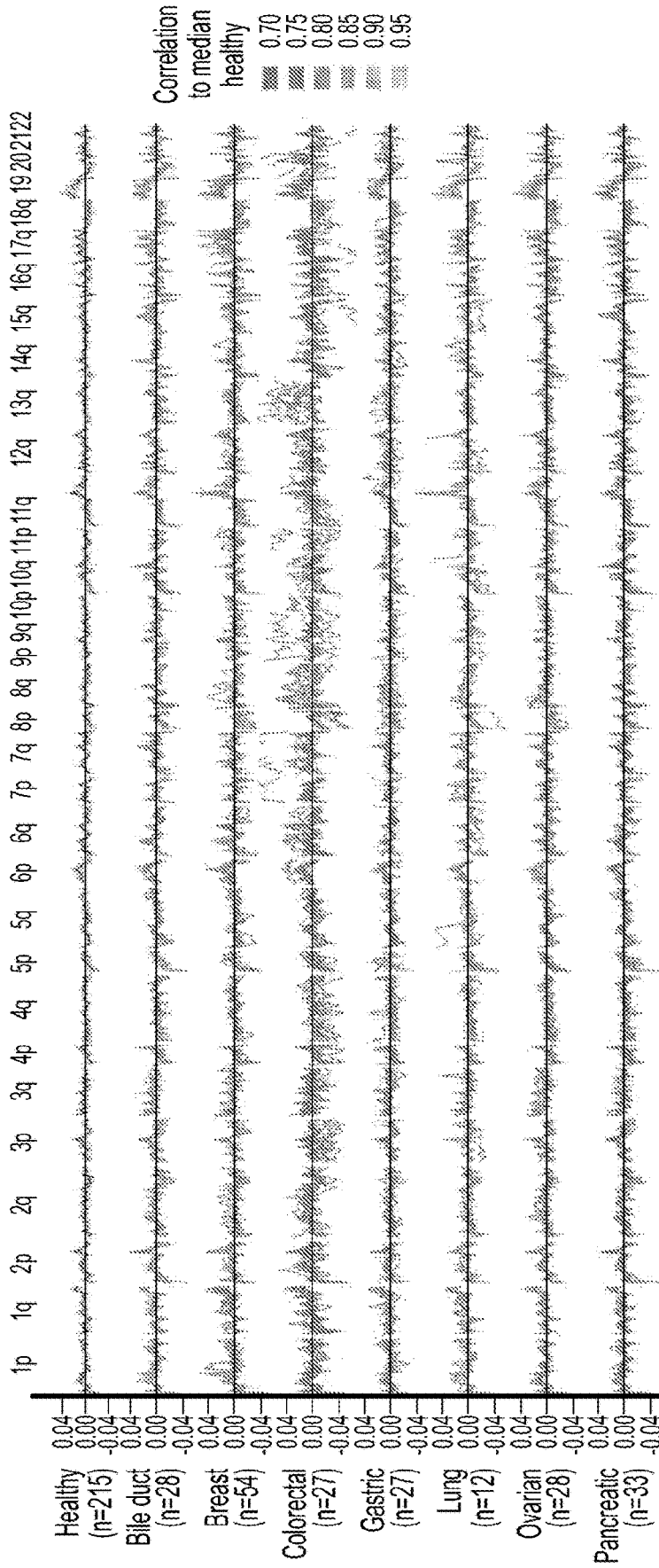


FIG. 11B

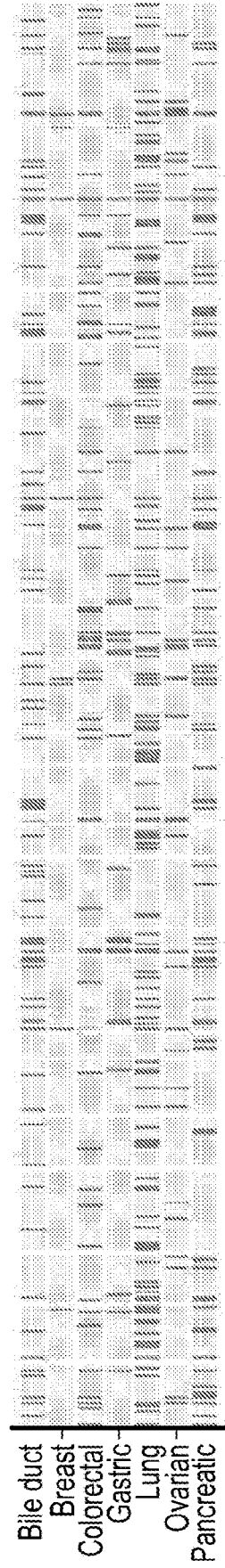


FIG. 11C

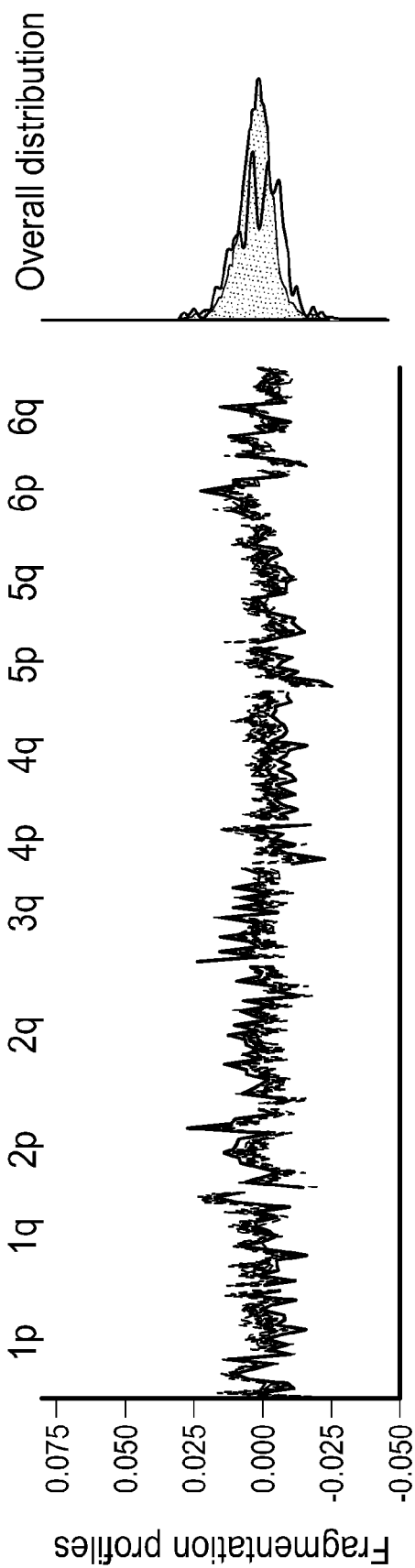


FIG. 12A

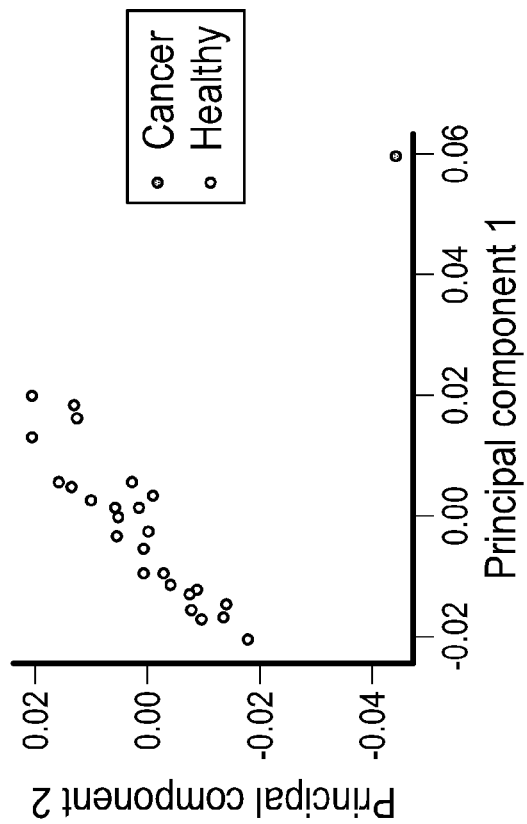


FIG. 12B

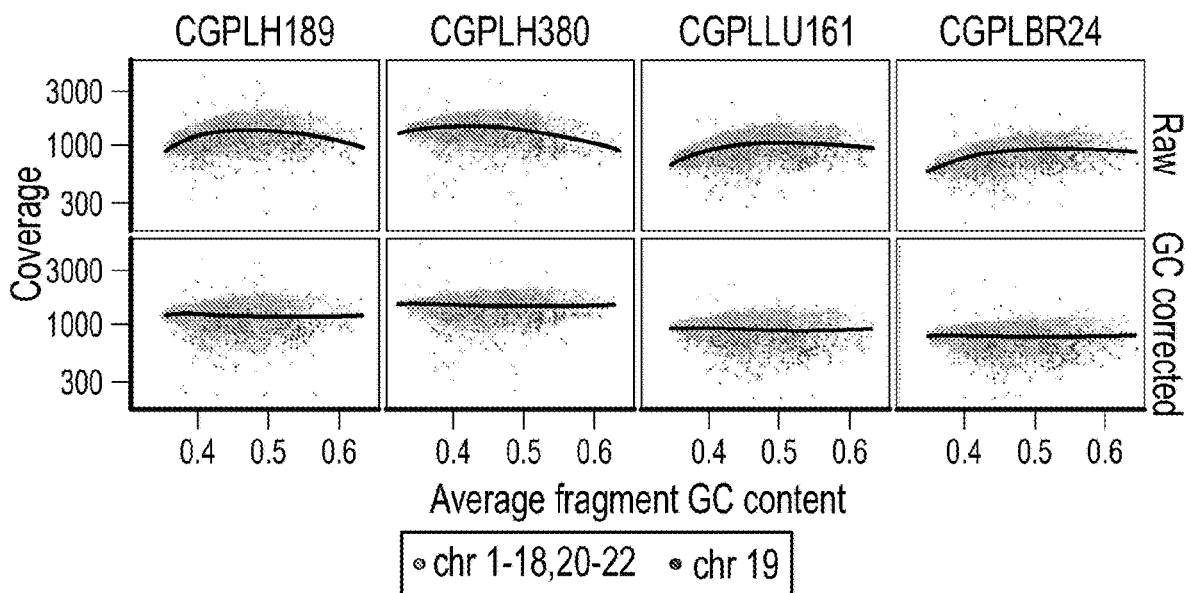


FIG. 13A

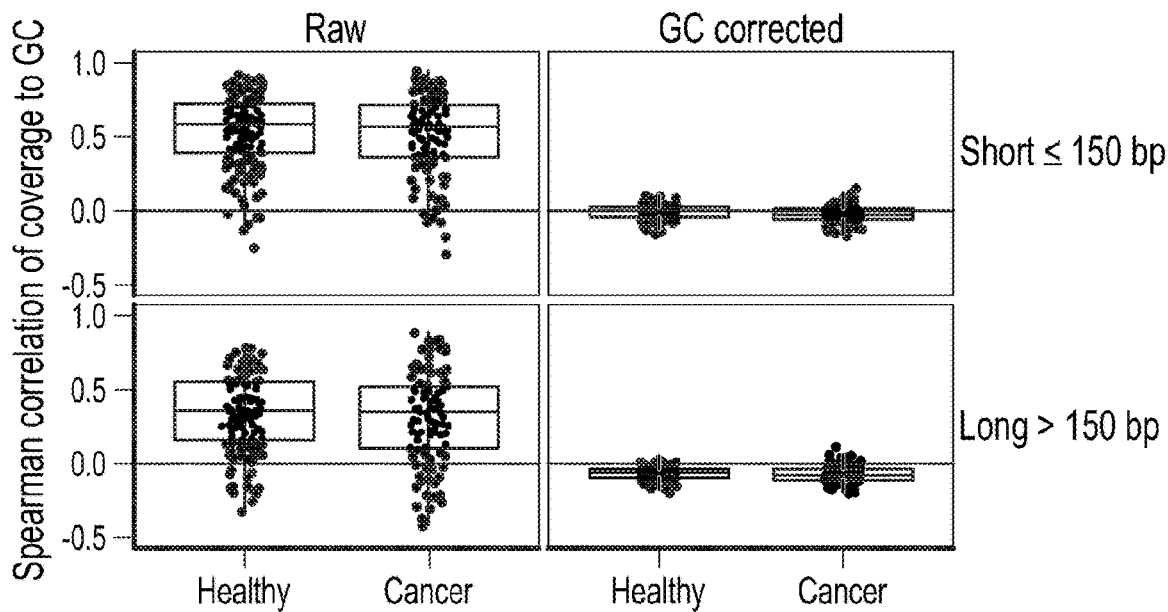


FIG. 13B

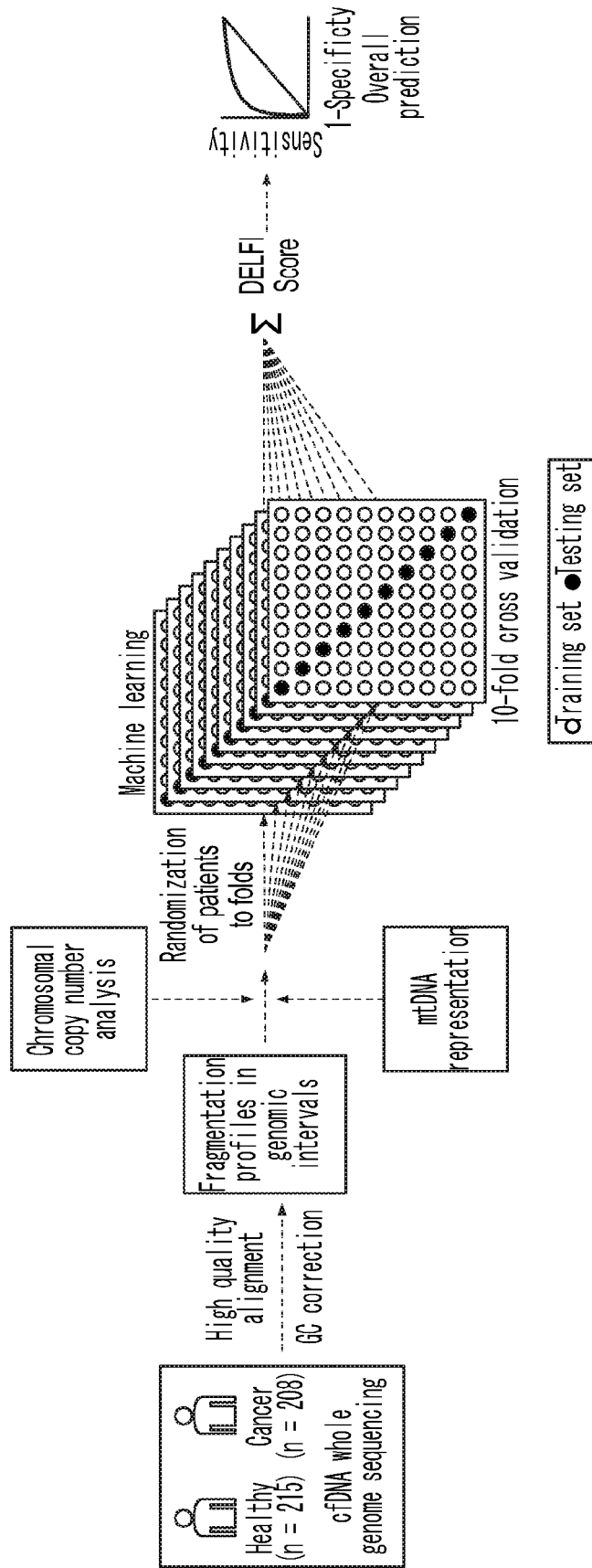


FIG. 14

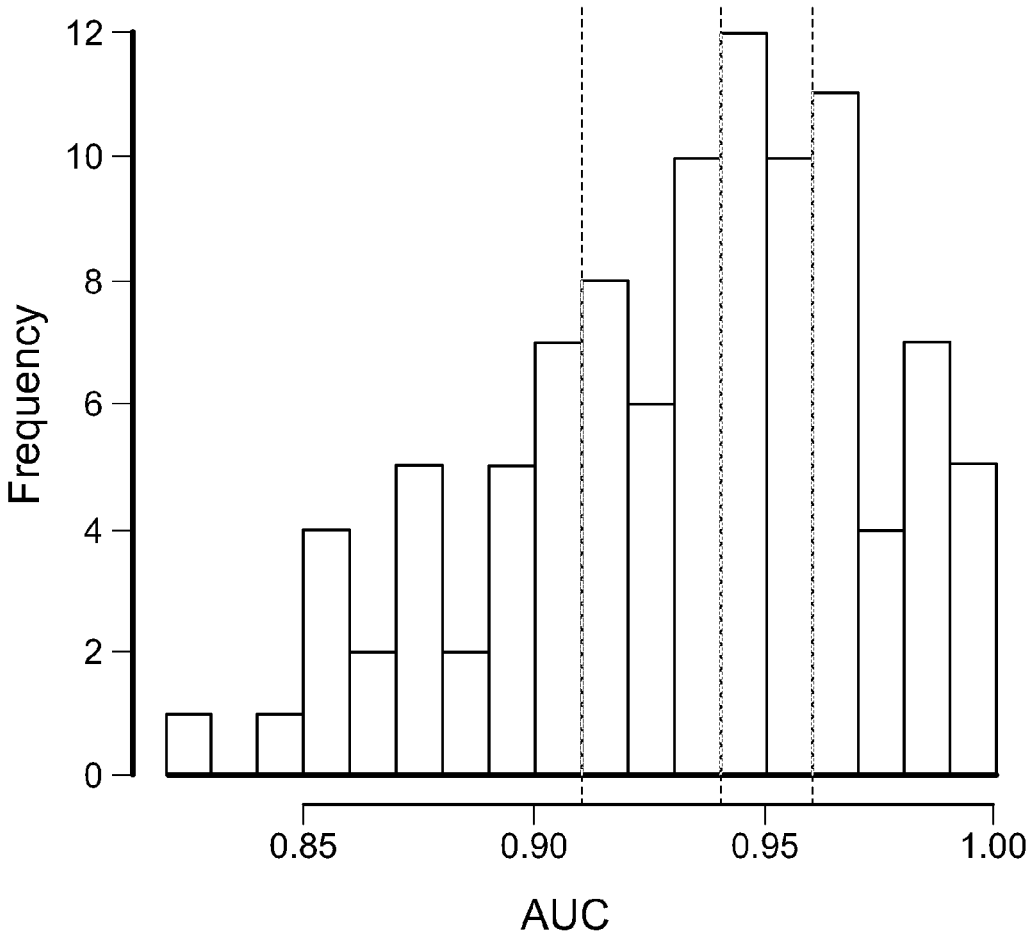


FIG. 15

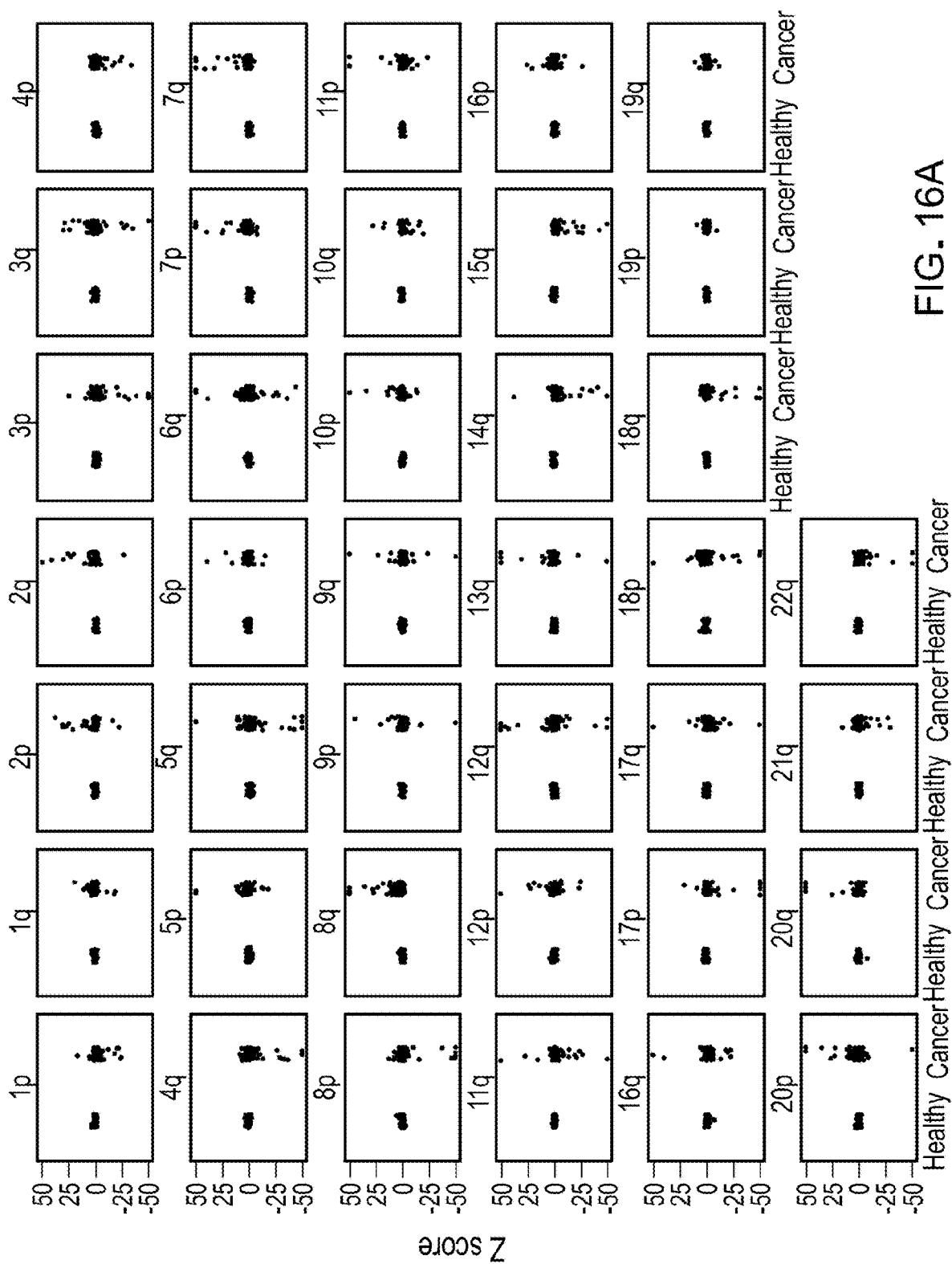


FIG. 16A

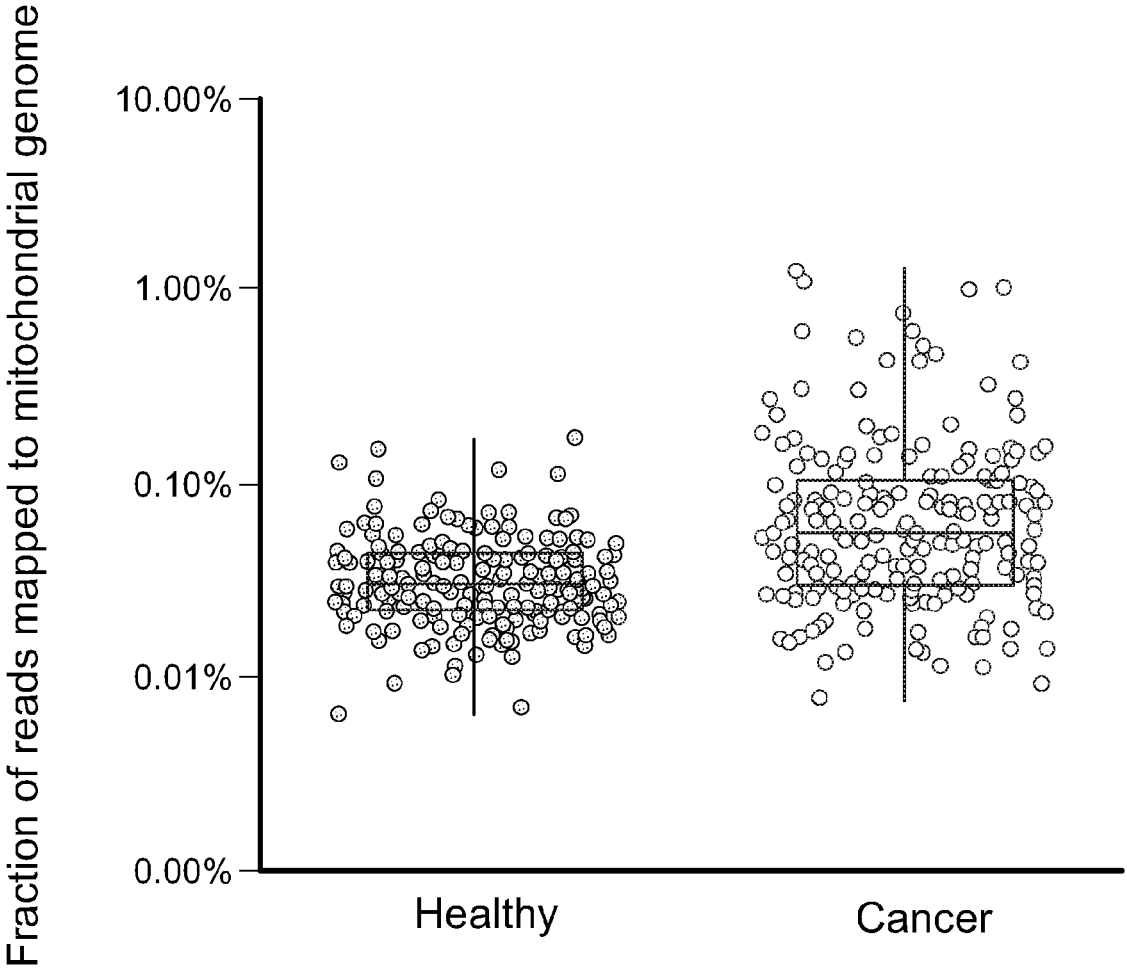


FIG. 16B

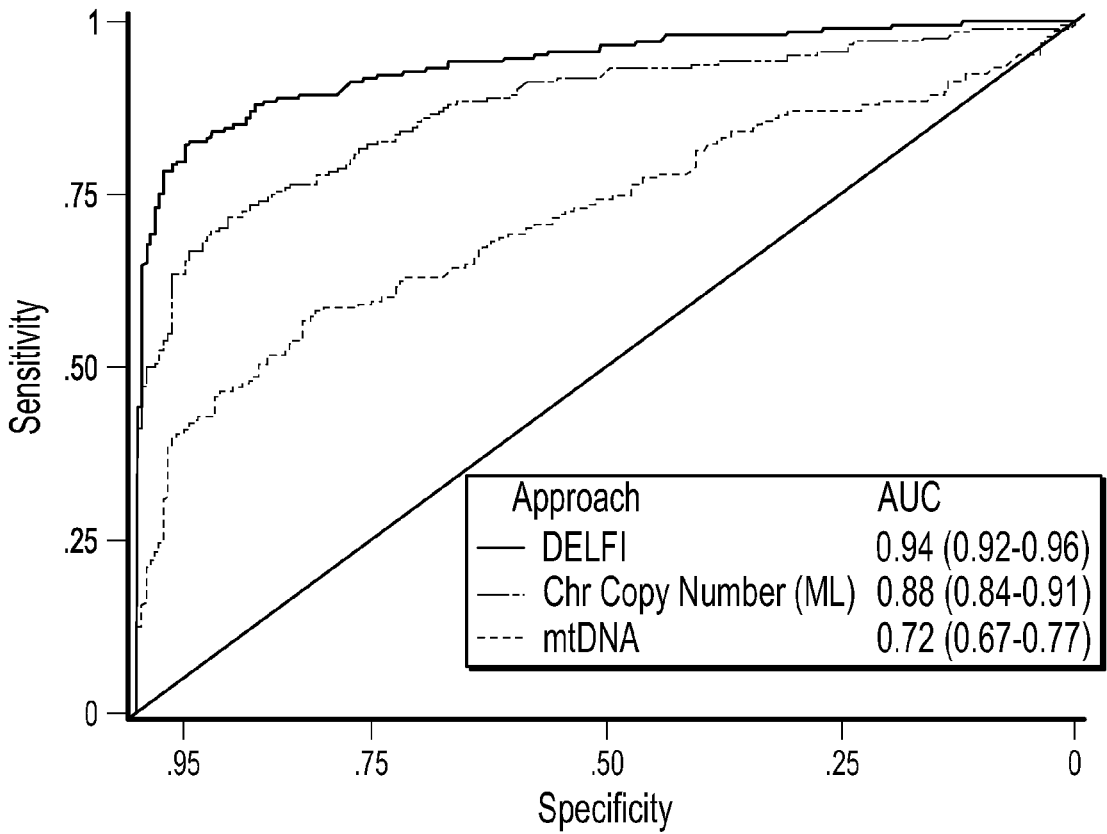
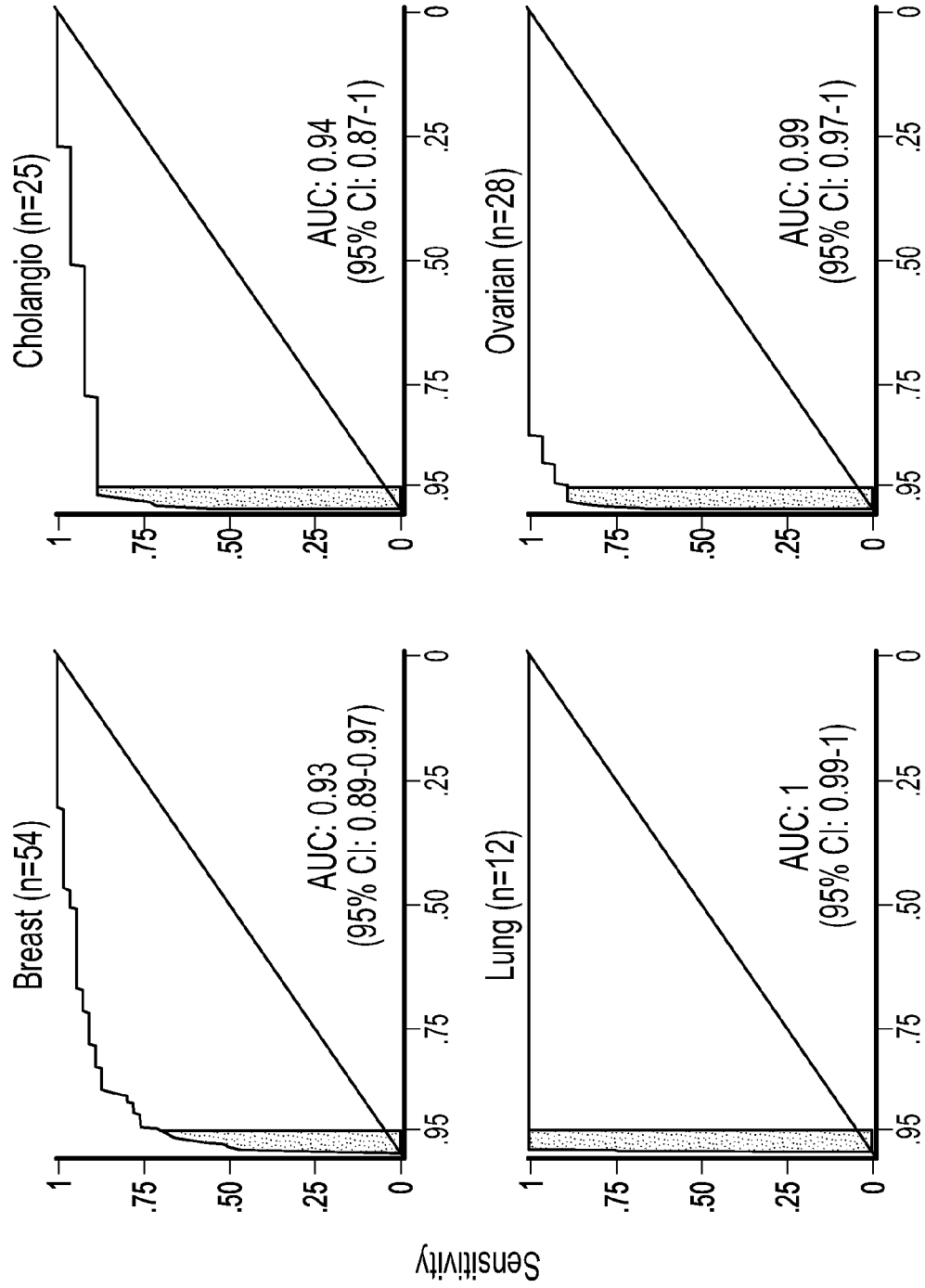
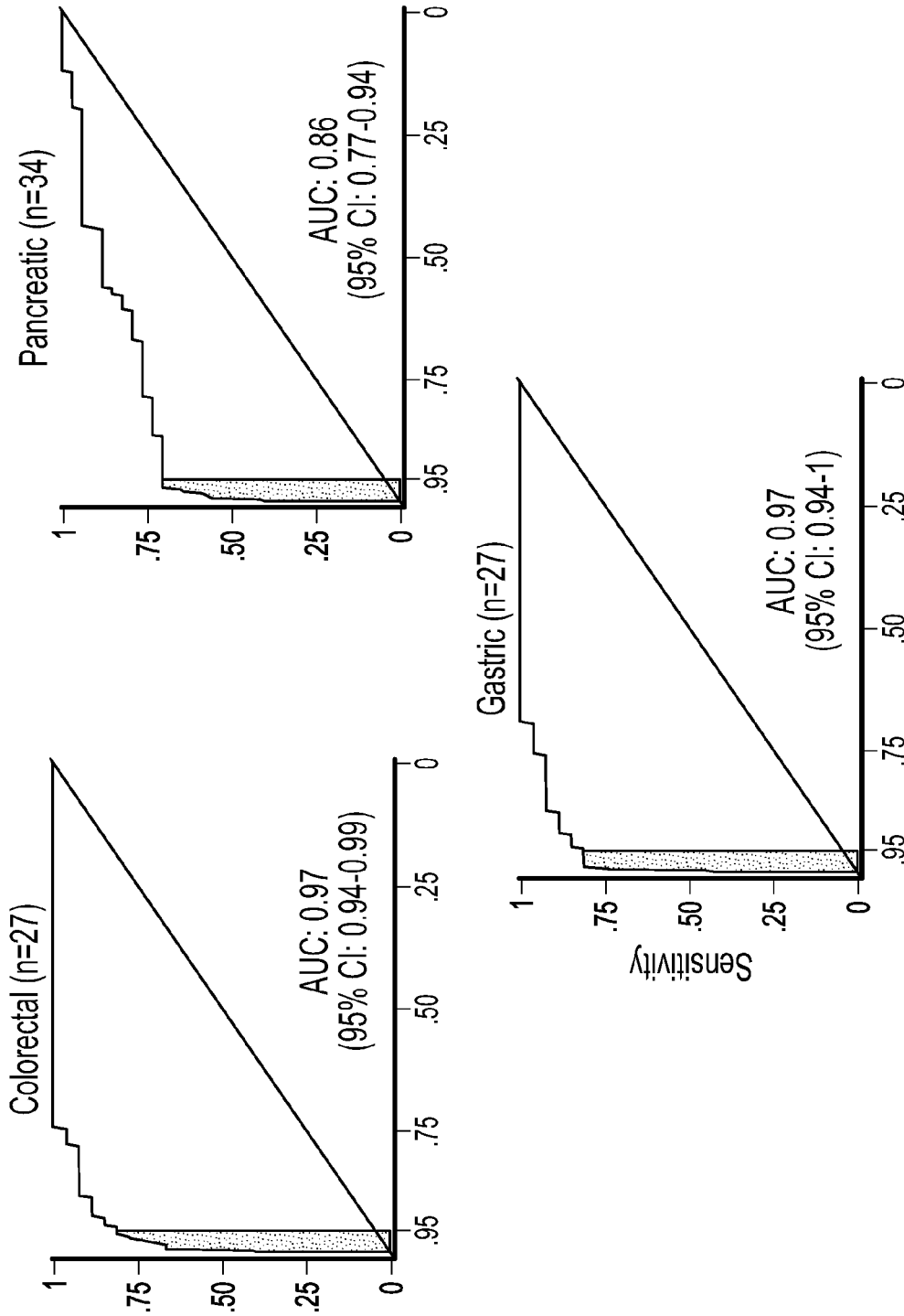


FIG. 17A



Specificity
FIG. 17B



Specificity
FIG. 17B (Cont.)

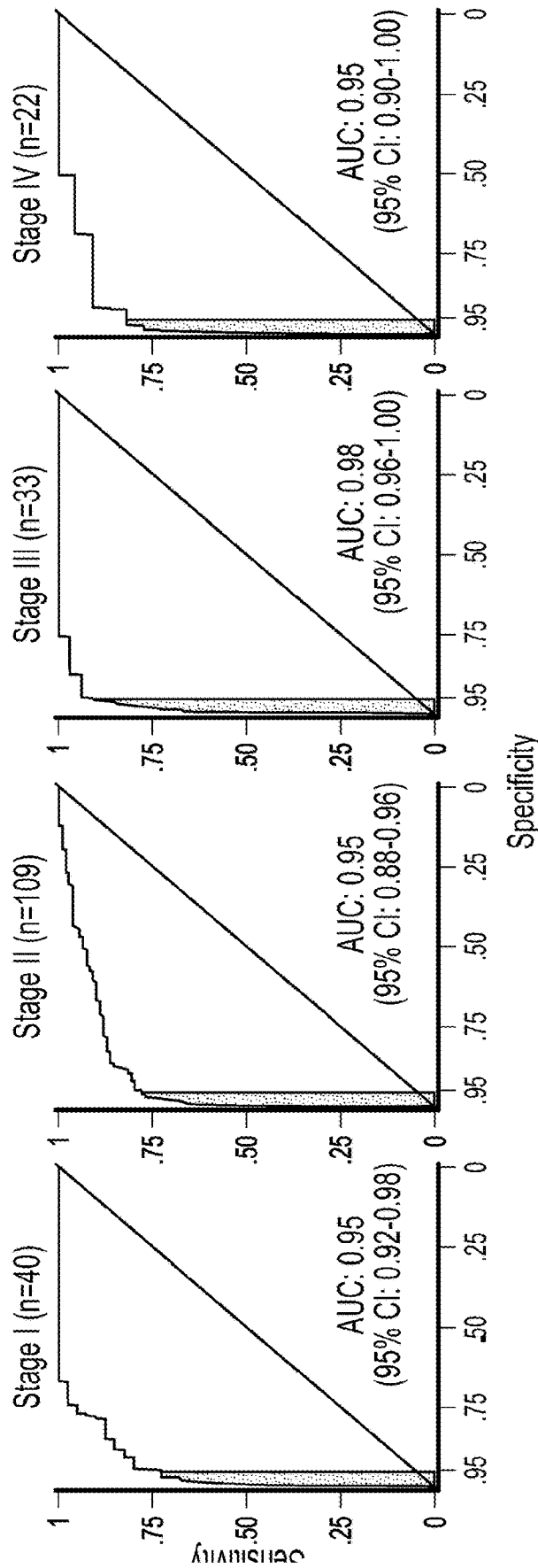


FIG. 18

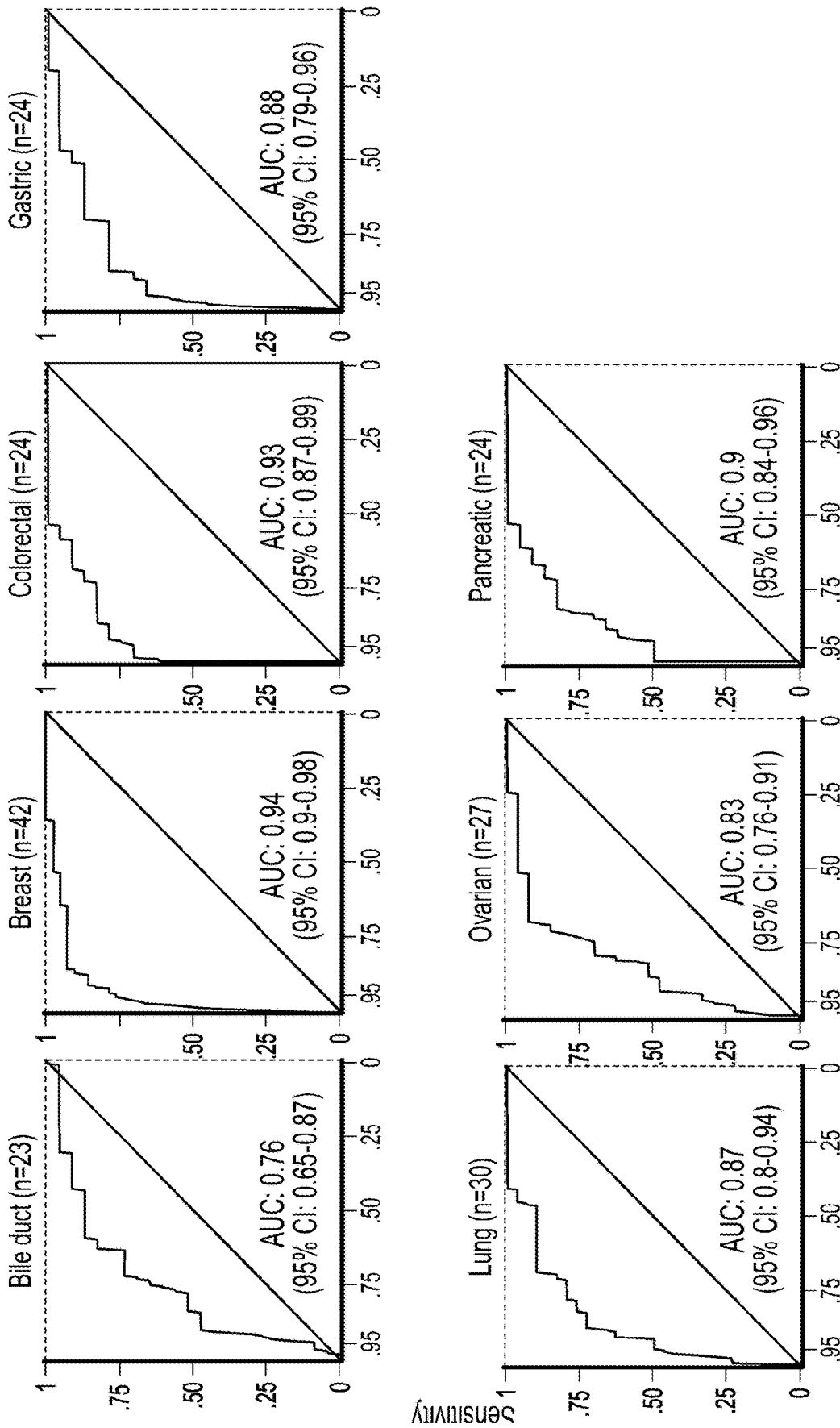
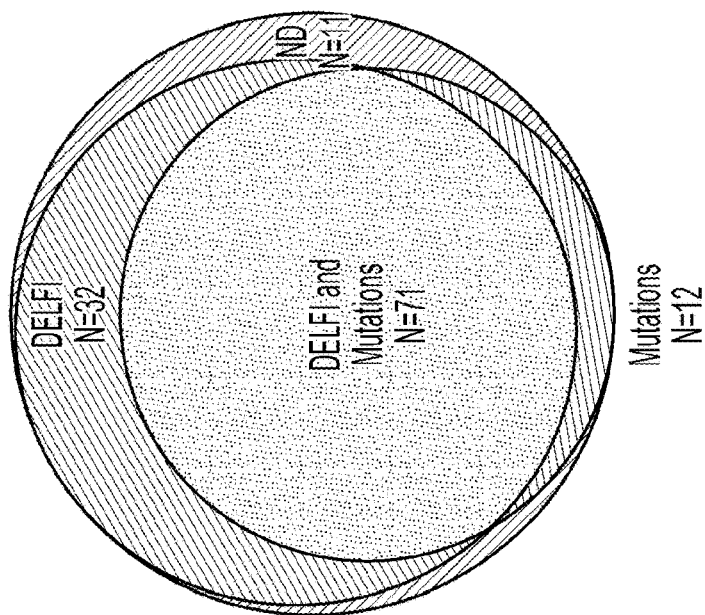


FIG. 19



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%
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 Detection 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

CELL-FREE DNA FOR ASSESSING AND/OR TREATING CANCER

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Patent Application Ser. No. 62/673,516, filed on May 18, 2018, and claims the benefit of U.S. Patent Application Ser. No. 62/795,900, filed on Jan. 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

[0002] 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

I. Technical Field

[0003] 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

[0004] 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 markers* 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

[0005] 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).

[0006] 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.

[0007] 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, DNA Evaluation of Fragments for early Interception (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.

[0008] 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).

[0009] 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.

[0010] 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.

[0011] 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, pat-

ents, 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.

[0012] 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

[0013] FIG. 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.

[0014] FIG. 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.

[0015] FIG. 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.

[0016] FIGS. 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.

[0017] FIG. 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).

[0018] FIG. 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).

[0019] FIGS. 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 $\sim 9\times$ 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 to median fragmentation profiles of lymphocytes (D), healthy cfDNA (E), and lymphocyte nucleosome (F) distances.

[0020] FIG. 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).

[0021] FIGS. 9A and 9B. Subsampling of whole genome sequence data for analysis of cfDNA fragmentation profiles. A, High coverage ($9\times$) whole-genome sequencing data were subsampled to $2\times$, $1\times$, $0.5\times$, $0.2\times$, and $0.1\times$ 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 $9\times$ coverage for healthy individuals and patients with lung cancer.

[0022] FIG. 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.

[0023] FIGS. 11A-11C. cfDNA fragmentation profiles in healthy individuals and patients with cancer. A, Fragmentation

tation 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.

[0024] FIGS. 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).

[0025] FIGS. 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 100 kb 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 resealed 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.

[0026] FIG. 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 num-

bers. 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.

[0027] FIG. 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.

[0028] FIGS. 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.

[0029] FIGS. 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.

[0030] FIG. 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 >95% specificity shaded in blue.

[0031] FIG. 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).

[0032] FIG. 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

[0033] 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.

[0034] 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.

[0035] 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).

[0036] 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.

[0037] 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).

[0038] 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).

[0039] 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 cases, 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, 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 cases, 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).

[0040] 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.

[0041] 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).

[0042] 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.

[0043] 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 FIG. 1.

[0044] 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).

[0045] 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.

[0046] 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.

[0047] 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).

[0048] 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 profile as described herein and, optionally, can be treated with one or more cancer treatments as described herein.

[0049] 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 profile as described herein.

[0050] 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).

[0051] 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).

[0052] 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.

[0053] 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.

[0054] 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.

[0055] 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; U.S. Pat. No. 9,233,125; incorporated by reference in their entirety herein.

[0056] 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, fludarabine, floxuridine, fludarabine, fluorouracil, gemcitabine, hydroxyurea, idarubicin, ifosfamide, irinotecan, lomustine, mechlorethamine, melphalan, mercaptopurine, methotrexate, 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).

[0057] 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 of 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).

[0058] 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 swallow), 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 esophagogastroduodenoscopy, 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).

[0059] 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

[0060] 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.

[0061] 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 (FIG. 2).

[0062] This study presents a novel method called DELFI for detection of cancer and further identification of tissue of origin using whole genome sequencing (FIG. 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

[0063] 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.

[0064] 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

[0065] Viably frozen lymphocytes were elutriated from leukocytes obtained from a healthy male (C0618) and female (D0808-L) (Advanced Biotechnologies Inc., Eldersburg, Md.). Aliquots of 1×10^6 cells were used for nucleosomal DNA purification using EZ Nucleosomal DNA Prep Kit (Zymo Research, Irvine, Calif.). Cells were initially treated with 100 μ l 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 1000 of Atlantis Digestion Buffer or with 100 μ l of micrococcal nuclease (MN) Digestion Buffer. Finally, cellular nucleic DNA was fragmented with 0.5 U of Atlantis dsDNase at 42° C. for 20 minutes or 1.5 U of MNase at 37° C. for 20 minutes. Reactions were stopped using 5xMN 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, Calif.).

Sample Preparation and Sequencing of cfDNA

[0066] 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 800 g for 10 min at 4° C. Plasma was centrifuged a second time at 18,000 g 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).

[0067] 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.

[0068] 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 the DNA1000 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

[0069] 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.

[0070] 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.

[0071] 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

[0072] 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.

[0073] 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/wgEn-

codeMappability/). 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 as having a length between 151 and 220 bp.

[0074] To account for biases in coverage attributable to GC content of the genome, the locally weighted smoother loess with span $\frac{3}{4}$ was applied to the scatterplot of average fragment GC versus coverage calculated for each 100 kb 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.

[0075] 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

[0076] 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 50 KB bins for which GC-corrected log₂ read depth was obtained after correction by loess with span $\frac{3}{4}$. 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

[0077] 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

[0078] 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.minobsinnode*=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

[0079] 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

[0080] 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 60 bp 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 nucleosomal 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, N Y, 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 individu-

als with sequence coverage of 9× 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

[0081] 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

[0082] 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

[0083] 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

[0084] 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 1-2× 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.

[0085] 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 manner could therefore serve as a unique biomarker for cancer detection.

[0086] 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.

[0087] 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 (FIGS. 7b and 7d) and nucleosome distances (FIGS. 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.

[0088] In contrast to healthy cfDNA, patients with cancer had multiple distinct genomic differences with increases and decreases in fragment sizes at different regions (FIGS. 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.

[0089] 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 (FIGS. 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 (FIGS. 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 patients to healthy=0.83) (Table 5; Appendix E).

[0090] 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.

[0091] 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).

[0092] 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).

[0093] 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.								
		95% specificity				98% specificity		
Type	Individuals analyzed	Individuals detected	Sensitivity	95% CI	Individuals detected	Sensitivity	95% CI	
Healthy	215	10	—	—	4	—	—	
Cancer	208	166	80%	74%-85%	152	73%	67%-79%	
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%	

TABLE 9-continued

DELFI performance for cancer detection.							
	Individuals analyzed	95% specificity		98% specificity		Individuals detected	95% CI
		Individuals detected	Sensitivity	Sensitivity	95% CI		
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%

[0094] 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.

[0095] 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).

[0096] 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).

[0097] 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

TABLE 10

DELFI tissue of origin prediction									
Cancer Type	Patients	Top Prediction			Top Two Predictions			Random Assignment	
		Detected*	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.

(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.

[0098] 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

[0099] 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 Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGCRC291	Colorectal Cancer	cfDNA	Preoperative treatment naïve	69	F	IV	T3N2M1	Cecum	Adenocarcinoma	Moderate	Synchronous Liver	7.9	7.80	7.80	Y	Y	Y
CGCRC292	Colorectal Cancer	cfDNA	Preoperative treatment naïve	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 naïve	55	M	IV	T3N2M1	Rectum	Adenocarcinoma	Moderate	Synchronous Liver	7.2	3.83	3.83	Y	Y	Y
CGCRC294	Colorectal Cancer	cfDNA	Preoperative treatment naïve	67	F	II	T3N0M0	Sigmoid Colon	Adenocarcinoma	Moderate	None	8.4	18.87	18.87	Y	Y	Y
CGCRC296	Colorectal Cancer	cfDNA	Preoperative treatment naïve	76	F	II	T4N0M0	Cecum	Adenocarcinoma	Poor	None	4.3	31.24	31.24	Y	Y	Y
CGCRC299	Colorectal Cancer	cfDNA	Preoperative treatment naïve	71	M	I	T1N0M0	Rectum	Adenocarcinoma	Moderate	None	8.8	10.18	10.18	Y	Y	Y
CGCRC300	Colorectal Cancer	cfDNA	Preoperative treatment naïve	65	M	I	T2N0M0	Rectum	Adenocarcinoma	Moderate	None	4.3	10.48	10.48	Y	Y	Y
CGCRC301	Colorectal Cancer	cfDNA	Preoperative treatment naïve	76	F	I	T2N0M0	Rectum	Adenocarcinoma	Moderate	None	4.1	6.51	6.51	Y	Y	Y
CGCRC302	Colorectal Cancer	cfDNA	Preoperative treatment naïve	73	M	II	T3N0M0	Transverse Colon	Adenocarcinoma	Moderate	None	4.3	52.13	52.13	Y	Y	Y
CGCRC304	Colorectal Cancer	cfDNA	Preoperative treatment naïve	86	F	II	T3N0M0	Rectum	Adenocarcinoma	Moderate	None	4.1	30.19	30.19	Y	Y	Y
CGCRC305	Colorectal Cancer	cfDNA	Preoperative treatment naïve	83	F	II	T3N0M0	Transverse Colon	Adenocarcinoma	Moderate	None	8.6	9.10	9.10	Y	Y	Y
CGCRC306	Colorectal Cancer	cfDNA	Preoperative treatment naïve	80	F	II	T4N0M0	Ascending Colon	Adenocarcinoma	Moderate	None	4.5	24.31	24.31	Y	Y	Y
CGCRC307	Colorectal Cancer	cfDNA	Preoperative treatment naïve	78	F	II	T3N0M0	Ascending Colon	Adenocarcinoma	Moderate	None	8.5	14.26	14.26	Y	Y	Y
CGCRC308	Colorectal Cancer	cfDNA	Preoperative treatment naïve	72	F	III	T4N2M0	Ascending Colon	Adenocarcinoma	Moderate	None	4.3	46.37	46.37	Y	Y	Y
CGCRC311	Colorectal Cancer	cfDNA	Preoperative treatment naïve	59	M	I	T2N0M0	Sigmoid Colon	Adenocarcinoma	Moderate	None	8.5	3.91	3.91	Y	Y	Y
CGCRC315	Colorectal Cancer	cfDNA	Preoperative treatment naïve	74	M	III	T3N1M0	Sigmoid Colon	Adenocarcinoma	Moderate	None	8.6	9.67	9.67	Y	Y	Y
CGCRC316	Colorectal Cancer	cfDNA	Preoperative treatment naïve	80	M	III	T3N2M0	Transverse Colon	Adenocarcinoma	Moderate	None	4.9	52.16	52.16	Y	Y	Y
CGCRC317	Colorectal Cancer	cfDNA	Preoperative treatment naïve	74	M	III	T3N2M0	Descending Colon	Adenocarcinoma	Moderate	None	8.8	16.08	16.08	Y	Y	Y
CGCRC318	Colorectal Cancer	cfDNA	Preoperative treatment naïve	81	M	I	T2N0M0	Cecum	Adenocarcinoma	Moderate	None	9.8	18.24	18.24	Y	Y	Y
CGCRC319	Colorectal Cancer	cfDNA	Preoperative treatment naïve	80	F	III	T2N1M0	Descending Colon	Adenocarcinoma	Moderate	None	4.2	53.84	53.84	Y	N	Y
CGCRC320	Colorectal Cancer	cfDNA	Preoperative treatment naïve	73	F	I	T2N0M0	Ascending Colon	Adenocarcinoma	Moderate	None	4.5	30.37	30.37	Y	Y	Y

APPENDIX A-continued

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
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, Pentoneum	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, Pentoneum	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, Pentoneum	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, Pentoneum	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

APPENDIX A-continued

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
CGLU369	Lung Cancer	cfDNA	Post-treatment, Day 88	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	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

APPENDIX A-continued

Table 1. Summary of patients and samples analyzed

Patient	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
CGPLBR30	Breast Cancer	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	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	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	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	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	Preoperative treatment naive	43	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	22.58	22.58	Y	N	N
CGPLBR36	Breast Cancer	Preoperative treatment naive	36	F	II	NA	Breast	Infiltrating Ductal Carcinoma with Microinvasion	NA	None	4.4	17.73	17.73	Y	N	N
CGPLBR37	Breast Cancer	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	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	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	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	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	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	Preoperative treatment naive	54	F	I	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	13.89	13.89	Y	N	N

APPENDIX A-continued

Table 1. Summary of patients and samples analyzed

Patient	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 Ex-tracted (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLBR48	Breast Cancer	Preoperative treatment naïve	47	F	II	T2N1M0	Left Breast	Infiltrating Ductal Carcinoma	Poor	None	3.9	7.07	7.07	Y	Y	Y
CGPLBR49	Breast Cancer	Preoperative treatment naïve	37	F	II	T2N1M0	Left Breast	Infiltrating Ductal Carcinoma	Poor	None	4.0	5.74	5.74	Y	N	Y
CGPLBR50	Breast Cancer	Preoperative treatment naïve	51	F	I	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	45.58	27.78	Y	N	N
CGPLBR51	Breast Cancer	Preoperative treatment naïve	53	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.0	8.83	8.83	Y	N	N
CGPLBR52	Breast Cancer	Preoperative treatment naïve	68	F	III	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	80.71	27.78	Y	N	N
CGPLBR55	Breast Cancer	Preoperative treatment naïve	53	F	III	T3N1M0	Right Breast	Infiltrating Ductal Carcinoma	Poor	None	4.3	4.57	4.57	Y	Y	Y
CGPLBR56	Breast Cancer	Preoperative treatment naïve	56	F	II	NA	Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	22.16	22.16	Y	N	N
CGPLBR57	Breast Cancer	Preoperative treatment naïve	54	F	III	T2N2M0	Left Breast	Infiltrating Ductal Carcinoma	NA	None	4.3	4.02	4.02	Y	N	Y
CGPLBR59	Breast Cancer	Preoperative treatment naïve	42	F	I	T1N0M0	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.1	8.24	8.24	Y	N	Y
CGPLBR60	Breast Cancer	Preoperative treatment naïve	61	F	II	NA	Left Breast	Infiltrating Ductal Carcinoma	NA	None	4.5	11.09	11.09	Y	N	N
CGPLBR61	Breast Cancer	Preoperative treatment naïve	67	F	II	T2N1M0	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.1	13.25	13.25	Y	N	Y
CGPLBR63	Breast Cancer	Preoperative treatment naïve	48	F	II	T2N1M0	Left Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.0	6.19	6.19	Y	Y	Y
CGPLBR65	Breast Cancer	Preoperative treatment naïve	50	F	II	NA	Left Breast	Infiltrating Ductal Carcinoma	NA	None	3.5	41.75	35.71	Y	N	N
CGPLBR68	Breast Cancer	Preoperative treatment naïve	64	F	III	T4N1M0	Breast	Infiltrating Ductal Carcinoma	Poor	None	3.4	10.41	10.41	Y	N	Y
CGPLBR69	Breast Cancer	Preoperative treatment naïve	43	F	II	T2N0M0	Breast	Infiltrating Ductal Carcinoma	Moderate	None	4.4	4.07	4.07	Y	Y	Y

APPENDIX A-continued

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
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
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

APPENDIX A-continued

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
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

APPENDIX A-continued

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
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	27.79	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, technical replicate	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.4	3.42	3.42	Y	N	N
CGPLH328	Healthy	cfDNA	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

APPENDIX A-continued

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
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	59.44	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	3.84	3.84	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	21.08	21.08	Y	N	N

APPENDIX A-continued

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
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	2.53	2.53	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

APPENDIX A-continued

Table 1. Summary of patients and samples analyzed

Patient	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
CGPLH386	Healthy	Preoperative treatment naive	62	M	NA	NA	NA	NA	NA	NA	4.6	6.54	6.54	Y	N	N
CGPLH387	Healthy	Preoperative treatment naive	71	F	NA	NA	NA	NA	NA	NA	4.5	6.19	6.19	Y	N	N
CGPLH388	Healthy	Preoperative treatment naive	57	F	NA	NA	NA	NA	NA	NA	4.5	6.62	6.62	Y	N	N
CGPLH389	Healthy	Preoperative treatment naive	73	F	NA	NA	NA	NA	NA	NA	4.6	14.78	14.78	Y	N	N
CGPLH390	Healthy	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	12.14	12.14	Y	N	N
CGPLH391	Healthy	Preoperative treatment naive	58	M	NA	NA	NA	NA	NA	NA	4.5	8.88	8.88	Y	N	N
CGPLH391	Healthy	Preoperative treatment naive	58	M	NA	NA	NA	NA	NA	NA	4.5	8.37	8.37	Y	N	N
CGPLH392	Healthy	Preoperative treatment naive	57	F	NA	NA	NA	NA	NA	NA	4.5	8.39	8.39	Y	N	N
CGPLH393	Healthy	Preoperative treatment naive	54	M	NA	NA	NA	NA	NA	NA	4.5	5.27	5.27	Y	N	N
CGPLH394	Healthy	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.4	3.79	3.79	Y	N	N
CGPLH395	Healthy	Preoperative treatment naive	56	F	NA	NA	NA	NA	NA	NA	4.4	9.56	9.56	Y	N	N
CGPLH395	Healthy	Preoperative treatment naive	56	F	NA	NA	NA	NA	NA	NA	4.4	5.40	5.40	Y	N	N
CGPLH396	Healthy	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.4	20.31	20.31	Y	N	N
CGPLH398	Healthy	Preoperative treatment naive	68	M	NA	NA	NA	NA	NA	NA	4.3	13.01	13.01	Y	N	N
CGPLH399	Healthy	Preoperative treatment naive	62	F	NA	NA	NA	NA	NA	NA	4.4	4.79	4.79	Y	N	N
CGPLH400	Healthy	Preoperative treatment naive	64	M	NA	NA	NA	NA	NA	NA	4.4	7.70	7.70	Y	N	N
CGPLH400	Healthy	Preoperative treatment naive	64	M	NA	NA	NA	NA	NA	NA	4.4	6.26	6.26	Y	N	N
CGPLH401	Healthy	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.3	13.01	13.01	Y	N	N
CGPLH401	Healthy	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.4	11.13	11.13	Y	N	N
CGPLH402	Healthy	Preoperative treatment naive	57	F	NA	NA	NA	NA	NA	NA	4.5	2.89	2.89	Y	N	N

APPENDIX A-continued

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
CGPLH403	Healthy	cfDNA	Preoperative treatment naive	64	M	NA	NA	NA	NA	NA	NA	4.3	4.41	4.41	Y	N	N
CGPLH404	Healthy	cfDNA	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.2	6.38	6.38	Y	N	N
CGPLH405	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.4	7.28	7.28	Y	N	N
CGPLH406	Healthy	cfDNA	Preoperative treatment naive	57	M	NA	NA	NA	NA	NA	NA	4.2	5.40	5.40	Y	N	N
CGPLH407	Healthy	cfDNA	Preoperative treatment naive	75	F	NA	NA	NA	NA	NA	NA	4.0	13.30	13.30	Y	N	N
CGPLH408	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.2	5.18	5.18	Y	N	N
CGPLH409	Healthy	cfDNA	Preoperative treatment naive	53	M	NA	NA	NA	NA	NA	NA	3.7	3.98	3.98	Y	N	N
CGPLH410	Healthy	cfDNA	Preoperative treatment naive	52	M	NA	NA	NA	NA	NA	NA	4.1	6.91	6.91	Y	N	N
CGPLH411	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.1	3.30	3.30	Y	N	N
CGPLH412	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.1	5.55	5.55	Y	N	N
CGPLH413	Healthy	cfDNA	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.5	8.18	8.18	Y	N	N
CGPLH414	Healthy	cfDNA	Preoperative treatment naive	56	M	NA	NA	NA	NA	NA	NA	3.8	5.85	5.85	Y	N	N
CGPLH415	Healthy	cfDNA	Preoperative treatment naive	59	M	NA	NA	NA	NA	NA	NA	4.7	10.20	10.20	Y	N	N
CGPLH416	Healthy	cfDNA	Preoperative treatment naive	58	F	NA	NA	NA	NA	NA	NA	4.5	11.73	11.73	Y	N	N
CGPLH417	Healthy	cfDNA	Preoperative treatment naive	70	M	NA	NA	NA	NA	NA	NA	4.2	10.98	10.98	Y	N	N
CGPLH418	Healthy	cfDNA	Preoperative treatment naive	70	F	NA	NA	NA	NA	NA	NA	4.5	10.96	10.96	Y	N	N
CGPLH419	Healthy	cfDNA	Preoperative treatment naive	65	F	NA	NA	NA	NA	NA	NA	4.5	10.17	10.17	Y	N	N
CGPLH42	Healthy	cfDNA	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.0	14.30	14.30	Y	N	Y
CGPLH420	Healthy	cfDNA	Preoperative treatment naive	51	M	NA	NA	NA	NA	NA	NA	4.2	12.32	12.32	Y	N	N
CGPLH422	Healthy	cfDNA	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.6	5.42	5.42	Y	N	N
CGPLH423	Healthy	cfDNA	Preoperative treatment naive	54	M	NA	NA	NA	NA	NA	NA	4.2	2.85	2.85	Y	N	N
CGPLH424	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.7	1.66	1.66	Y	N	N

APPENDIX A-continued

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
CGPLH425	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.4	5.98	5.98	Y	N	N
CGPLH426	Healthy	cfDNA	Preoperative treatment naive	68	M	NA	NA	NA	NA	NA	NA	4.4	2.84	2.84	Y	N	N
CGPLH427	Healthy	cfDNA	Preoperative treatment naive	68	M	NA	NA	NA	NA	NA	NA	4.4	10.86	10.86	Y	N	N
CGPLH428	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	6.27	6.27	Y	N	N
CGPLH429	Healthy	cfDNA	Preoperative treatment naive	63	F	NA	NA	NA	NA	NA	NA	4.5	3.89	3.89	Y	N	N
CGPLH43	Healthy	cfDNA	Preoperative treatment naive	49	F	NA	NA	NA	NA	NA	NA	4.0	8.50	8.50	Y	N	Y
CGPLH430	Healthy	cfDNA	Preoperative treatment naive	69	F	NA	NA	NA	NA	NA	NA	4.2	10.33	10.33	Y	N	N
CGPLH431	Healthy	cfDNA	Preoperative treatment naive	59	F	NA	NA	NA	NA	NA	NA	4.8	12.81	12.81	Y	N	N
CGPLH432	Healthy	cfDNA	Preoperative treatment naive	59	F	NA	NA	NA	NA	NA	NA	4.8	2.42	2.42	Y	N	N
CGPLH434	Healthy	cfDNA	Preoperative treatment naive	59	M	NA	NA	NA	NA	NA	NA	4.6	8.83	8.83	Y	N	N
CGPLH435	Healthy	cfDNA	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.5	8.95	8.95	Y	N	N
CGPLH436	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	4.29	4.29	Y	N	N
CGPLH437	Healthy	cfDNA	Preoperative treatment naive	56	M	NA	NA	NA	NA	NA	NA	4.6	18.07	18.07	Y	N	N
CGPLH438	Healthy	cfDNA	Preoperative treatment naive	69	M	NA	NA	NA	NA	NA	NA	4.8	16.62	16.62	Y	N	N
CGPLH439	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.7	4.38	4.38	Y	N	N
CGPLH440	Healthy	cfDNA	Preoperative treatment naive	72	M	NA	NA	NA	NA	NA	NA	4.7	4.32	4.32	Y	N	N
CGPLH441	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.7	7.80	7.80	Y	N	N
CGPLH442	Healthy	cfDNA	Preoperative treatment naive	59	F	NA	NA	NA	NA	NA	NA	4.5	6.15	6.15	Y	N	N
CGPLH443	Healthy	cfDNA	Preoperative treatment naive	52	F	NA	NA	NA	NA	NA	NA	4.4	3.44	3.44	Y	N	N
CGPLH444	Healthy	cfDNA	Preoperative treatment naive	60	F	NA	NA	NA	NA	NA	NA	4.4	4.12	4.12	Y	N	N
CGPLH445	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.4	4.36	4.36	Y	N	N
CGPLH446	Healthy	cfDNA	Preoperative treatment naive	51	F	NA	NA	NA	NA	NA	NA	4.4	2.92	2.92	Y	N	N

APPENDIX A-continued

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
CGPLH447	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.6	3.87	3.87	Y	N	N
CGPLH448	Healthy	cfDNA	Preoperative treatment naive	51	F	NA	NA	NA	NA	NA	NA	4.4	5.29	5.29	Y	N	N
CGPLH449	Healthy	cfDNA	Preoperative treatment naive	51	F	NA	NA	NA	NA	NA	NA	4.5	3.77	3.77	Y	N	N
CGPLH45	Healthy	cfDNA	Preoperative treatment naive	58	F	NA	NA	NA	NA	NA	NA	4.0	10.85	10.85	Y	N	Y
CGPLH450	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	5.62	5.62	Y	N	N
CGPLH451	Healthy	cfDNA	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.6	7.24	7.24	Y	N	N
CGPLH452	Healthy	cfDNA	Preoperative treatment naive	69	M	NA	NA	NA	NA	NA	NA	4.4	2.54	2.54	Y	N	N
CGPLH453	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.6	9.11	9.11	Y	N	N
CGPLH455	Healthy	cfDNA	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.4	2.64	2.64	Y	N	N
CGPLH455	Healthy	cfDNA, technical replicate	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.5	2.42	2.42	Y	N	N
CGPLH456	Healthy	cfDNA	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.5	3.11	3.11	Y	N	N
CGPLH457	Healthy	cfDNA	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.4	5.92	5.92	Y	N	N
CGPLH458	Healthy	cfDNA	Preoperative treatment naive	52	F	NA	NA	NA	NA	NA	NA	4.5	16.04	16.04	Y	N	N
CGPLH459	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.4	6.52	6.52	Y	N	N
CGPLH46	Healthy	cfDNA	Preoperative treatment naive	35	F	NA	NA	NA	NA	NA	NA	4.0	8.25	8.25	Y	N	Y
CGPLH460	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.6	5.24	5.24	Y	N	N
CGPLH463	Healthy	cfDNA	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.5	22.77	22.77	Y	N	N
CGPLH464	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.4	2.90	2.90	Y	N	N
CGPLH465	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	4.76	4.76	Y	N	N
CGPLH466	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.6	5.68	5.68	Y	N	N
CGPLH466	Healthy	cfDNA, technical replicate	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	6.75	6.75	Y	N	N

APPENDIX A-continued

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 Ex-traced (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLH467	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	4.59	4.59	Y	N	N
CGPLH468	Healthy	cfDNA	Preoperative treatment naive	53	M	NA	NA	NA	NA	NA	NA	4.5	11.19	11.19	Y	N	N
CGPLH469	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	3.25	3.25	Y	N	N
CGPLH47	Healthy	cfDNA	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.0	7.43	7.43	Y	N	Y
CGPLH470	Healthy	cfDNA	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.5	13.64	13.64	Y	N	N
CGPLH471	Healthy	cfDNA	Preoperative treatment naive	70	F	NA	NA	NA	NA	NA	NA	4.3	13.00	13.00	Y	N	N
CGPLH472	Healthy	cfDNA	Preoperative treatment naive	69	F	NA	NA	NA	NA	NA	NA	4.2	10.17	10.17	Y	N	N
CGPLH473	Healthy	cfDNA	Preoperative treatment naive	62	M	NA	NA	NA	NA	NA	NA	4.3	2.98	2.98	Y	N	N
CGPLH474	Healthy	cfDNA	Preoperative treatment naive	63	M	NA	NA	NA	NA	NA	NA	4.3	29.15	29.15	Y	N	N
CGPLH475	Healthy	cfDNA	Preoperative treatment naive	67	F	NA	NA	NA	NA	NA	NA	4.0	7.26	7.26	Y	N	N
CGPLH476	Healthy	cfDNA	Preoperative treatment naive	65	F	NA	NA	NA	NA	NA	NA	4.3	6.16	6.16	Y	N	N
CGPLH477	Healthy	cfDNA	Preoperative treatment naive	61	F	NA	NA	NA	NA	NA	NA	4.3	15.21	15.21	Y	N	N
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

APPENDIX A-continued

Table 1. Summary of patients and samples analyzed

Patient	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 Ex-traced (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLH487	Healthy	Preoperative treatment naive	50	M	NA	NA	NA	NA	NA	NA	4.4	6.11	6.11	Y	N	N
CGPLH488	Healthy	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	7.88	7.88	Y	N	N
CGPLH49	Healthy	Preoperative treatment naive	39	F	NA	NA	NA	NA	NA	NA	4.0	6.60	6.60	Y	N	Y
CGPLH490	Healthy	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	4.18	4.18	Y	N	N
CGPLH491	Healthy	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.5	13.16	13.16	Y	N	N
CGPLH492	Healthy	Preoperative treatment naive	51	F	NA	NA	NA	NA	NA	NA	4.5	3.83	3.83	Y	N	N
CGPLH493	Healthy	Preoperative treatment naive	64	M	NA	NA	NA	NA	NA	NA	4.5	25.06	25.06	Y	N	N
CGPLH494	Healthy	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.4	5.24	5.24	Y	N	N
CGPLH495	Healthy	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.4	5.03	5.03	Y	N	N
CGPLH496	Healthy	Preoperative treatment naive	74	M	NA	NA	NA	NA	NA	NA	4.5	34.01	27.78	Y	N	N
CGPLH497	Healthy	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.5	8.24	8.24	Y	N	N
CGPLH497	Healthy	Preoperative treatment naive	68	F	NA	NA	NA	NA	NA	NA	4.4	5.88	5.88	Y	N	N
CGPLH498	Healthy	Preoperative treatment naive	54	F	NA	NA	NA	NA	NA	NA	4.4	5.33	5.33	Y	N	N
CGPLH499	Healthy	Preoperative treatment naive	52	F	NA	NA	NA	NA	NA	NA	4.5	7.85	7.85	Y	N	N
CGPLH50	Healthy	Preoperative treatment naive	55	F	NA	NA	NA	NA	NA	NA	4.0	7.05	7.05	Y	N	Y
CGPLH500	Healthy	Preoperative treatment naive	51	F	NA	NA	NA	NA	NA	NA	4.5	3.49	3.49	Y	N	N
CGPLH501	Healthy	Preoperative treatment naive	50	F	NA	NA	NA	NA	NA	NA	4.3	6.29	6.29	Y	N	N
CGPLH502	Healthy	Preoperative treatment naive	53	F	NA	NA	NA	NA	NA	NA	4.5	2.24	2.24	Y	N	N
CGPLH503	Healthy	Preoperative treatment naive	67	M	NA	NA	NA	NA	NA	NA	4.5	11.01	11.01	Y	N	N
CGPLH504	Healthy	Preoperative treatment naive	57	F	NA	NA	NA	NA	NA	NA	4.3	6.60	6.60	Y	N	N
CGPLH504	Healthy	Preoperative treatment naive	57	F	NA	NA	NA	NA	NA	NA	4.2	10.02	10.02	Y	N	N

APPENDIX A-continued

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
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	F	NA	NA	NA	NA	NA	NA	4.1	9.89	9.89	Y	N	N
CGPLH508	Healthy	cfDNA	Preoperative treatment naive	54	M	NA	NA	NA	NA	NA	NA	4.5	8.66	8.66	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

APPENDIX A-continued

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
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	1.69	1.69	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

APPENDIX A-continued

Table 1. Summary of patients and samples analyzed

Patient	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
CGPLH82	cfDNA	Preoperative treatment naive	38	F	NA	NA	NA	NA	NA	NA	4.0	3.30	3.30	Y	N	Y
CGPLH83	cfDNA	Preoperative treatment naive	60	F	NA	NA	NA	NA	NA	NA	4.0	5.04	5.04	Y	N	Y
CGPLH84	cfDNA	Preoperative treatment naive	45	F	NA	NA	NA	NA	NA	NA	4.0	3.33	3.33	Y	N	Y
CGPLLU13	cfDNA	Preoperative treatment naive	72	F	IV	T1BN2bM1a	Right Lung	Adenocarcinoma	NA	Bone	5.0	7.67	7.67	Y	N	Y
CGPLLU13	cfDNA	Post-treatment, Day 2	72	F	IV	T1BN2bM1a	Right Lung	Adenocarcinoma	NA	Bone	4.5	8.39	8.39	Y	N	Y
CGPLLU13	cfDNA	Post-treatment, Day 5	72	F	IV	T1BN2bM1a	Right Lung	Adenocarcinoma	NA	Bone	3.2	8.66	8.66	Y	N	Y
CGPLLU13	cfDNA	Post-treatment, Day 28	72	F	IV	T1BN2bM1a	Right Lung	Adenocarcinoma	NA	Bone	5.0	5.97	5.97	Y	N	Y
CGPLLU13	cfDNA	Post-treatment, Day 91	72	F	IV	T1BN2bM1a	Right Lung	Adenocarcinoma	NA	Bone	5.0	5.97	5.97	Y	N	Y
CGPLLU14	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	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	cfDNA	Pre-treatment, Day -8	55	F	IV	T1N1M0	Right Lower Lobe of Lung	Adenocarcinoma	Moderate	NA	2.0	2.55	2.55	Y	N	Y
CGPLLU14	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	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	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	cfDNA	Preoperative treatment naive	52	M	II	T2aN1M0	Lung	Adenocarcinoma	Poor	None	3.5	31.51	31.51	Y	Y	Y
CGPLLU147	cfDNA	Preoperative treatment naive	60	M	III	T3N2M0	Lung	Adenosquamous Carcinoma	Poor	None	3.8	6.72	6.72	Y	Y	Y
CGPLLU151	cfDNA	Preoperative treatment naive	41	F	II	T3N2M0	Lung	Adenocarcinoma	Well	None	4.0	83.04	83.04	Y	N	Y
CGPLLU162	cfDNA	Preoperative treatment naive	38	M	II	T1N1M0	Right Lung	Adenocarcinoma	Moderate	None	3.1	40.32	40.32	Y	Y	Y
CGPLLU163	cfDNA	Preoperative treatment naive	66	M	II	T1N1M0	Left Lung	Adenocarcinoma	Poor	None	5.0	54.03	54.03	Y	Y	Y
CGPLLU165	cfDNA	Preoperative treatment naive	68	F	II	T1N1M0	Right Lung	Adenocarcinoma	Well	None	4.5	20.13	20.13	Y	Y	Y
CGPLLU168	cfDNA	Preoperative treatment naive	70	F	I	T2aN0M0	Lung	Adenocarcinoma	Poor	None	4.3	19.38	19.38	Y	Y	Y
CGPLLU169	cfDNA	Preoperative treatment naive	64	M	I	T1bN0M0	Lung	Squamous Cell Carcinoma	Moderate	None	4.2	13.70	13.70	Y	N	Y
CGPLLU175	cfDNA	Preoperative treatment naive	47	M	I	T2N0M0	Lung	Squamous Cell Carcinoma	Moderate	None	4.4	16.84	16.84	Y	Y	Y

APPENDIX A-continued

Table 1. Summary of patients and samples analyzed

Patient	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 Ex-tracted (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLLU176	cfDNA	Preoperative treatment naive	58	M	I	T2N0M0	Lung	Adenosquamous Carcinoma	Moderate	None	3.2	7.86	7.86	Y	Y	Y
CGPLLU177	cfDNA	Preoperative treatment naive	45	M	II	T3N0M0	Right Lung	Adenocarcinoma	NA	None	3.9	19.07	19.07	Y	Y	Y
CGPLLU180	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	cfDNA	Preoperative treatment naive	49	F	I	T2N0M0	Left Lung	Adenocarcinoma	Moderate	None	4.2	14.09	14.09	Y	Y	Y
CGPLLU202	cfDNA	Preoperative treatment naive	68	M	I	T2aN0M0	Right Lung	Adenocarcinoma	NA	None	4.4	24.72	24.72	Y	Y	Y
CGPLLU203	cfDNA	Preoperative treatment naive	68	M	II	T3N0M0	Right Lung	Squamous Cell Carcinoma	Well	None	4.2	26.24	26.24	Y	N	Y
CGPLLU205	cfDNA	Preoperative treatment naive	65	M	II	T3N0M0	Left Lung	Adenocarcinoma	Poor	None	4.0	18.56	18.56	Y	Y	Y
CGPLLU206	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	cfDNA	Preoperative treatment naive	60	F	II	T2N1M0	Lung	Adenocarcinoma	Well	None	4.0	17.29	17.29	Y	Y	Y
CGPLLU208	cfDNA	Preoperative treatment naive	56	F	II	T2N1M0	Lung	Adenocarcinoma	Moderate	None	3.0	24.34	24.34	Y	Y	Y
CGPLLU209	cfDNA	Preoperative treatment naive	65	M	II	T2aN0M0	Lung	Large Cell Carcinoma	Poor	None	5.5	53.95	53.95	Y	Y	Y
CGPLLU244	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	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	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	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	cfDNA	Pre-treatment, Day 32	49	M	IV	T2a2M1B	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42	Y	N	Y
CGPLLU245	cfDNA	Pre-treatment, Day 0	49	M	IV	T2a2M1B	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42	Y	N	Y
CGPLLU245	cfDNA	Post-treatment, Day 7	49	M	IV	T2a2M1B	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42	Y	N	Y
CGPLLU245	cfDNA	Post-treatment, Day 21	49	M	IV	T2a2M1B	Left Upper Lobe of Lung	Adenocarcinoma	NA	Brain	4.7	19.42	19.42	Y	N	Y
CGPLLU246	cfDNA	Pre-treatment, Day -21	65	F	IV	NA	Right Lower Lobe of Lung	Adenocarcinoma	Poor	Petra	5.5	18.51	18.51	Y	N	Y

APPENDIX A-continued

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 Ex-tracted (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLLU246	Lung Cancer	cfDNA	Pre-treatment, Day 0	65	F	IV	NA	Right Lower Lobe of Lung	Adenocarcinoma	Poor	Petra	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	Petra	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	Petra	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 8	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, Petra	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, Petra	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, Petra	3.5	17.79	17.79	Y	N	Y

APPENDIX A-continued

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
CGPLLU271	Lung Cancer	cfDNA	Post-treatment, Day 259	73	M	IV	T1aNxM1	Left Upper Lobe of Lung	Adenocarcinoma	Moderate	Petua	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	Moderate	Petua	5.0	18.86	18.86	Y	N	Y
CGPLLU271	Lung Cancer	cfDNA	Post-treatment, Day 8	73	M	IV	T1aNxM1	Left Upper Lobe of Lung	Adenocarcinoma	Moderate	Petua	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	Moderate	Petua	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	Moderate	Petua	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
CGPFOV11	Ovarian Cancer	cfDNA	Preoperative treatment naive	51	F	IV	T3cN0M1	Right Ovary	Endometrioid Adenocarcinoma	Moderate	Omentum	3.4	17.35	17.35	Y	Y	Y
CGPFOV12	Ovarian Cancer	cfDNA	Preoperative treatment naive	45	F	I	T1aN0MX	Ovary	Endometrioid Adenocarcinoma	NA	None	3.2	12.44	12.44	Y	N	Y

APPENDIX A-continued

Table 1. Summary of patients and samples analyzed

Patient	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 Ex-traced (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLOV13	Ovarian Cancer	Preoperative treatment naive	62	F	IV	T1bN0M1	Right Ovary	Endometrioid Adenocarcinoma	Poor	Omentum	3.8	27.00	27.00	Y	Y	Y
CGPLOV15	Ovarian Cancer	Preoperative treatment naive	54	F	III	T3N1M0	Ovary	Adenocarcinoma	Poor	None	5.0	4.77	4.77	Y	Y	Y
CGPLOV16	Ovarian Cancer	Preoperative treatment naive	40	F	III	T3aN0M0	Ovary	Serous Adenocarcinoma	Moderate	None	4.5	27.28	27.28	Y	N	Y
CGPLOV19	Ovarian Cancer	Preoperative treatment naive	52	F	II	T2aN0M0	Ovary	Endometrioid Adenocarcinoma	Moderate	None	5.0	23.46	23.46	Y	Y	Y
CGPLOV20	Ovarian Cancer	Preoperative treatment naive	52	F	II	T2aN0M0	Left Ovary	Endometrioid Adenocarcinoma	Poor	None	4.2	5.67	5.67	Y	Y	Y
CGPLOV21	Ovarian Cancer	Preoperative treatment naive	51	F	IV	TanyN1M1	Ovary	Serous Adenocarcinoma	Poor	Omentum, Appendix	4.3	56.32	56.32	Y	Y	Y
CGPLOV22	Ovarian Cancer	Preoperative treatment naive	64	F	III	T1cNXMX	Left Ovary	Serous Adenocarcinoma	Well	None	4.6	17.42	17.42	Y	Y	Y
CGPLOV23	Ovarian Cancer	Preoperative treatment naive	47	F	I	T1aN0M0	Ovary	Serous Adenocarcinoma	Poor	None	5.0	26.73	26.73	Y	N	Y
CGPLOV24	Ovarian Cancer	Preoperative treatment naive	14	F	I	T1aN0M0	Ovary	Germ Cell Tumor	Poor	None	4.2	10.71	10.71	Y	N	Y
CGPLOV25	Ovarian Cancer	Preoperative treatment naive	18	F	I	T1aN0M0	Ovary	Germ Cell Tumor	Poor	None	4.8	6.78	6.78	Y	N	Y
CGPLOV26	Ovarian Cancer	Preoperative treatment naive	35	F	I	T1aN0M0	Ovary	Germ Cell Tumor	Poor	None	4.5	27.90	27.90	Y	N	Y
CGPLOV28	Ovarian Cancer	Preoperative treatment naive	63	F	I	T1aN0M0	Right Ovary	Serous Carcinoma	NA	None	3.2	10.74	10.74	Y	N	Y
CGPLOV31	Ovarian Cancer	Preoperative treatment naive	45	F	III	T3aNxM0	Right Ovary	Clear Cell adenocarcinoma	NA	None	4.0	14.45	14.45	Y	N	Y
CGPLOV32	Ovarian Cancer	Preoperative treatment naive	53	F	I	T1aNxM0	Left Ovary	Mucinous Cystadenoma	NA	None	3.2	27.36	27.36	Y	N	Y
CGPLOV37	Ovarian Cancer	Preoperative treatment naive	40	F	I	T1cN0M0	Ovary	Serous Carcinoma	NA	None	3.2	46.88	46.88	Y	N	Y
CGPLOV38	Ovarian Cancer	Preoperative treatment naive	46	F	I	T1cN0M0	Ovary	Serous Carcinoma	NA	None	2.4	34.29	34.29	Y	N	Y
CGPLOV40	Ovarian Cancer	Preoperative treatment naive	53	F	IV	T3N0M1	Ovary	Serous Carcinoma	NA	Omentum, Uterus, Appendix	1.6	193.60	156.25	Y	N	Y
CGPLOV41	Ovarian Cancer	Preoperative treatment naive	57	F	IV	T3N0M1	Ovary	Serous Carcinoma	NA	Omentum, Uterus, Cervix	4.4	10.03	10.03	Y	N	Y
CGPLOV42	Ovarian Cancer	Preoperative treatment naive	52	F	I	T3aN0M0	Ovary	Serous Carcinoma	NA	None	4.2	49.51	49.51	Y	N	Y
CGPLOV43	Ovarian Cancer	Preoperative treatment naive	30	F	I	T1aN0M0	Ovary	Mucinous Cyst-adenocarcinoma	NA	None	4.4	9.09	9.09	Y	N	Y
CGPLOV44	Ovarian Cancer	Preoperative treatment naive	69	F	I	T1aN0M0	Ovary	Mucinous Adenocarcinoma	NA	None	4.5	8.79	8.79	Y	N	Y

APPENDIX A-continued

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
CGPLOV46	Ovarian Cancer	cfDNA	Preoperative treatment naive	58	F	I	T1bN0M0	Ovary	Serous Carcinoma	NA	None	4.1	8.97	8.97	Y	N	Y
CGPLOV47	Ovarian Cancer	cfDNA	Preoperative treatment naive	41	F	I	T1aN0M0	Ovary	Serous Adenocarcinoma	NA	None	4.5	19.35	19.35	Y	N	Y
CGPLOV48	Ovarian Cancer	cfDNA	Preoperative treatment naive	52	F	I	T1bN0M0	Ovary	Serous Carcinoma	NA	None	3.5	22.80	22.80	Y	N	Y
CGPLOV49	Ovarian Cancer	cfDNA	Preoperative treatment naive	68	F	III	T3bN0M0	Ovary	Serous Carcinoma	NA	None	4.2	16.48	16.48	Y	N	Y
CGPLOV50	Ovarian Cancer	cfDNA	Preoperative treatment naive	30	F	III	T3cN0M0	Ovary	Serous Carcinoma	NA	None	4.5	8.89	8.89	Y	N	Y
CGPLPA112	Pancreatic Cancer	cfDNA	Preoperative treatment naive	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 naive	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 naive	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 naive	NA	M	IV	NA	Intra-Hepatic Bile Duct	NA	NA	NA	5.0	31.41	31.41	Y	N	N
CGPLPA117	Bile Duct Cancer	cfDNA	Preoperative treatment naive	NA	M	II	NA	Intra-Pancreatic Bile Duct	NA	NA	NA	3.4	2.29	2.29	Y	N	N
CGPLPA118	Bile Duct Cancer	cfDNA	Preoperative treatment naive	68	F	I	NA	Bile Duct	Intra-Amпулярary 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-Amпулярary 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	4.2	80.56	29.07	Y	N	Y
CGPLPA127	Bile Duct Cancer	cfDNA	Preoperative treatment naive	71	F	IV	NA	Bile Duct	Intra-Extra-Pancreatic Bile Duct	NA	NA	3.0	20.60	20.60	Y	N	N

APPENDIX A-continued

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 Ex-traced (ng/ml)	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
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-Pancreatic 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	58.98	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

APPENDIX A-continued

Table 1. Summary of patients and samples analyzed

Patient	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
CGPLPA168	Bile Duct Cancer	Preoperative treatment naive	58	M	II	NA	Bile Duct	NA	NA	NA	3.0	139.12	34.72	Y	N	N
CGPLPA17	Pancreatic Cancer	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	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	Preoperative treatment naive	67	F	II	NA	Bile Duct	Intra-Pancreatic Bile Duct	NA	None	NA	NA	NA	Y	N	N
CGPLPA23	Pancreatic Cancer	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	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	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	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	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	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	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	Preoperative treatment naive	65	M	II	NA	Pancreas	Ductal Adenocarcinoma	Moderate	None	4.0	5.29	5.29	Y	N	N
CGPLPA39	Pancreatic Cancer	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	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	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	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	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	Preoperative treatment naive	72	F	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	NA	NA	NA	Y	N	N
CGPLPA52	Pancreatic Cancer	Preoperative treatment naive	63	M	II	NA	Pancreas	Ductal Adenocarcinoma	Moderate	None	2.5	9.86	9.86	Y	N	N
CGPLPA53	Pancreatic Cancer	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	Preoperative treatment naive	74	F	II	NA	Pancreas	Ductal Adenocarcinoma	NA	None	3.0	6.87	6.87	Y	N	N

APPENDIX A-continued

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)	NA	cfDNA Input (ng/ml)	Whole Genome Fragment Profile Analysis	Targeted Fragment Profile Analysis	Targeted Mutation Analysis
CGPLPA59	Pancreatic Cancer	cfDNA	Preoperative treatment naive	59	F	II	NA	Pancreas	Ductal Adenocarcinoma or Adenoma	Well	Lymph Node	NA	NA	NA	Y	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	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	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	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	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	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	Y	N	N
CGPLPA86	Pancreatic Cancer	cfDNA	Preoperative treatment naive	66	M	II	NA	Pancreas	Ductal Adenocarcinoma	Moderate	Lymph Node	2.5	11.92	11.92	Y	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	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	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	Y	N	N
CGPLPA95	Pancreatic Cancer	cfDNA	Preoperative treatment naive	64	F	II	NA	Pancreas	Ductal Adenocarcinoma	Well	Lymph Node	NA	NA	NA	Y	Y	N	N
CGSTI02	Gastric Cancer	cfDNA	Preoperative treatment naive	76	F	II	T3N0M0	Stomach	Tubular Adenocarcinoma	Moderate	None	4.1	8.03	8.03	Y	Y	Y	Y
CGSTI11	Gastric Cancer	cfDNA	Preoperative treatment naive	49	M	IV	TXNXM1	Stomach	Mixed Carcinoma	Moderate	None	3.8	3.57	3.57	Y	Y	N	N
CGSTI10	Gastric Cancer	cfDNA	Preoperative treatment naive	77	M	III	T4AN3aM0	Stomach	Tubular Adenocarcinoma	Moderate	None	3.8	5.00	5.00	Y	Y	Y	Y
CGSTI14	Gastric Cancer	cfDNA	Preoperative treatment naive	65	M	III	T4N1M0	Stomach	Tubular Adenocarcinoma	Poor	None	4.4	10.35	10.35	Y	Y	Y	Y
CGSTI3	Gastric Cancer	cfDNA	Preoperative treatment naive	72	F	II	T1AN2M0	Stomach	Adenocarcinoma Signet Ring Cell Carcinoma	Poor	None	4.4	24.33	24.33	Y	Y	Y	Y
CGSTI31	Gastric Cancer	cfDNA	Preoperative treatment naive	63	M	III	T2N3aM0	Stomach	Signet ring cell Carcinoma	Poor	None	4.0	4.28	4.28	Y	Y	N	N
CGSTI41	Gastric Cancer	cfDNA	Preoperative treatment naive	33	F	III	T3N2M0	Stomach	Signet Ring Cell Carcinoma	Poor	None	4.4	10.84	10.84	Y	Y	Y	Y
CGSTI6	Gastric Cancer	cfDNA	Preoperative treatment naive	78	M	III	T4AN3aM0	Stomach	Tubular Adenocarcinoma	Poor	None	4.0	40.69	40.69	Y	Y	Y	Y
CGSTI8	Gastric Cancer	cfDNA	Preoperative treatment naive	50	M	II	T3N0M0	Stomach	Mucinous Adenocarcinoma	Well	None	4.3	9.78	9.78	Y	Y	Y	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	Y	N	N

APPENDIX A-continued

Table 1. Summary of patients and samples analyzed

Patient	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
CGST26	Gastric Cancer	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	Preoperative treatment naive	55	M	X	TXNXMX	Stomach	Undifferentiated Carcinoma	Poor	None	4.0	5.86	5.86	Y	N	Y
CGST30	Gastric Cancer	Preoperative treatment naive	64	F	III	T3N2M0	Stomach	Signet Ring Tubular	Poor	None	3.0	4.22	4.22	Y	N	Y
CGST32	Gastric Cancer	Preoperative treatment naive	67	M	II	T3N1M0	Stomach	Cell Carcinoma	Moderate	None	4.0	11.49	11.49	Y	N	Y
CGST33	Gastric Cancer	Preoperative treatment naive	61	M	I	T2N0M0	Stomach	Adenocarcinoma Tubular	Moderate	None	3.5	5.71	5.71	Y	N	Y
CGST38	Gastric Cancer	Preoperative treatment naive	71	F	0	TON0M0	Stomach	Adenocarcinoma Mucinous	NA	None	4.0	NA	NA	Y	N	N
CGST39	Gastric Cancer	Preoperative treatment naive	51	M	IV	TXNXM1	Stomach	Adenocarcinoma Signet Ring Cell Carcinoma	Poor	None	3.5	20.69	20.69	Y	N	Y
CGST41	Gastric Cancer	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	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	Preoperative treatment naive	74	F	I	TLAN0M0	Stomach	Adenocarcinoma Tubular	Moderate	None	4.0	4.55	4.55	Y	N	Y
CGST48	Gastric Cancer	Preoperative treatment naive	62	M	IV	TXNXM1	Stomach	Adenocarcinoma Tubular	Poor	None	4.5	8.79	8.79	Y	N	Y
CGST53	Gastric Cancer	Preoperative treatment naive	70	M	0	TON0M0	Stomach	Adenocarcinoma NA	NA	None	3.8	15.82	15.82	Y	N	N
CGST58	Gastric Cancer	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	Preoperative treatment naive	69	M	I	T1RN0M0	Stomach	Tubular adenocarcinoma	Moderate	None	3.0	23.01	23.01	Y	N	N
CGST77	Gastric Cancer	Preoperative treatment naive	70	M	IV	TXNXM1	Stomach	Tubular adenocarcinoma	Moderate	None	4.5	15.09	15.09	Y	N	N
CGST80	Gastric Cancer	Preoperative treatment naive	58	M	III	T3N3aM0	Stomach	Adenocarcinoma Mucinous	Poor	None	4.5	8.56	8.56	Y	N	Y
CGST81	Gastric Cancer	Preoperative treatment naive	64	F	I	T2N0M1	Stomach	Signet Ring Cell Carcinoma	Poor	None	3.5	37.32	37.32	Y	N	Y
CGH14	Healthy	NA	NA	M	NA	NA	NA	NA	NA	NA	NA	NA	NA	Y	N	N
CGH15	Healthy	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 naïve	Y	Y	100	80930	7501485600	37711359756	50%	44345	10359
CGCRC292	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	6736035200	3098886973	46%	36448	8603
CGCRC293	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	6300244000	2818734206	45%	33117	5953
CGCRC294	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7766872600	3911796709	50%	46016	12071
CGCRC295	Colorectal Cancer	Preoperative, Treatment naïve	Y	N	100	80930	8240660200	3478059753	42%	40787	5826
CGCRC296	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	5718556500	2898549356	51%	33912	10180
CGCRC297	Colorectal Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7550826100	3717222432	49%	43545	5870
CGCRC298	Colorectal Cancer	Preoperative, Treatment naïve	Y	N	100	80930	12501036400	6096393764	49%	71196	9617
CGCRC299	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7812602900	4121569690	53%	48098	10338
CGCRC300	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8648090300	3962285136	46%	46364	5756
CGCRC301	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7538758100	3695480348	49%	43024	6618
CGCRC302	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8573658300	4349420574	51%	51006	13799
CGCRC303	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	5224046400	2505714343	48%	29365	8372
CGCRC304	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	5762112600	2942170530	51%	34462	10208
CGCRC305	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7213384100	3726953480	52%	43516	8589
CGCRC306	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7075579700	3552441899	50%	41507	7372
CGCRC307	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7572687100	3492191519	46%	40793	9680
CGCRC308	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7945738000	3895908986	49%	45224	11809
CGCRC309	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8487455800	3921079811	46%	45736	10739
CGCRC310	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	9003580500	4678812441	52%	54713	11139
CGCRC311	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	6528162700	3276653864	50%	38324	6044
CGCRC312	Colorectal Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7683294300	3316719187	43%	38652	4622
CGCRC313	Colorectal Cancer	Preoperative, Treatment naïve	Y	N	100	80930	5874099200	2896148722	49%	33821	6506
CGCRC314	Colorectal Cancer	Preoperative, Treatment naïve	Y	N	100	80930	6883148500	3382767492	49%	39414	6664
CGCRC315	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7497252500	3775556051	50%	44034	8666
CGCRC316	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	10684720400	5533857153	52%	64693	14289
CGCRC317	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7086877600	3669434216	52%	43538	10944
CGCRC318	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	6880041100	3326357413	48%	39077	11571
CGCRC319	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7485342900	3982677483	53%	47327	10502
CGCRC320	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7058703200	3450648135	49%	40888	10198
CGCRC321	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7203625900	3633396892	50%	43065	6499
CGCRC322	Colorectal Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7202969100	3758323705	52%	44580	3243
CGCRC323	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8767144700	4199126827	48%	49781	8336
CGCRC324	Colorectal Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7771869100	3944518280	51%	46518	5014
CGCRC325	Colorectal Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7972524600	4064901201	51%	48308	6151
CGCRC326	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8597346400	4333410573	50%	51390	7551
CGCRC327	Colorectal Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7399611700	3800666199	51%	45083	8092
CGCRC328	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	8029493700	4179383804	52%	49380	5831
CGCRC329	Colorectal Cancer	Preoperative, Treatment naïve	Y	Y	100	80930	7938963500	4095555110	52%	48397	3808
CGCRC330	Colorectal Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7214889500	3706643098	51%	43805	3014
CGCRC331	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8803159200	3668208527	42%	43106	11957
CGCRC332	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8478811500	3425408889	40%	40328	9592
CGCRC333	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6942167800	3098232737	45%	36823	2300
CGCRC334	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8182868200	2383173431	29%	28233	7973
CGCRC335	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7448272300	3925056341	53%	46679	5582
CGCRC336	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	5804744500	2986809912	51%	35490	4141

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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
CGRC349	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	69434511600	3533145275	51%	41908	5762
CGRC350	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7434818400	3848923016	52%	45678	4652
CGRC351	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7306546400	3636910409	50%	43162	5205
CGRC352	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7864655000	3336939252	42%	39587	4502
CGRC353	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7501674800	3642919375	49%	43379	4666
CGRC354	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7938270200	2379068977	30%	28256	4858
CGRC355	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6013175900	3046754994	51%	36127	3425
CGRC357	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6013454600	3022035300	50%	35813	4259
CGRC358	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7227212400	3188723303	44%	37992	5286
CGRC359	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7818567700	425110101	5%	5040	2566
CGRC367	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6582043200	3363063597	51%	39844	5839
CGRC368	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	8042242400	4101646000	51%	48636	11471
CGRC370	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6940330100	3198954121	46%	38153	4826
CGRC373	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6587201700	3120088035	47%	37234	5190
CGRC376	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6727983100	3162416807	47%	37735	3445
CGRC377	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	3131415570	3131415570	47%	37160	4524
CGRC378	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6523969900	2411096720	37%	28728	3239
CGRC379	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6996252100	3371081103	48%	39999	2891
CGRC380	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7097496300	2710244446	38%	32020	3251
CGRC381	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6961936100	3287050681	47%	38749	9357
CGRC382	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6959048700	2552325859	37%	30040	5148
CGRC384	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7012798900	3293884583	47%	39158	3653
CGRC385	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7542017900	3356570505	45%	39884	3686
CGRC386	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6876059600	3064412286	45%	36431	2787
CGRC387	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7399564700	3047254560	41%	36141	6675
CGRC386	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6592692900	3137284885	48%	37285	5114
CGRC389	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6651206300	3102100941	47%	36764	6123
CGRC390	Colorectal Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7260616800	3376667585	47%	40048	4368
CGRC391	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
CGLU344	Lung Cancer	Pre-treatment, Day -21	Y	N	100	80930	6587281800	1947630979	30%	23094	4439
CGLU344	Lung Cancer	Pre-treatment, Day -21	Y	N	100	80930	7842910900	1147703178	45%	32462	8063
CGLU344	Lung Cancer	Pre-treatment, Day -21	Y	N	100	80930	5838083100	2291108925	15%	13565	4303
CGLU344	Lung Cancer	Pre-treatment, Day -21	Y	N	100	80930	7078131900	1482448715	39%	27067	4287
CGLU369	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	6904701700	3722274529	48%	43945	3471
CGLU369	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	7003452200	1271457982	18%	15109	2354
CGLU369	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	6346267200	3053520676	21%	17583	4275
CGLU373	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	6517189900	3192984468	31%	25230	5278
CGLU373	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	7767146300	3572598842	45%	37509	6062
CGLU373	Lung Cancer	Pre-treatment, Day -2	Y	N	100	80930	7190999100	3273648804	48%	36137	6251
CGPLBR101	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	7420822800	3810365416	49%	38066	8040
CGPLBR101	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6679304900	3269688319	46%	38784	5306
CGPLBR102	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6679304900	3269688319	46%	38784	5306
CGPLBR102	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	80930	6679304900	3269688319	46%	38784	5306

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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
CGPLBR103	Breast Cancer	Preoperative, Treatment naïve	N	Y	100	60930	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	3836800101	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	Y	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	8264533900	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
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	4006693338	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	Y	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	Y	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

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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
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
CGRLH56	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	3464444000	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
CGPLJU13	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
CGPLLU14	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	398731089	46%	48628	3148
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
CGPLJU14	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
CGPLLU161	Lung Cancer	Preoperative, Treatment naïve	Y	N	100	80930	7789148700	3280139772	42%	38568	12229
CGPLLU162	Lung Cancer	Preoperative, Treatment naïve	N	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	7600630000	3868237773	50%	45625	9711
CGPLLU169	Lung Cancer	Preoperative, Treatment naïve	N	Y	100	80930	9378333000	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	N	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%	36768	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	79066779200	3082397881	39%	36381	5388

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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
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	Y	Y	100	80930	7458749900	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	Y	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
CGPLLU264	Lung Cancer	Pre-treatment, Day -1	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	8388
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	7785
CGPLLU266	Lung Cancer	Pre-treatment, Day 0	Y	N	100	80930	6513702000	2096370387	32%	25142	6598
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	6156402000	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

APPENDIX B-continued

Table 2. Summary of targeted cfDNA analyses

Patient	Patient Type	Timepoint	Fragment Profile Analysis	Mutation Analysis	Read Length	Bases in		Bases Mapped to Genome	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage	Distinct Coverage
						Target	Region					
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	36413	50%	3560	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	N	Y	100	80930	6509178000	3316053733	51%	39274	2651	
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	7005599600	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	3402306123	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	N	Y	100	80930	8173037600	4064432407	50%	47714	5182	
CGPLOV19	Ovarian Cancer	Preoperative, Treatment naïve	Y	N	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	8961384000	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	3927	
CGPLOV46	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	9346036300	5037820346	44%	61204	4067	
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	5096	
CGPLOV49	Ovarian Cancer	Preoperative, Treatment naïve	N	Y	100	80930	100762098000	5519656698	55%	67117	5097	
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	4002	
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	

APPENDIX B-continued

Table 2. Summary of targeted cfDNA analyses

Patient	Patient Type	Timepoint	Fragment Profile Analysis	Mutation Analysis	Read Length	Bases in		Bases Mapped to Genome	Bases Mapped to Target Regions	Percent Mapped to Target Regions	Total Coverage	Distinct Coverage
						Target	Region					
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	2992501875	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	6388064600	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)
CGCRC291	Colorectal Cancer	IV	Tumor-derived	STK11	39R > C
CGCRC291	Colorectal Cancer	IV	Tumor-derived	TP53	272V > M
CGCRC291	Colorectal Cancer	IV	Tumor-derived	TP53	167Q > X
CGCRC291	Colorectal Cancer	IV	Tumor-derived	KRAS	12G > A
CGCRC291	Colorectal Cancer	IV	Tumor-derived	APC	1260Q > X
CGCRC291	Colorectal Cancer	IV	Tumor-derived	APC	1450R > X
CGCRC291	Colorectal Cancer	IV	Tumor-derived	PIK3CA	542E > K
CGCRC292	Colorectal Cancer	IV	Tumor-derived	KRAS	146A > V
CGCRC292	Colorectal Cancer	IV	Tumor-derived	CTNNB1	41T > A
CGCRC292	Colorectal Cancer	IV	Germline	EGFR	2284 - 4C > 3
CGCRC293	Colorectal Cancer	IV	Tumor-derived	TP53	176C > S
CGCRC294	Colorectal Cancer	II	Tumor-derived	APC	213R > X
CGCRC294	Colorectal Cancer	II	Tumor-derived	APC	1367Q > X
CGCRC295	Colorectal Cancer	IV	Tumor-derived	PDBFRA	49 + 4C > T
CGCRC295	Colorectal Cancer	IV	Hematopoietic	IDH1	104G > V
CGCRC296	Colorectal Cancer	II	Germline	EGFR	922E > K
CGCRC297	Colorectal Cancer	III	Germline	KIT	18L > F
CGCRC298	Colorectal Cancer	II	Hematopoietic	DNMT3A	882R > H
CGCRC298	Colorectal Cancer	II	Hematopoietic	DNMT3A	714S > C
CGCRC298	Colorectal Cancer	II	Tumor-derived	PIK3CA	414G > V
CGCRC299	Colorectal Cancer	I	Hematopoietic	DNMT3A	735Y > C
CGCRC299	Colorectal Cancer	I	Hematopoietic	DNMT3A	710C > S
CGCRC300	Colorectal Cancer	I	Hematopoietic	DNMT3A	720R > G
CGCRC301	Colorectal Cancer	I	Tumor-derived	ATM	2397Q > X
CGCRC302	Colorectal Cancer	II	Tumor-derived	TP53	141C > Y
CGCRC302	Colorectal Cancer	II	Tumor-derived	BRAF	600V > E
CGCRC303	Colorectal Cancer	III	Tumor-derived	TP53	173V > L
CGCRC303	Colorectal Cancer	III	Hematopoietic	DNMT3A	755F > S
CGCRC303	Colorectal Cancer	III	Hematopoietic	DNMT3A	2173 + 1G > A
CGCRC304	Colorectal Cancer	II	Tumor-derived	EGFR	1131T > S
CGCRC304	Colorectal Cancer	II	Tumor-derived	ATM	3077 + 1G > A
CGCRC304	Colorectal Cancer	II	Hematopoietic	ATM	3008R > C
CGCRC305	Colorectal Cancer	II	Tumor-derived	GNA11	213R > Q
CGCRC305	Colorectal Cancer	II	Tumor-derived	TP53	273R > H
CGCRC306	Colorectal Cancer	II	Tumor-derived	TP53	196R > X
CGCRC306	Colorectal Cancer	II	Tumor-derived	CDKN2A	107R > C
CGCRC306	Colorectal Cancer	II	Tumor-derived	KRAS	61Q > K
CGCRC306	Colorectal Cancer	II	Germline	PDGFRA	200T > S
CGCRC306	Colorectal Cancer	II	Tumor-derived	EGFR	618H > R
CGCRC306	Colorectal Cancer	II	Tumor-derived	PIK3CA	545E > A
CGCRC306	Colorectal Cancer	II	Germline	ERBB4	1155R > X
CGCRC307	Colorectal Cancer	II	Tumor-derived	JAK2	805L > V
CGCRC307	Colorectal Cancer	II	Tumor-derived	SMARCB1	501 - 2A > G
CGCRC307	Colorectal Cancer	II	Tumor-derived	GNAS	201R > C
CGCRC307	Colorectal Cancer	II	Tumor-derived	BRAF	600V > E
CGCRC307	Colorectal Cancer	II	Tumor-derived	FBXW7	465R > C
CGCRC307	Colorectal Cancer	II	Tumor-derived	ERBB4	17A > V
CGCRC308	Colorectal Cancer	III	Hematopoietic	DNMT3A	882R > H
CGCRC308	Colorectal Cancer	III	Germline	EGFR	848P > L
CGCRC308	Colorectal Cancer	III	Tumor-derived	APC	1480Q > X
CGCRC309	Colorectal Cancer	III	Tumor-derived	AKT1	17E > K
CGCRC309	Colorectal Cancer	III	Tumor-derived	BRAF	600V > E
CGCRC310	Colorectal Cancer	II	Tumor-derived	KRAS	12G > V
CGCRC310	Colorectal Cancer	II	Tumor-derived	APC	1513E > X
CGCRC310	Colorectal Cancer	II	Tumor-derived	APC	1521E > X
CGCRC311	Colorectal Cancer	I	Hematopoietic	DNMT3A	882R > H
CGCRC312	Colorectal Cancer	III	Tumor-derived	APC	960S > X
CGCRC312	Colorectal Cancer	III	Tumor-derived	NRAS	61Q > K
CGCRC313	Colorectal Cancer	III	Tumor-derived	KRAS	12G > S
CGCRC313	Colorectal Cancer	III	Tumor-derived	APC	876R > X
CGCRC314	Colorectal Cancer	I	Tumor-derived	KRAS	12G > D
CGCRC314	Colorectal Cancer	I	Hematopoietic	DNMT3A	738L > Q
CGCRC314	Colorectal Cancer	I	Tumor-derived	APC	1379E > X
CGCRC315	Colorectal Cancer	III	Tumor-derived	NRAS	12G > D
CGCRC315	Colorectal Cancer	III	Tumor-derived	FBXW7	505R > C

Patient	Nucleotide	Mutation Type	Hotspot Alteration	Alteration Detected in Tissue	Mutant Allele Fraction
CGCRC291	chr19_1207027-127027_C_T	Substitution	No	No	0.14%
CGCRC291	chr17_7577124-7577124_C_T	Substitution	Yes	No	0.10%

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

CGCRC291	chr17_7578431-7578431_G_A	Substitution	Yes	Yes	22.85%
CGCRC291	chr12_25398284-25398284_C_G	Substitution	Yes	Yes	14.65%
CGCRC291	chr5_112175069-112175069_C_T	Substitution	No	Yes	11.23%
CGCRC291	chr5_11215639-11215639_C_T	Substitution	Yes	Yes	11.05%
CGCRC291	chr3_178936082-178936082_G_A	Substitution	Yes	Yes	18.11%
CGCRC292	chr12_25378561-25378561_G_A	Substitution	Yes	No	1.41%
CGCRC292	chr3_41266124-41266124_A_G	Substitution	Yes	Yes	0.13%
CGCRC292	chr7_55248982-55248982_C_G	Substitution	NA	Yes	31.99%
CGCRC293	chr17_7578404-7578404_A_T	Substitution	No	No	0.35%
CGCRC294	chr5_12116592-12116592_C_T	Substitution	Yes	Yes	0.14%
CGCRC294	chr5_12175390-12175390_C_T	Substitution	Yes	Yes	0.13%
CGCRC295	chr4_55124988-55124988_C_T	Substitution	No	No	0.45%
CGCRC295	chr2_209113196-209113196_C_A	Substitution	No	Yes	0.34%
CGCRC296	chr7_55266472-55266472_G_A	Substitution	NA	Yes	30.48%
CGCRC297	chr4_55524233-55524233_C_T	Substitution	NA	Yes	41.39%
CGCRC298	chr2_25457242-25457242_C_T	Substitution	Yes	Yes	0.08%
CGCRC298	chr2_25463541-25463541_G_C	Substitution	No	No	0.11%
CGCRC298	chr3_178927478-178927478_G_T	Substitution	No	No	0.55%
CGCRC299	chr2_25463289-25463289_T_C	Substitution	No	Yes	0.30%
CGCRC299	chr2_25463553-25463553_C_G	Substitution	No	Yes	0.12%
CGCRC300	chr2_25463524-25463524_G_C	Substitution	No	No	0.15%
CGCRC301	chr11_108199847-108199847_C_T	Substitution	No	No	0.21%
CGCRC302	chr17_7578508-7578508_C_T	Substitution	Yes	Yes	0.05%
CGCRC302	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	0.12%
CGCRC303	chr17_7578413-7578413_C_A	Substitution	Yes	Yes	0.08%
CGCRC303	chr2_25463229-25463229_A_G	Substitution	No	No	0.21%
CGCRC303	chr2_25463508-25463508_C_T	Substitution	No	No	0.17%
CGCRC304	chr7_55273068-55273068_A_T	Substitution	No	No	0.22%
CGCRC304	chr11_108142134-108142134_G_A	Substitution	No	No	0.27%
CGCRC304	chr11_108236086-108236086_C_T	Substitution	No	Yes	0.43%
CGCRC305	chr19_3118954-3118954_G_A	Substitution	No	Yes	0.11%
CGCRC305	chr17_7577120-7577120_C_T	Substitution	Yes	No	0.19%
CGCRC306	chr17_7578263-7578263_G_A	Substitution	Yes	No	0.12%
CGCRC306	chr9_21971039-21971039_G_A	Substitution	No	Yes	8.02%
CGCRC306	chr12_25380277-25380277_G_T	Substitution	Yes	Yes	7.30%
CGCRC306	chr4_55130065-55130065_C_G	Substitution	NA	Yes	34.78%
CGCRC306	chr7_55233103-55233103_A_G	Substitution	No	Yes	8.32%
CGCRC306	chr3_178936092-178936092_A_C	Substitution	Yes	No	0.96%
CGCRC306	chr2_2122596-2122596_G_A	Substitution	NA	Yes	38.70%
CGCRC307	chr9_5080662-5080662_C_G	Substitution	No	No	0.56%
CGCRC307	chr22_24145480-24145480_A_G	Substitution	No	Yes	0.34%
CGCRC307	chr20_57484420-57484420_C_T	Substitution	Yes	Yes#	0.24%
CGCRC307	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	0.38%
CGCRC307	chr4_153249385-153249385_G_A	Substitution	Yes	Yes	0.31%
CGCRC307	chr2_213403205-213403205_G_A	Substitution	No	No	0.15%
CGCRC308	chr2_25457242-25457242_C_T	Substitution	Yes	No	0.06%
CGCRC308	chr7_55259485-55259485_C_T	Substitution	NA	Yes	27.69%
CGCRC308	chr5_112175242-112175242_C_T	Substitution	No	Yes	0.11%
CGCRC309	chr14_105246551-105246551_C_T	Substitution	Yes	Yes	2.70%
CGCRC309	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	3.00%
CGCRC310	chr12_25398284-25398284_C_A	Substitution	Yes	Yes	0.13%
CGCRC310	chr5_11215828-11215828_G_T	Substitution	No	Yes	0.11%
CGCRC310	chr5_11215852-11215852_G_T	Substitution	No	Yes	0.15%
CGCRC311	chr2_25457242-25457242_C_T	Substitution	Yes	No	0.86%
CGCRC312	chr5_112174170-112174170_C_G	Substitution	No	Yes	0.59%
CGCRC312	chr1_115256530-115256530_G_T	Substitution	Yes	Yes	0.47%
CGCRC313	chr12_25398285-25398285_C_T	Substitution	Yes	Yes	0.17%
CGCRC313	chr5_112173917-112173917_C_T	Substitution	Yes	Yes	0.07%
CGCRC314	chr12_25398284-25398284_C_T	Substitution	Yes	Yes	0.30%
CGCRC314	chr2_25463280-25463280_A_T	Substitution	No	Yes	2.50%
CGCRC314	chr5_112175426-112175426_G_T	Substitution	Yes	Yes	0.38%
CGCRC315	chr1_115258747-115258747_C_T	Substitution	Yes	Yes	0.27%
CGCRC315	chr4_153247289-153247289_G_A	Substitution	Yes	Yes	0.25%

Wild-type Fragments

Patient	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)
CGCRC291	11688	100	151	167	159
CGCRC291	11779	100	155	171	159

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

CGCRC291	11026	100	156	166	159
CGCRC291	7632	97	152	169	157
CGCRC291	7218	101	155	167	159
CGCRC291	10757	86	154	166	167
CGCRC291	5429	100	151	171	167
CGCRC292	8120	101	157	167	169
CGCRC292	10693	100	155	169	168
CGCRC292	7587	97	158	166	171
CGCRC293	7672	95	159	168	170
CGCRC294	7339	84	155	166	167
CGCRC294	12054	89	159	167	170
CGCRC295	5602	101	157	164	170
CGCRC295	8330	100	157	166	169
CGCRC296	8375	89	161	166	172
CGCRC297	3580	102	159	164	170
CGCRC298	13032	100	159	168	171
CGCRC298	13475	93	158	169	170
CGCRC298	5815	100	156	168	169
CGCRC299	11995	100	154	164	165
CGCRC299	15363	96	151	166	164
CGCRC300	7487	100	162	170	173
CGCRC301	5881	100	156	169	169
CGCRC302	24784	84	154	165	164
CGCRC302	11763	95	159	165	165
CGCRC303	13967	95	160	169	171
CGCRC303	10161	81	160	169	172
CGCRC303	10845	100	160	169	172
CGCRC304	16168	90	153	167	164
CGCRC304	10502	100	152	165	163
CGCRC304	12987	101	154	165	165
CGCRC305	12507	100	159	169	171
CGCRC305	10301	100	156	168	168
CGCRC306	8594	101	157	165	169
CGCRC306	9437	90	159	167	171
CGCRC306	8090	100	152	163	168
CGCRC306	4585	103	158	167	170
CGCRC306	7395	81	160	166	171
CGCRC306	4885	100	152	167	167
CGCRC306	3700	100	159	166	171
CGCRC307	6860	100	158	170	170
CGCRC307	10065	95	157	168	169
CGCRC307	7520	102	156	167	168
CGCRC307	6623	76	157	169	168
CGCRC307	10606	100	155	167	168
CGCRC307	13189	90	158	168	171
CGCRC308	16287	90	159	168	169
CGCRC308	7729	100	160	164	170
CGCRC308	14067	92	157	170	169
CGCRC309	13036	85	157	170	169
CGCRC309	9084	101	157	166	168
CGCRC310	7393	100	153	165	164
CGCRC310	11689	100	152	166	164
CGCRC310	10273	100	153	166	164
CGCRC311	8456	94	160	171	172
CGCRC312	4719	100	160	165	173
CGCRC312	3391	101	157	172	170
CGCRC313	5013	100	163	166	174
CGCRC313	8150	72	161	171	174
CGCRC314	4684	100	158	165	169
CGCRC314	6902	85	159	165	170
CGCRC314	7229	102	158	167	170
CGCRC315	8739	94	155	167	169
CGCRC315	9623	101	158	166	170

Patient	Patient Type	Stage at Diagnosis	Alteration Type	Gene	Amino Acid (Protein)
CGCRC316	Colorectal Cancer	III	Tumor-derived	TP53	245G > S
CGCRC316	Colorectal Cancer	III	Tumor-derived	CDKN2A	1M > R
CGCRC316	Colorectal Cancer	III	Tumor-derived	CTNNB1	37S > C
CGCRC316	Colorectal Cancer	III	Tumor-derived	EGFR	2732 - 3C > T
CGCRC316	Colorectal Cancer	III	Hematopoietic	ATM	3008R > P
CGCRC317	Colorectal Cancer	III	Tumor-derived	TP53	220Y > C
CGCRC317	Colorectal Cancer	III	Tumor-derived	ATM	1026W > R
CGCRC317	Colorectal Cancer	III	Tumor-derived	APC	216R > X

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

CGCRC318	Colorectal Cancer	I	Hematopoietic	DNMT3A	698W > X
CGCRC320	Colorectal Cancer	I	Germline	KIT	18L > F
CGCRC320	Colorectal Cancer	I	Tumor-derived	ERBB4	78R > W
CGCRC321	Colorectal Cancer	I	Tumor-derived	CDKN2A	12S > L
CGCRC321	Colorectal Cancer	I	Hematopoietic	DNMT3A	882R > H
CGCRC321	Colorectal Cancer	I	Germline	EGFR	511S > Y
CGCRC332	Colorectal Cancer	IV	Tumor-derived	TP53	125T > R
CGCRC333	Colorectal Cancer	IV	Tumor-derived	TP53	673 - 2A > G
CGCRC333	Colorectal Cancer	IV	Tumor-derived	BRAF	600V > E
CGCRC333	Colorectal Cancer	IV	Tumor-derived	ERBB4	891E > A
CGCRC334	Colorectal Cancer	IV	Tumor-derived	TP53	245G > S
CGCRC334	Colorectal Cancer	IV	Germline	EGFR	638T > M
CGCRC334	Colorectal Cancer	IV	Tumor-derived	PIK3CA	104P > R
CGCRC335	Colorectal Cancer	IV	Tumor-derived	BRAF	600V > E
CGCRC336	Colorectal Cancer	IV	Tumor-derived	TP53	175R > H
CGCRC336	Colorectal Cancer	IV	Tumor-derived	KRAS	12G > V
CGCRC336	Colorectal Cancer	IV	Tumor-derived	APC	1286E > X
CGCRC337	Colorectal Cancer	IV	Tumor-derived	STK11	734 + ST > A
CGCRC337	Colorectal Cancer	IV	Germline	APC	485M > I
OGORC338	Colorectal Cancer	IV	Tumor-derived	KRAS	12G > D
CGCRC339	Colorectal Cancer	IV	Tumor-derived	KRAS	13G > D
CGCRC339	Colorectal Cancer	IV	Tumor-derived	APC	876R > X
CGCRC339	Colorectal Cancer	IV	Tumor-derived	PIK3CA	407C > F
CGCRC339	Colorectal Cancer	IV	Tumor-derived	PIK3CA	1047H > L
CGCRC340	Colorectal Cancer	IV	Tumor-derived	TP53	196R > X
CGCRC340	Colorectal Cancer	IV	Tumor-derived	APC	1306E > X
CGPLBR38	Breast Cancer	I	Tumor-derived	TP53	241S > P
CGPLBR40	Breast Cancer	III	Germline	AR	392P > R
CGPLBR44	Breast Cancer	III	Hematopoietic	DNMT3A	882R > H
CGPLBR44	Breast Cancer	III	Hematopoietic	DNMT3A	705I > T
CGPLBR44	Breast Cancer	III	Tumor-derived	PDGFRA	859V > M
CGPLBR48	Breast Cancer	II	Germline	ALK	1231R > Q
CGPLBR48	Breast Cancer	II	Tumor-derived	EGFR	669R > Q
CGPLBR55	Breast Cancer	III	Hematopoietic	DNMT3A	743P > S
CGPLBR55	Breast Cancer	III	Tumor-derived	GNAS	201R > H
CGPLBR55	Breast Cancer	III	Tumor-derived	PIK3CA	345N > K
CGPLBR63	Breast Cancer	II	Germline	FGFR3	403K > E
CGPLBR67	Breast Cancer	II	Hematopoietic	DNMT3A	882R > H
CGPLBR67	Breast Cancer	II	Tumor-derived	PIK3CA	545E > K
CGPLBR67	Breast Cancer	II	Tumor-derived	ERBB4	1000D > A
CGPLBR69	Breast Cancer	II	Hematopoietic	DNMT3A	774E > V
CGPLBR69	Breast Cancer	II	Germline	CTNNB1	30Y > S
CGPLBR69	Breast Cancer	II	Germline	IDH1	231Y > N
CGPLBR70	Breast Cancer	II	Tumor-derived	ATM	2832R > H
CGPLBR70	Breast Cancer	II	Germline	APC	1577E > D
CGPLBR71	Breast Cancer	II	Tumor-derived	TP53	273R > H
CGPLBR72	Breast Cancer	II	Germline	APC	1532D > G
CGPLBR73	Breast Cancer	II	Tumor-derived	ALK	708S > P
CGPLBR73	Breast Cancer	II	Germline	ERBB4	158A > E
CGPLBR74	Breast Cancer	II	Germline	AR	20 + G1G > T
CGPLBR75	Breast Cancer	II	Tumor-derived	PIK3CA	1047H > R
CGPLBR76	Breast Cancer	II	Germline	KDR	1290S > N
CGPLBR76	Breast Cancer	II	Tumor-derived	PIK3CA	1047H > R
CGPLBR77	Breast Cancer	III	Tumor-derived	PTEN	170S > I
CGPLBR80	Breast Cancer	II	Tumor-derived	CDKN2A	12S > L
CGPLBR83	Breast Cancer	II	Germline	AR	728N > D
CGPLBR83	Breast Cancer	II	Tumor-derived	ATM	322E > S
CGPLBR83	Breast Cancer	II	Germline	ERBB4	539Y > K
CGPLBR86	Breast Cancer	II	Germline	STK11	354F > L

Patient	Nucleotide	Mutation Type	Hotspot Alteration	Alteration Detected in Tissue	Mutant Allele Fraction
CGCRC316	chr17_7577548-7577548_C_T	Substitution	Yes	Yes	6.52%
CGCRC316	chr9_21974625-21974825_A_C	Substitution	No	Yes	5.74%
CGCRC316	chr3_41266113-41266113_C_G	Substitution	Yes	Yes	5.47%
CGCRC316	chr7_55266407-55266407_C_T	Substitution	No	No	0.11%
CGCRC316	chr11_108236087-108236087_G_C	Substitution	No	Yes	0.13%
CGCRC317	chr17_7578190-7578190_T_C	Substitution	Yes	Yes	0.36%
CGCRC317	chr11_108142132-108142132_T_C	Substitution	No	Yes	0.23%
CGCRC317	chr5_112128143-112128143_C_T	Substitution	Yes	No	0.29%
CGCRC318	chr2_25463589-25463589_C_T	Substitution	No	Yes	0.25%
CGCRC320	chr4_55524233-55524233_C_T	Substitution	NA	Yes	34.76%
CGCRC320	chr2_212989479-212989479_G_A	Substitution	No	No	0.12%

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

CGCRC321	chr9_21974792-21974792_C_T	Substitution	No	No	0.20%
CGCRC321	chr2_25457242-25457242_C_A	Substitution	You	No	0.08%
CGCRC321	chr7_55229225-55229225_G_C	Substitution	NA	Yes	41.86%
CGCRC332	chr17_7579313-7579313_T_C	Substitution	No	Yes	19.98%
CGCRC333	chr17_7577610-7577610_A_T	Substitution	No	Yes	43.03%
CGCRC333	chr7_140453136-140453136_T_G	Substitution	Yes	Yes	22.26%
CGCRC333	chr2_212495194-212495194_C_T	Substitution	No	No	1.00%
CGCRC334	chr17_7577548-7577548_C_T	Substitution	Yes	Yes	13.44%
CGCRC334	chr7_55238900-55238900_C_T	Substitution	NA	Yes	35.28%
CGCRC334	chr3_178916924-178916924_C_G	Substitution	No	No	3.85%
CGCRC335	chr7_140453136-140453136_A_T	Substitution	Yes	Yes	0.32%
CGCRC336	chr17_7578406-7578406_C_T	Substitution	Yes	Yes	75.76%
CGCRC336	chr12_25398284-25398284_C_A	Substitution	Yes	Yes	42.87%
CGCRC336	chr5_112175147-112175147_G_T	Substitution	No	Yes	81.61%
CGCRC337	chr19_1220718-1220718_T_A	Substitution	No	No	0.12%
CGCRC337	chr5_112162851-112162851_G_A	Substitution	NA	Yes	46.26%
OGORC338	chr12_25398284-25398284_C_T	Substitution	Yes	Yes	27.03%
CGCRC339	chr12_25398281-25398281_C_T	Substitution	Yes	Yes	1.94%
CGCRC339	chr5_112173917-112173917_C_T	Substitution	Yes	Yes	2.35%
CGCRC339	chr3_178927457-178927457_G_T	Substitution	No	Yes	3.14%
CGCRC339	chr3_178952085-178952085_A_T	Substitution	Yes	Yes	1.71%
CGCRC340	chr17_7578263-7578263_G_A	Substitution	Yes	Yes	18.26%
CGCRC340	chr5_112175207-112175207_G_T	Substitution	Yes	Yes	22.57%
CGPLBR38	chr17_7577560-7577560_A_G	Substitution	No	Yes	0.53%
CGPLBR40	chrX_66766163-66766163_C_G	Substitution	NA	Yes	28.99%
CGPLBR44	chr2_25457242-25457242_C_T	Substitution	Yes	Yes	1.82%
CGPLBR44	chr2_25463568-25463568_A_G	Substitution	No	Yes	0.41%
CGPLBR44	chr4_55153609-55153609_G_A	Substitution	No	Yes	0.13%
CGPLBR48	chr2_2936301-2936301_C_T	Substitution	NA	Yes	34.61%
CGPLBR48	chr7_55240762-55240762_G_A	Substitution	No	No	0.18%
CGPLBR55	chr2_25463266-25463266_G_A	Substitution	No	No	0.18%
CGPLBR55	chr20_57484421-57484421_G_A	Substitution	Yes	Yes	0.68%
CGPLBR55	chr178921553-178921553_T_A	Substitution	Yes	Yes	0.42%
CGPLBR63	chr3_1806188-1806188_A_G	Substitution	NA	Yes	34.82%
CGPLBR67	chr4_25457242-25457242_C_T	Substitution	Yes	Yes	0.11%
CGPLBR67	chr3_178936091-178936091_G_A	Substitution	Yes	Yes	0.68%
CGPLBR67	chr2_212285302-212285302_T_G	Substitution	No	No	0.28%
CGPLBR69	chr2_25463172-25463172_T_A	Substitution	No	No	0.29%
CGPLBR69	chr3_41266092-41266092_A_C	Substitution	NA	Yes	41.74%
CGPLBR69	chr2_209108158-209108158_A_T	Substitution	NA	Yes	41.86%
CGPLBR70	chr11_108216546-108216546_G_A	Substitution	No	No	0.36%
CGPLBR70	chr5_112176022-112176022_A_C	Substitution	NA	Yes	40.28%
CGPLBR71	chr17_7577120-7577120_C_T	Substitution	Yes	Yes	0.10%
CGPLBR72	chr5_112175886-112175886_A_G	Substitution	NA	Yes	44.03%
CGPLBR73	chr2_29474053-29474053_A_G	Substitution	No	No	0.27%
CGPLBR73	chr2_212652833-212652833_G_T	Substitution	NA	Yes	35.58%
CGPLBR74	chrX_66788865-66788865_G_T	Substitution	NA	Yes	36.23%
CGPLBR75	chr3_178952085-178952085_A_G	Substitution	Yes	Yes	0.14%
CGPLBR76	chr4_55946310-55946310_C_T	Substitution	NA	Yes	36.57%
CGPLBR76	chr3_178952085-178952085_A_G	Substitution	Yes	Yes	0.12%
CGPLBR77	chr10_89711891-89711891_G_T	Substitution	No	Yes	2.29%
CGPLBR80	chr9_21974792-21974792_G_A	Substitution	No	No	0.54%
CGPLBR83	chrX_66937328-66937328_A_G	Substitution	NA	Yes	42.66%
CGPLBR83	chr11_108117753-108117753_G_A	Substitution	No	No	0.28%
CGPLBR83	chr2_212543783-212543783_T_G	Substitution	NA	Yes	44.91%
CGPLBR86	chr19_1223125-1223125_C_G	Substitution	NA	Yes	42.32%

Wild-type Fragments

Patient	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)
CGCRC316	12880	100	150	166	163
CGCRC316	7479	93	157	164	168
CGCRC316	13682	100	149	165	162
CGCRC316	16716	85	153	166	156
CGCRC316	17060	100	150	166	153
CGCRC317	14587	84	152	166	154
CGCRC317	10483	100	152	164	155
CGCRC317	3497	101	149	166	163
CGCRC318	16436	98	158	170	170

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

CGCRC320	6521	100	163	170	175
CGCRC320	11633	100	162	174	174
CGCRC321	6918	88	161	167	174
CGCRC321	9559	94	159	171	170
CGCRC321	5545	100	159	172	172
CGCRC332	605	104	164	170	176
CGCRC333	1265	89	159	165	171
CGCRC333	3338	102	153	165	169
CGCRC333	3008	102	153	169	109
CGCRC334	1725	105	160	170	175
CGCRC334	1168	100	159	164	174
CGCRC334	1798	103	159	166	173
CGCRC335	2411	99	155	167	167
CGCRC336	757	104	156	171	170
CGCRC336	1080	102	150	166	167
CGCRC336	391	102	161	165	171
CGCRC337	6497	72	153	169	177
CGCRC337	1686	100	147	170	153
OGORC338	1408	105	153	164	156
CGCRC339	1256	105	158	168	159
CGCRC339	1639	101	158	165	172
CGCRC339	1143	100	154	170	167
CGCRC339	1584	108	161	171	173
CGCRC340	876	101	162	170	175
CGCRC340	796	105	159	164	174
CGPLBR38	9684	95	156	166	168
CGPLBR40	10277	78	162	168	173
CGPLBR44	10715	99	162	171	173
CGPLBR44	10837	100	159	169	171
CGPLBR44	12640	100	159	168	171
CGPLBR48	5631	100	164	170	179
CGPLBR48	12467	101	167	174	180
CGPLBR55	10527	101	158	169	169
CGPLBR55	6011	101	153	166	167
CGPLBR55	3973	101	153	166	166
CGPLBR63	3405	97	165	170	176
CGPLBR67	10259	87	157	166	168
CGPLBR67	5163	100	151	167	165
CGPLBR67	6250	100	155	166	187
CGPLBR69	7558	100	159	166	170
CGPLBR69	3938	101	154	169	166
CGPLBR69	2387	101	157	166	168
CGPLBR70	6916	100	158	171	169
CGPLBR70	3580	107	160	169	173
CGPLBR71	7930	85	156	166	158
CGPLBR72	2389	100	157	160	170
CGPLBR73	11348	95	161	173	174
CGPLBR73	3422	102	157	168	169
CGPLBR74	9784	101	163	175	174
CGPLBR75	7290	103	162	173	172
CGPLBR76	4342	104	166	171	179
CGPLBR76	11785	100	165	168	177
CGPLBR77	6161	100	158	166	169
CGPLBR80	3643	96	166	166	185
CGPLBR83	3479	105	162	164	174
CGPLBR83	3496	103	165	170	177
CGPLBR83	1748	100	164	173	175
CGPLBR86	4241	98	160	168	175

Patient	Patient Type	Stage at Diagnosis	Alteration Type	Gene	Amino Acid (Protein)
CGPLBR86	Breast Cancer	II	Germline	SMARCB1	795 + 3A > G
CGPLBR87	Breast Cancer	II	Tumor-derived	JAK2	215R > X
CGPLBR87	Breast Cancer	II	Hematopoietic	DNMT3A	882R > H
CGPLBR87	Breast Cancer	II	Tumor-derived	SMAD4	496R > C
CGPLBR87	Breast Cancer	II	Germline	AR	651S > N
CGPLBR88	Breast Cancer	II	Tumor-derived	CDK6	51E > K
CGPLBR88	Breast Cancer	II	Germline	APC	1125V > A
CGPLBR92	Breast Cancer	II	Tumor-derived	TP53	257L > P
CGPLBR96	Breast Cancer	II	Tumor-derived	TP53	213R > X
CGPLBR96	Breast Cancer	II	Hematopoietic	DNMT3A	531D > G
CGPLBR96	Breast Cancer	II	Tumor-derived	AR	13R > Q
CGPLBR97	Breast Cancer	II	Hematopoietic	DNMT3A	882R > H
CGPLBR97	Breast Cancer	II	Germline	PDGFRA	401A > D

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

CGPLBR97	Breast Cancer	II	Tumor-derived	GNAS	201R > H
CGPLLU144	Lung Cancer	II	Tumor-derived	TP53	241S > F
CGPLLU144	Lung Cancer	II	Tumor-derived	KRAS	12G > C
CGPLLU144	Lung Cancer	II	Tumor-derived	EGFR	373P > S
CGPLLU144	Lung Cancer	II	Tumor-derived	ATM	292P > L
CGPLLU144	Lung Cancer	II	Tumor-derived	PIK3CA	545E > K
CGPLLU144	Lung Cancer	II	Tumor-derived	ERBB4	426R > K
CGPLLU146	Lung Cancer	II	Tumor-derived	JAK2	617V > F
CGPLLU146	Lung Cancer	II	Tumor-derived	TP53	282R > P
CGPLLU146	Lung Cancer	II	Tumor-derived	DNMT3A	737L > H
CGPLLU146	Lung Cancer	II	Tumor-derived	RB1	861 + 2T > C
CGPLLU146	Lung Cancer	II	Tumor-derived	ATM	581L > F
CGPLLU147	Lung Cancer	III	Tumor-derived	TP53	248R > Q
CGPLLU147	Lung Cancer	III	Tumor-derived	TP53	201L > X
CGPLLU147	Lung Cancer	III	Tumor-derived	ALK	1537G > E
CGPLLU147	Lung Cancer	III	Germline	PDGFRA	200T > S
CGPLLU162	Lung Cancer	II	Tumor-derived	CDKN2A	12S > L
CGPLLU162	Lung Cancer	II	Tumor-derived	EGFR	858L > R
CGPLLU162	Lung Cancer	II	Tumor-derived	BRAF	354R > Q
CGPLLU163	Lung Cancer	II	Tumor-derived	CDKN2A	12S > L
CGPLLU163	Lung Cancer	II	Hematopoietic	DNMT3A	528Y > D
CGPLLU164	Lung Cancer	II	Tumor-derived	STK11	216S > Y
CGPLLU164	Lung Cancer	II	Germline	STK11	354F > L
CGPLLU164	Lung Cancer	II	Tumor-derived	GNA11	606 - 3C > T
CGPLLU164	Lung Cancer	II	Tumor-derived	TP53	278P > S
CGPLLU164	Lung Cancer	II	Tumor-derived	TP53	161A > S
CGPLLU164	Lung Cancer	II	Tumor-derived	TP53	160M > I
CGPLLU164	Lung Cancer	II	Tumor-derived	ERBB4	1299P > L
CGPLLU164	Lung Cancer	II	Tumor-derived	ERBB4	253N > S
CGPLLU165	Lung Cancer	II	Tumor-derived	STK11	354F > L
CGPLLU165	Lung Cancer	I	Tumor-derived	GNAS	201R > H
CGPLLU168	Lung Cancer	I	Tumor-derived	TP53	136Q > X
CGPLLU168	Lung Cancer	I	Hematopoietic	DNMT3A	736R > S
CGPLLU168	Lung Cancer	I	Tumor-derived	EGFR	858L > R
CGPLLU174	Lung Cancer	I	Tumor-derived	STK11	597 + 1G > T
CGPLLU174	Lung Cancer	I	Tumor-derived	JAK2	160D > Y
CGPLLU174	Lung Cancer	I	Tumor-derived	KRAS	12G > C
CGPLLU174	Lung Cancer	I	Hematopoietic	DNMT3A	891R > W
CGPLLU174	Lung Cancer	I	Hematopoietic	DNMT3A	715I > M
CGPLLU175	Lung Cancer	I	Tumor-derived	TP53	179H > R
CGPLLU175	Lung Cancer	I	Hematopoietic	DNMT3A	2598 - 1I > A
CGPLLU175	Lung Cancer	I	Hematopoietic	DNMT3A	755F > L
CGPLLU175	Lung Cancer	I	Germline	ATM	337R > C
CGPLLU175	Lung Cancer	I	Tumor-derived	ERBB4	941Q > X
CGPLLU176	Lung Cancer	I	Hematopoietic	DNMT3A	750P > S
CGPLLU176	Lung Cancer	I	Hematopoietic	DNMT3A	735Y > C
CGPLLU177	Lung Cancer	II	Tumor-derived	KRAS	12G > V
CGPLLU177	Lung Cancer	II	Hematopoietic	DNMT3A	897V > G
CGPLLU177	Lung Cancer	II	Hematopoietic	DNMT3A	862R > C
CGPLLU177	Lung Cancer	II	Hematopoietic	DNMT3A	2173 + 1 > A
CGPLLU178	Lung Cancer	I	Tumor-derived	CDH1	251 > M
CGPLLU178	Lung Cancer	I	Tumor-derived	PIK3CA	861Q > X
CGPLLU179	Lung Cancer	I	Hematopoietic	DNMT3A	879N > D
CGPLLU179	Lung Cancer	I	Germline	APC	2611T > I

Patient	Nucleotide	Mutation Type	Hotspot Alteration	Alteration Detected in Tissue	Mutant Allele Fraction
CGPLBR86	chr22_24159126-24159124_A_G	Substitution	NA	Yes	42.38%
CGPLBR87	chr9_5054591-5054591_C_T	Substitution	No	No	0.35%
CGPLBR87	chr2_25457242-25457242_C_T	Substitution	You	No	0.31%
CGPLBR87	chr18_48604664-48604664_C_T	Substitution	No	No	0.40%
CGPLBR87	chrX_66931310-66931310_G_A	Substitution	NA	Yes	42.94%
CGPLBR88	chr7_92462487-92462487_C_T	Substitution	No	No	0.13%
CGPLBR88	chr5_112174665-112174665_T_C	Substitution	NA	Yes	31.19%
CGPLBR92	chr17_7577511-7577511_A_G	Substitution	No	Yes	0.20%
CGPLBR96	chr17_fa:7578212-7578212_G_A	Substitution	Yes	No	0.10%
CGPLBR96	chr2_25467484-25467484_C_T	Substitution	No	Yes	5.81%
CGPLBR96	chrX_66765026-66765026_G_A	Substitution	No	No	0.60%
CGPLBR97	chr2_25457242-25457242_C_T	Substitution	Yes	Yes	0.11%
CGPLBR97	chr4_55136880-55136880_C_A	Substitution	NA	Yes	34.12%
CGPLBR97	chr20_57484421-57484421_G_A	Substitution	Yes	Yes	0.13%
CGPLLU144	chr17_7577559-7577559_G_A	Substitution	Yes	Yes	1.95%
CGPLLU144	chr12_25398285-25398285_C_A	Substitution	Yes	Yes	5.10%

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

CGPLLU144	chr7_55224336-55224336_C_T	Substitution	No	Yes	0.16%
CGPLLU144	chr11_108115727-108115727_C_T	Substitution	No	No	0.22%
CGPLLU144	chr3_178936091-178936091_G_A	Substitution	Yes	Yes	2.94%
CGPLLU144	chr2_212568841-212568841_C_T	Substitution	No	No	0.18%
CGPLLU146	chr9_5073770-5073770_G_T	Substitution	Yes	No	0.25%
CGPLLU146	chr17_7577093-7577093_C_G	Substitution	No	Yes	1.30%
CGPLLU146	chr2_25463283-25463283_A_T	Substitution	No	Yes	0.84%
CGPLLU146	chr13_48937095-48937095_T_C	Substitution	No	Yes	0.87%
CGPLLU146	chr11_108122699-108122699_A_T	Substitution	No	No	0.20%
CGPLLU147	chr17_7577538-7577538_C_T	Substitution	Yes	No	0.15%
CGPLLU147	chr17_7578247-7578247_A_T	Substitution	No	Yes	0.55%
CGPLLU147	chr2_29416343-29416343_C_T	Substitution	No	Yes	0.94%
CGPLLU147	chr4_55130065-55130065_C_G	Substitution	NA	Yes	43.47%
CGPLLU162	chr9_21974792-21974792_G_A	Substitution	No	No	0.22%
CGPLLU162	chr7_55259515-55259515_T_G	Substitution	Yes	Yes	0.22%
CGPLLU162	chr7_140494187-140494187_C_T	Substitution	No	No	0.14%
CGPLLU163	chr9_21974792-21974792_G_A	Substitution	No	No	0.21%
CGPLLU163	chr2_25467494-25467494_A_C	Substitution	No	Yes	0.15%
CGPLLU164	chr19_1220629-1220629_C_A	Substitution	No	Yes	1.23%
CGPLLU164	chr19_1223125-1223125_C_G	Substitution	NA	Yes	45.52%
CGPLLU164	chr19_3118919-3118919_C_T	Substitution	No	No	0.20%
CGPLLU164	chr17_7577106-7577106_G_A	Substitution	Yes	No	0.10%
CGPLLU164	chr17_7578449-7578449_C_A	Substitution	No	Yes	1.78%
CGPLLU164	chr17_7578450-7578450_C_A	Substitution	No	Yes	1.86%
CGPLLU164	chr2_212248371-212248371_G_A	Substitution	No	Yes	0.96%
CGPLLU164	chr2_212587243-212587243_T_C	Substitution	No	No	0.22%
CGPLLU165	chr19_1223125-1223125_C_G	Substitution	NA	Yes	36.62%
CGPLLU165	chr20_57484421-57484421_G_A	Substitution	Yes	Yes	0.16%
CGPLLU168	chr17_fa:7578524-7578524_G_A	Substitution	Yes	Yes	0.06%
CGPLLU168	chr2_25463287-25463287_G_T	Substitution	No	No	0.39%
CGPLLU168	chr7_fa:55259515-55259515_T_G	Substitution	Yes	Yes	0.07%
CGPLLU174	chr19_1220505-1220505_G_T	Substitution	No	Yes	0.33%
CGPLLU174	chr9_5050695-5050695_G_T	Substitution	No	Yes	0.40%
CGPLLU174	chr12_25398285-25398285_C_A	Substitution	Yes	Yes	0.16%
CGPLLU174	chr2_25457216-25457216_G_A	Substitution	No	Yes	0.29%
CGPLLU174	chr2_25463537-25463537_G_C	Substitution	No	Yes	0.26%
CGPLLU175	chr17_7578394-7578394_T_C	Substitution	Yes	Yes	8.03%
CGPLLU175	chr2_25457216-25457216_C_T	Substitution	No	No	0.21%
CGPLLU175	chr2_25463230-25463230_A_G	Substitution	No	No	0.15%
CGPLLU175	chr11_108117798-108117798_C_T	Substitution	NA	Yes	43.84%
CGPLLU175	chr2_212288925-212288925_G_A	Substitution	No	Yes	3.64%
CGPLLU176	chr2_25463245-25463245_G_A	Substitution	No	Yes	0.92%
CGPLLU176	chr2_25463289-25463289_T_C	Substitution	No	Yes	0.12%
CGPLLU177	chr12_25398284-25398284_C_A	Substitution	Yes	Yes	2.49%
CGPLLU177	chr2_25457197-25457197_A_C	Substitution	No	Yes	1.53%
CGPLLU177	chr2_25457243-25457243_G_A	Substitution	Yes	No	0.29%
CGPLLU177	chr2_25463508-25463508_C_T	Substitution	No	No	0.13%
CGPLLU178	chr16_68844164-68844164_C_T	Substitution	No	No	0.29%
CGPLLU178	chr3_178947145-178947145_C_T	Substitution	No	No	0.17%
CGPLLU179	chr2_25457252-25457252_T_C	Substitution	No	Yes	0.38%
CGPLLU179	chr5_112179123-112179123_C_T	Substitution	NA	Yes	39.91%

Wild-type Fragments

Patient	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)
CGPLBR86	3096	88	160	167	174
CGPLBR87	3680	101	162	168	175
CGPLBR87	6180	101	163	164	175
CGPLBR87	7746	86	160	167	175
CGPLBR87	2286	106	160	166	172
CGPLBR88	17537	89	185	200	223
CGPLBR88	5919	101	162	172	173
CGPLBR92	15530	77	150	164	152
CGPLBR96	9893	100	159	164	171
CGPLBR96	8620	95	162	167	173
CGPLBR96	8036	85	162	169	175
CGPLBR97	14856	93	160	168	170
CGPLBR97	5329	100	161	165	171
CGPLBR97	7010	97	158	169	170

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

CGPLLU144	11371	100	156	165	167
CGPLLU144	7641	100	155	167	166
CGPLLU144	9996	100	158	168	169
CGPLLU144	4956	101	159	166	169
CGPLLU144	6540	100	153	170	168
CGPLLU144	7648	101	156	164	166
CGPLLU146	5920	100	155	164	168
CGPLLU146	9356	100	155	166	168
CGPLLU146	7284	101	158	165	170
CGPLLU146	4183	103	160	166	170
CGPLLU146	6778	100	157	166	158
CGPLLU147	4807	100	155	166	170
CGPLLU147	5282	100	156	167	171
CGPLLU147	7122	100	158	174	173
CGPLLU147	2825	101	160	165	173
CGPLLU162	9940	95	161	164	174
CGPLLU162	13855	87	160	174	173
CGPLLU162	11251	100	153	167	165
CGPLLU163	10805	85	159	165	173
CGPLLU163	20185	83	158	166	170
CGPLLU164	8795	91	156	161	169
CGPLLU164	4561	92	157	164	169
CGPLLU164	8097	100	158	170	170
CGPLLU164	9241	100	155	165	157
CGPLLU164	10806	100	157	168	159
CGPLLU164	10919	100	157	168	159
CGPLLU164	5412	103	159	175	170
CGPLLU164	5151	101	160	166	169
CGPLLU165	7448	95	155	167	167
CGPLLU165	5822	102	154	166	166
CGPLLU168	15985	97	152	165	166
CGPLLU168	11070	100	156	165	168
CGPLLU168	11063	83	157	166	169
CGPLLU174	5881	88	162	165	174
CGPLLU174	3696	100	162	167	172
CGPLLU174	4941	101	162	167	172
CGPLLU174	7527	100	163	168	173
CGPLLU174	8353	101	162	168	173
CGPLLU175	10214	100	160	166	170
CGPLLU175	9739	100	157	168	158
CGPLLU175	9509	100	157	165	158
CGPLLU175	2710	101	157	165	157
CGPLLU175	6565	100	158	166	158
CGPLLU176	6513	101	164	168	175
CGPLLU176	5962	100	164	174	175
CGPLLU177	7044	102	160	165	170
CGPLLU177	9950	88	160	169	171
CGPLLU177	11233	100	160	168	171
CGPLLU177	10966	75	160	169	172
CGPLLU178	5378	100	162	176	172
CGPLLU178	7235	101	159	167	170
CGPLLU179	6350	103	161	169	171
CGPLLU179	2609	108	162	171	173

Patient	Patient Type	Stage at Diagnosis	Alteration Type	Gene	Amino Acid (Protein)
CGPLLU180	Lung Cancer	I	Tumor-derived	STK11	237D > Y
CGPLLU180	Lung Cancer	I	Tumor-derived	TP53	293G > V
CGPLLU180	Lung Cancer	I	Tumor-derived	TP53	282R > P
CGPLLU180	Lung Cancer	I	Tumor-derived	TP53	177P > L
CGPLLU180	Lung Cancer	I	Tumor-derived	RB1	565S > X
CGPLLU197	Lung Cancer	I	Hematopoietic	DNMT3A	882R > C
CGPLLU197	Lung Cancer	I	Hematopoietic	DNMT3A	879N > D
CGPLLU198	Lung Cancer	I	Tumor-derived	TP53	162I > N
CGPLLU198	Lung Cancer	I	Tumor-derived	EGFR	858L > R
CGPLLU202	Lung Cancer	I	Tumor-derived	EGFR	790T > M
CGPLLU202	Lung Cancer	I	Tumor-derived	EGFR	868E > X
CGPLLU204	Lung Cancer	I	Tumor-derived	KIT	956R > Q
CGPLLU205	Lung Cancer	II	Hematopoietic	DNMT3A	736R > C
CGPLLU205	Lung Cancer	II	Hematopoietic	DNMT3A	696Q > X
CGPLLU206	Lung Cancer	III	Tumor-derived	TP53	672 + 1G > A
CGPLLU206	Lung Cancer	III	Tumor-derived	TP53	131N > S
CGPLLU207	Lung Cancer	II	Tumor-derived	TP53	376 - 1G > A
CGPLLU207	Lung Cancer	II	Germline	ALK	419P > L

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

CGPLLU207	Lung Cancer	II	Tumor-derived	EGFR	790T > M
CGPLLU208	Lung Cancer	II	Tumor-derived	TP53	250P > L
CGPLLU208	Lung Cancer	II	Germline	EGFR	224R > H
CGPLLU208	Lung Cancer	II	Tumor-derived	EGFR	858L > R
CGPLLU208	Lung Cancer	II	Tumor-derived	MYC	98R > W
CGPLLU209	Lung Cancer	II	Germline	STK11	354F > L
CGPLLU209	Lung Cancer	II	Tumor-derived	TP53	100Q > X
CGPLLU209	Lung Cancer	II	Tumor-derived	CDKN2A	88E > X
CGPLLU209	Lung Cancer	II	Tumor-derived	PDGFRA	921A > T
CGPLLU209	Lung Cancer	II	Germline	EGFR	567M > V
CGPLOV10	Ovarian Cancer	I	Tumor-derived	TP53	342R > X
CGPLOV11	Ovarian Cancer	IV	Tumor-derived	TP53	248R > Q
CGPLOV11	Ovarian Cancer	IV	Germline	TP53	63A > V
CGPLOV13	Ovarian Cancer	IV	Tumor-derived	ALK	444W > C
CGPLOV13	Ovarian Cancer	IV	Germline	PDGFRA	401A > D
CGPLOV13	Ovarian Cancer	IV	Tumor-derived	KIT	135R > H
CGPLOV14	Ovarian Cancer	I	Tumor-derived	HNF1A	230E > K
CGPLOV15	Ovarian Cancer	III	Tumor-derived	TP53	278P > S
CGPLOV15	Ovarian Cancer	III	Tumor-derived	EGFR	433H > D
CGPLOV17	Ovarian Cancer	I	Tumor-derived	TP53	248R > Q
CGPLOV17	Ovarian Cancer	I	Germline	PDGFRA	1071D > N
CGPLOV18	Ovarian Cancer	I	Germline	APC	1125V > A
CGPLOV19	Ovarian Cancer	II	Germline	FGFR3	403K > E
CGPLOV19	Ovarian Cancer	II	Tumor-derived	TP53	273R > H
CGPLOV19	Ovarian Cancer	II	Germline	AR	176S > R
CGPLOV19	Ovarian Cancer	II	Tumor-derived	APC	1378Q > X
CGPLOV20	Ovarian Cancer	II	Tumor-derived	TP53	195I > T
CGPLOV20	Ovarian Cancer	II	Germline	EGFR	253K > R
CGPLOV21	Ovarian Cancer	IV	Germline	STK11	354F > L
CGPLOV21	Ovarian Cancer	IV	Tumor-derived	TP53	275C > Y
CGPLOV21	Ovarian Cancer	IV	Tumor-derived	ERBB4	602S > T
CGPLOV22	Ovarian Cancer	III	Tumor-derived	TP53	193H > P
CGPLOV22	Ovarian Cancer	III	Tumor-derived	CTNNB1	41T > A

Patient	Nucleotide	Mutation Type	Hotspot Alteration	Alteration Detected in Tissue	Mutant Allele Fraction
CGPLLU180	chr19_1220691-1220691_G_T	Substitution	No	You	2.43%
CGPLLU180	chr17_7577060-7577060_C_A	Substitution	No	Yes	2.07%
CGPLLU180	chr17_7577093-7577093_C_G	Substitution	No	Yes	1.94%
CGPLLU180	chr17:fa_7578400-7578400_G_A	Substitution	Yes	No	0.08%
CGPLLU180	chr13_48955578-48955578_C_G	Substitution	No	Yes	1.01%
CGPLLU197	chr2_25457243-25457243_G_A	Substitution	Yes	No	0.16%
CGPLLU197	chr2_25457252-25457252_T_C	Substitution	No	No	0.38%
CGPLLU198	chr17_7578445-7578445_A_T	Substitution	No	Yes	0.87%
CGPLLU198	chr7_55259515-55259515_T_G	Substitution	Yes	Yes	0.52%
CGPLLU202	chr7:fa_55249071-55249071_C_T	Substitution	Yes	Yes	0.05%
CGPLLU202	chr7_55259544-55259544_G_T	Substitution	No	No	0.13%
CGPLLU204	chr4_55604659-55604659_G_A	Substitution	No	No	0.26%
CGPLLU205	chr2_25463287-25463287_G_A	Substitution	No	Yes	0.70%
CGPLLU205	chr2_25463598-25463598_G_A	Substitution	No	Yes	3.47%
CGPLLU206	chr17_7578176-7578176_C_T	Substitution	Yes	Yes	26.13%
CGPLLU206	chr17_7578538-7578538_T_C	Substitution	No	No	0.21%
CGPLLU207	chr17_7578555-7578555_C_T	Substitution	Yes	Yes	0.32%
CGPLLU207	chr2_29606625-29606625_A_G	Substitution	NA	Yes	34.38%
CGPLLU207	chr7:fa_55249071-55249071_C_T	Substitution	Yes	No	0.09%
CGPLLU208	chr17_7577532-7577532_G_A	Substitution	Yes	Yes	1.33%
CGPLLU208	chr7_55220281-55220281_G_A	Substitution	NA	Yes	39.34%
CGPLLU208	chr7_55259515-55259515_T_G	Substitution	Yes	Yes	0.86%
CGPLLU208	chr8_128750755-128750755_C_T	Substitution	No	No	0.17%
CGPLLU209	chr19_1223125-1223125_C_G	Substitution	NA	Yes	26.84%
CGPLLU209	chr17_7579389-7579389_G_A	Substitution	No	Yes	9.97%
CGPLLU209	chr9_21971096-21971096_C_A	Substitution	Yes	Yes	9.13%
CGPLLU209	chr4_55155052-55155052_G_A	Substitution	No	Yes	9.82%
CGPLLU209	chr7_55231493-55231493_A_G	Substitution	NA	Yes	30.41%
CGPLOV10	chr17_7574003-7574003_G_A	Substitution	Yes	Yes	3.14%
CGPLOV11	chr17_7577538-7577538_C_T	Substitution	Yes	Yes	0.87%
CGPLOV11	chr17_7579499-7579499_G_A	Substitution	NA	Yes	37.77%
CGPLOV13	chr2_29551296-29551296_C_A	Substitution	No	Yes	0.12%
CGPLOV13	chr4_55136880-55136880_C_A	Substitution	NA	Yes	37.98%
CGPLOV13	chr4_55564516-55564516_G_A	Substitution	No	Yes	0.35%
CGPLOV14	chr12_121431484-121431484_G_A	Substitution	No	No	0.14%
CGPLOV15	chr17_7577106-7577106_G_A	Substitution	Yes	Yes	3.54%
CGPLOV15	chr7_55225445-55225445_C_G	Substitution	No	No	0.19%

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

CGPLOV17	chr17_7577538-7577538_C_T	Substitution	Yes	Yes	0.32%
CGPLOV17	chr4_55161382-55161382_G_A	Substitution	NA	Yes	44.10%
CGPLOV18	chr5_112174665-112174665_T_C	Substitution	NA	Yes	40.81%
CGPLOV19	chr4_1806186-1806186_A_G	Substitution	NA	Yes	23.80%
CGPLOV19	chr17_7577120-7577120_C_T	Substitution	Yes	Yes	36.83%
CGPLOV19	chrX_66765516-66765516_C_A	Substitution	NA	Yes	65.29%
CGPLOV19	chr5_112175423-112175423_C_T	Substitution	Yes	Yes	46.35%
CGPLOV20	chr17_7578265-7578265_A_G	Substitution	Yes	Yes	0.21%
CGPLOV20	chr7_55221714-55221714_A_G	Substitution	NA	Yes	44.05%
CGPLOV21	chr19_1223125-1223125_C_G	Substitution	NA	Yes	7.68%
CGPLOV21	chr17_7577114-7577114_C_T	Substitution	No	Yes	2.04%
CGPLOV21	chr2_212530114-212530114_C_G	Substitution	No	No	14.36%
CGPLOV22	chr17_7578271-7578271_T_G	Substitution	No	Yes	0.49%
CGPLOV22	chr3_41266124-41266124_A_G	Substitution	Yes	Yes	0.34%

Wild-type Fragments

Patient	Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)	Mode cfDNA Fragment Size (bp)	Median cfDNA Fragment Size (bp)
CGPLLU180	6065	91	158	165	170
CGPLLU180	6680	92	158	164	169
CGPLLU180	7790	92	158	167	168
CGPLLU180	9036	101	160	169	171
CGPLLU180	4679	100	157	169	158
CGPLLU197	7196	102	162	166	172
CGPLLU197	7147	100	161	166	172
CGPLLU198	9322	97	157	165	158
CGPLLU198	8303	100	160	173	172
CGPLLU202	14197	90	151	165	166
CGPLLU202	9279	51	150	168	167
CGPLLU204	7185	100	157	165	168
CGPLLU205	10739	96	156	165	166
CGPLLU205	12065	100	154	165	165
CGPLLU206	6746	94	148	165	164
CGPLLU206	11225	100	147	167	164
CGPLLU207	11224	100	159	165	170
CGPLLU207	4960	101	160	166	170
CGPLLU207	13216	85	161	165	172
CGPLLU208	9211	101	156	166	168
CGPLLU208	5253	100	159	164	170
CGPLLU208	10733	100	160	170	171
CGPLLU208	11421	100	158	165	171
CGPLLU209	11695	96	153	166	159
CGPLLU209	12771	94	155	163	168
CGPLLU209	16557	92	157	169	170
CGPLLU209	13057	97	158	167	171
CGPLLU209	8521	100	155	167	169
CGPLOV10	4421	101	161	165	172
CGPLOV11	7987	100	157	164	169
CGPLOV11	3782	97	160	166	171
CGPLOV13	12072	88	157	165	169
CGPLOV13	4107	103	159	166	169
CGPLOV13	6427	100	161	165	171
CGPLOV14	11418	92	154	166	171
CGPLOV15	7689	102	157	164	169
CGPLOV15	7617	101	159	167	171
CGPLOV17	4463	96	156	168	169
CGPLOV17	2884	110	157	170	170
CGPLOV18	2945	101	159	164	169
CGPLOV19	9727	95	158	167	172
CGPLOV19	4387	100	158	165	169
CGPLOV19	2775	93	161	171	171
CGPLOV19	3616	102	156	170	170
CGPLOV20	5404	94	159	165	170
CGPLOV20	3744	102	158	166	169
CGPLOV21	21823	81	158	166	169
CGPLOV21	18806	101	159	165	169

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

Table 3. Targeted cfDNA fragment analyses in cancer patients					
CGPLOC21	10801	89	160	166	169
CGPLOC22	11952	100	155	165	167
CGPLOC22	12399	92	150	165	164
Mutant Fragments					
Mean cfDNA Fragment Size (bp)	75th Percentile cfDNA Fragment Size (bp)	Maximum cfDNA Fragment Size (bp)	Mutant Fragments		
			Distinct Coverage	Minimum cfDNA Fragment Size (bp)	25th Percentile cfDNA Fragment Size (bp)
179	186	400	19	100	142
182	185	400	21	132	166
180	183	400	5411	92	152
177	182	400	1903	100	148
184	185	400	1344	108	155
181	182	400	2108	100	153
176	180	400	1951	101	149
176	183	399	75	123	162
177	182	400	28	101	130
183	188	399	6863	100	160
188	186	400	34	77	154
175	179	396	9	138	147
184	185	400	21	115	145
179	185	397	30	137	149
179	182	397	44	125	155
185	186	400	8167	101	180
187	186	400	3552	102	158
184	187	399	15	93	137
183	185	400	26	137	163
181	182	397	35	118	147
172	175	400	71	133	152
169	174	400	55	130	153
189	187	390	17	149	155
176	183	400	18	156	170
169	175	397	51	108	143
166	173	397	26	118	147
184	186	400	45	116	151
185	186	400	25	157	165
185	187	400	25	124	168
167	175	394	86	121	155
167	173	397	45	124	143
170	175	396	108	126	147
190	189	400	23	131	148
182	182	399	42	138	155
189	187	399	25	126	153
192	193	400	977	101	149
173	179	391	525	102	140
181	185	399	4010	100	158
178	184	399	625	100	140
175	179	398	37	111	143
181	186	398	3184	102	159
180	183	399	47	111	148
183	184	397	39	111	146
185	184	400	24	110	146
176	180	400	32	117	146
180	184	399	43	111	143
185	187	400	29	109	140
179	182	399	20	128	152
176	184	396	7515	101	160
182	182	399	31	85	145
181	182	395	428	100	135
176	180	397	352	97	136
165	172	397	15	131	137
170	173	398	25	107	138
171	173	400	27	122	147
189	169	400	91	112	165
189	169	400	27	124	144
178	184	399	24	105	143
188	189	399	8	122	143
194	192	400	17	144	163
180	183	394	15	132	159
183	185	399	233	131	162

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

Mutant Fragments					Difference between Median Mutant	Difference between Mean Mutant	Adjusted P Value of Difference between
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)	and Wild type cfDNA Fragment Size (bp)	and Wild-type cfDNA Fragment Size (bp)	Mutant and Wild-type cfDNA Fragment Size
186	186	186	186	398	27	136	155
192	195	195	195	399	23	137	144
182	184	184	184	399	29	131	157
233	165	180	230	305	-4.0	1.54	0.475
182	176	191	198	309	7.0	8.33	0.250
167	169	186	191	399	0.0	5.89	0.000
166	166	177	183	383	-1.0	-0.25	0.874
167	170	189	191	398	1.0	5.37	0.009
166	168	185	187	386	1.0	3.80	0.025
175	167	179	182	397	0.0	2.65	0.148
167	172	182	190	370	3.0	5.31	0.368
130	139	164	155	345	-29.5	-12.79	0.000
165	173	185	159	400	2.0	3.13	0.002
171	170	177	192	335	-0.5	-11.46	0.571
176	171	177	176	290	4.0	1.22	0.475
155	159	176	175	368	-11.0	-7.99	0.052
181	162	182	161	369	-8.0	3.49	0.061
155	169	185	194	338	0.0	5.78	0.623
166	171	184	187	400	-1.0	-1.27	0.212
168	170	185	185	399	0.0	-2.62	0.114
127	174	173	193	261	3.0	-11.00	0.507
166	167	179	180	364	-3.0	-4.34	0.430
176	163	172	176	336	-6.0	-9.35	0.166
170	165	169	173	301	0.0	3.57	0.668
165	164	166	166	325	0.0	-2.15	0.630
326	170	221	301	387	-3.0	32.43	0.453
174	174	210	219	372	5.0	33.84	0.368
268	152	164	176	268	-12.0	-5.12	0.000
153	156	174	158	327	-9.5	8.37	0.036
168	163	175	177	346	-8.0	-8.84	0.057
191	175	207	199	350	3.0	22.93	0.456
180	180	189	191	338	8.0	4.06	0.154
169	166	168	175	309	2.0	0.46	0.445
197	162	166	168	377	-1.0	-0.91	0.482
162	162	164	174	302	-3.0	-6.74	0.064
145	166	189	205	333	-5.0	-0.80	0.297
155	174	177	187	343	5.5	-4.51	0.171
176	176	188	229	305	7.0	-0.19	0.234
189	170	182	192	380	-1.0	-9.76	0.000
168	159	168	176	382	-7.0	-5.57	0.052
166	170	181	185	398	0.0	0.37	0.770
167	162	172	181	380	-9.0	-6.68	0.009
142	166	172	186	321	-1.0	-2.36	0.572
168	172	182	187	400	0.5	0.95	0.564
144	169	176	153	353	-1.0	-4.83	0.598
182	162	182	155	337	-7.0	-0.44	0.064
309	182	208	284	355	14.0	22.31	0.031
154	157	167	166	298	-11.0	-8.94	0.013
144	177	187	212	319	9.0	7.22	0.062
204	159	186	204	387	-12.0	3.32	0.031
180	163	166	180	219	-6.5	-13.04	0.155
170	171	177	185	400	1.0	1.08	0.166
137	166	167	176	316	-3.0	-14.62	0.469
138	149	158	166	340	-20.0	-23.47	0.000
132	147	149	159	326	21.0	26.04	0.000
132	144	163	171	323	-20.0	-1.73	0.000
159	161	175	190	299	-3.0	4.83	0.384
161	161	173	171	342	-3.0	2.54	0.354
168	173	196	192	397	1.0	6.83	0.571
154	154	167	172	320	-19.0	-22.39	0.000
132	159	183	190	367	-11.0	4.67	0.054
122	161	168	195	241	-13.0	-19.21	0.100

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

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)		
173	173	213	372	1.0	19.22	0.587	
186	166	174	185	265	-3.0	-5.62	0.461
167	172	190	187	394	2.0	7.27	0.137
183	163	170	178	262	-7.0	-16.03	0.131
175	152	190	212	327	-17.0	-1.78	0.018
177	171	183	179	319	-1.0	-0.74	0.564

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)
166	172	396	1616	100	146
175	180	400	806	96	158
165	172	399	1410	102	140
170	177	397	49	99	153
166	173	398	33	140	155
180	178	400	73	95	140
172	177	400	38	115	160
171	174	386	6	124	137
180	183	400	70	124	151
191	199	399	6586	96	162
184	188	400	41	112	172
181	198	399	35	149	168
182	184	399	20	166	180
183	186	397	5338	102	159
202	203	393	178	101	150
195	195	397	1350	104	153
185	189	400	1257	100	153
185	189	396	30	117	163
203	210	391	336	105	153
188	194	399	741	101	161
193	193	396	89	100	145
172	179	396	12	129	143
186	188	387	3559	91	155
177	183	392	873	102	149
194	200	377	1909	100	158
202	259	400	27	122	157
171	178	395	1818	103	147
178	182	374	546	102	151
179	184	397	26	132	142
195	194	400	53	117	157
176	179	397	40	124	150
188	191	390	38	107	153
205	207	399	217	102	146
196	195	397	266	111	147
186	184	400	76	123	157
179	186	400	9832	93	161
191	190	400	277	104	162
191	189	400	65	123	165
187	189	400	31	136	163
202	202	400	5286	102	166
196	201	400	102	138	166
181	182	397	30	138	158
181	181	400	64	113	158
176	179	398	27	121	163
191	192	398	2943	100	165
179	181	399	25	138	153
171	177	399	60	110	136
172	179	399	26	139	147
186	184	398	35	121	149
176	178	397	4000	103	155
176	178	385	2390	99	157
182	184	400	28	131	160
194	193	400	3545	100	161
179	180	398	15	121	146
188	187	400	2587	103	158
189	192	400	86	121	165
178	184	399	3339	101	157
179	187	391	3193	101	163
183	186	398	13	111	153

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

Mutant Fragments					Difference between Median Mutant	Difference between Mean Mutant	Adjusted P Value of Difference between
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)	and Wild type cfDNA Fragment Size (bp)	and Wild-type cfDNA Fragment Size (bp)	Mutant and Wild-type cfDNA Fragment Size
197	201	400	4140	102	166		
191	194	400	16	130	143		
183	183	400	209	125	154		
211	230	400	41	158	176		
193	193	400	3445	94	162		
197	199	400	23	123	182		
193	195	399	1787	100	163		
204	207	400	4100	100	159		
164	159	163	170	354	-3.5	-3.57	0.000
169	169	173	184	366	1.0	3.80	0.054
149	154	164	170	398	-8.0	-0.35	0.816
143	182	206	284	333	16.0	36.25	0.000
154	170	108	180	296	7.0	14.38	0.104
140	155	173	178	324	-9.0	-6.66	0.000
164	167	182	179	329	1.5	10.09	0.479
170	156	153	168	178	-7.5	-18.98	0.411
151	164	182	183	385	-6.0	1.71	0.064
168	175	193	196	399	0.0	-1.79	0.166
176	177	195	195	373	3.0	11.02	0.397
175	175	181	186	312	1.0	-13.40	0.587
185	191	205	219	357	21.0	23.48	0.013
175	171	183	185	394	-1.0	0.03	0.984
168	171	198	240	357	-5.0	-4.34	0.571
163	171	201	258	400	0.0	5.94	0.066
168	170	189	202	392	1.0	4.37	0.064
164	172	175	179	372	3.0	-10.29	0.463
141	171	200	240	399	4.0	3.10	0.571
169	176	190	194	400	2.0	1.96	0.571
171	171	197	229	393	-2.0	3.42	0.479
143	153	163	166	275	-14.0	-8.99	0.084
164	173	195	211	398	3.0	5.92	0.001
163	164	177	181	400	-3.0	-0.39	0.880
167	176	202	242	398	5.0	7.98	0.061
164	179	199	231	350	2.0	-3.82	0.685
169	162	173	180	396	1.0	1.92	0.372
166	166	180	182	381	0.0	2.87	0.416
138	171	183	188	351	1.5	3.29	0.572
165	169	192	198	336	-3.0	-2.86	0.451
169	166	181	176	309	-1.0	4.53	0.539
180	174	185	210	326	0.5	-2.59	0.576
144	163	188	212	360	-12.0	-17.11	0.004
150	166	188	204	379	-8.0	-7.53	0.208
171	169	182	182	346	1.0	-3.64	0.479
166	172	180	186	399	-1.0	1.04	0.155
160	176	201	200	384	3.0	9.95	0.061
166	172	198	192	371	1.0	7.08	0.560
171	167	201	199	387	-4.0	14.14	0.341
168	181	201	203	400	2.0	-0.86	0.587
161	179	199	209	372	-1.5	2.90	0.679
189	185	191	191	311	16.0	9.25	0.000
163	167	179	176	318	0.0	-2.85	0.679
200	171	187	190	392	5.0	10.89	0.314
176	176	187	192	398	0.0	-3.83	0.015
138	167	181	184	340	-1.0	2.00	0.571
147	147	161	159	327	-19.0	-9.77	0.000
180	176	176	184	344	9.0	3.52	0.015
360	161	197	195	360	-9.0	10.77	0.314
166	167	176	178	397	0.5	0.65	0.610
164	168	178	180	400	0.0	1.78	0.314
168	167	177	179	338	-2.0	-5.83	0.463
169	173	194	192	399	0.0	0.40	0.825
166	166	172	204	221	-2.0	-7.32	0.564

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

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)		
162	169	189	186	399	-1.0	1.12	0.598
183	177	189	193	373	3.0	-0.01	0.293
165	169	177	184	400	0.0	-1.73	0.598
178	173	180	186	389	1.0	0.22	0.839
153	161	171	179	323	-11.0	-12.36	0.061
169	179	197	200	400	0.0	-0.32	0.839
143	157	173	173	325	-20.0	-18.40	0.000
175	170	196	233	357	1.0	12.55	0.025
197	186	215	220	374	1.0	3.72	0.603
175	174	194	194	399	0.0	0.65	0.714
248	224	232	260	359	47.0	34.97	0.000
163	176	192	194	400	1.0	-0.85	0.718
164	173	200	202	400	-2.0	-3.65	0.062

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)
196	195	400	3096	79	159
202	203	400	73	142	178
205	203	400	23	161	168
195	196	400	170	125	158
195	192	400	2089	101	162
238	280	400	125	84	192
197	194	400	5715	108	163
172	173	398	109	78	148
196	191	399	35	119	161
189	190	400	826	102	162
194	195	400	95	135	160
184	184	400	27	128	150
179	184	399	4771	103	161
187	185	399	7	417	154
179	179	395	330	106	152
172	177	399	536	106	151
179	183	400	45	136	163
182	182	397	16	138	146
172	177	397	293	101	152
171	177	399	23	130	152
180	183	399	54	104	161
184	184	400	154	96	149
186	187	399	79	102	163
183	185	400	44	118	149
182	184	400	35	136	164
192	191	400	13	138	164
199	205	400	50	128	155
191	193	400	81	108	150
190	191	389	2597	101	159
192	197	400	58	92	173
183	189	400	74	90	147
175	178	400	37	144	163
194	202	400	61	93	164
184	186	400	66	104	158
191	190	396	101	126	155
188	185	394	4718	100	156
186	186	399	30	134	161
180	180	397	34	139	163
182	182	400	262	101	150
182	182	400	277	101	150
180	182	395	65	121	158
177	182	400	16	144	172
185	184	399	7186	100	154
181	179	394	21	108	164
177	180	400	18	111	127
179	181	400	72	121	156
177	182	400	30	106	160
200	199	399	36	131	147
184	185	392	20	144	173
182	184	395	16	147	156
186	187	399	34	159	168
186	186	396	5	116	182

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

Mutant Fragments					Difference between Median Mutant	Difference between Mean Mutant	Adjusted P Value of Difference between
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)	and Wild type cfDNA Fragment Size (bp)	and Wild-type cfDNA Fragment Size (bp)	Mutant and Wild-type cfDNA Fragment Size
185	183	399	1073	100	142		
179	180	400	46	109	151		
181	181	400	30	146	154		
176	179	392	2742	102	154		
174	180	399	298	103	140		
197	194	399	67	115	164		
195	194	399	19	156	165		
178	182	395	189	105	138		
183	185	398	227	123	160		
185	184	397	53	78	161		
190	188	395	50	130	161		
186	187	398	28	139	150		
179	184	400	24	130	153		
185	185	394	48	111	154		
189	187	398	2337	100	163		
161	173	194	191	397	-1.0	-2.45	0.251
178	184	237	338	377	9.0	35.30	0.114
168	171	189	186	380	-4.0	-16.38	0.435
173	173	188	190	400	-2.0	-6.17	0.293
169	176	203	203	400	4.5	8.80	0.000
194	207	243	324	400	-16.0	5.51	0.574
164	174	200	196	400	1.0	2.87	0.065
149	158	166	173	302	-4.0	-5.94	0.190
172	171	191	180	390	0.0	-4.34	0.627
166	171	187	187	395	-2.0	-1.94	0.475
161	170	182	184	400	-5.0	-11.54	0.155
150	169	174	185	319	-1.0	-9.68	0.571
168	171	179	183	400	0.0	0.15	0.880
154	167	164	174	117	-3.0	-22.90	0.155
165	166	178	178	361	-1.0	-1.35	0.685
167	163	172	175	363	-3.0	-0.34	0.880
175	172	185	191	380	3.0	6.52	0.368
146	155	162	170	224	-14.0	-19.82	0.007
169	164	170	174	392	2.0	1.37	0.646
162	162	163	177	232	-4.0	-7.62	0.252
154	176	195	206	383	7.5	14.58	0.064
157	163	176	185	347	-5.5	-7.87	0.154
177	174	200	203	372	4.0	14.61	0.270
163	163	185	186	338	-7.0	1.98	0.039
204	181	194	203	369	13.0	11.80	0.039
169	169	198	173	333	-1.0	6.05	0.610
161	171	216	301	360	0.0	17.02	0.623
108	173	198	224	385	0.0	6.48	0.624
165	172	185	187	397	-1.0	-5.17	0.005
192	192	202	200	397	18.0	9.79	0.007
142	167	176	182	391	-6.5	-6.78	0.061
185	172	192	186	375	6.0	17.15	0.005
181	181	197	211	370	8.0	3.34	0.169
194	174	189	194	379	3.5	4.60	0.270
176	176	194	213	331	7.0	2.50	0.718
164	168	190	187	393	-1.0	2.54	0.113
175	175	190	208	339	5.0	4.07	0.302
165	170	178	175	349	3.0	-1.65	0.407
152	165	181	186	393	-4.0	-0.65	0.876
147	166	182	185	393	-3.0	0.36	0.926
161	167	186	188	338	-4.0	6.15	0.234
179	179	187	180	376	10.0	9.98	0.130
167	166	183	181	396	-1.0	-1.73	0.154
164	173	196	200	357	7.0	14.95	0.213
127	158	189	186	352	-8.0	12.47	0.179
173	166	183	179	396	-2.0	4.31	0.427
174	174	180	156	282	5.0	3.09	0.252

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

143	177	196	227	298	2.5	-4.24	0.479
266	178	199	215	269	6.0	15.13	0.252
156	164	177	169	302	8.0	4.82	0.119
168	176	206	196	365	3.0	20.55	0.415
182	185	201	192	329	12.0	14.62	0.263
164	152	157	164	346	-18.0	-27.67	0.000
143	175	174	183	325	7.0	-5.22	0.054
146	168	186	181	367	-0.5	5.19	0.568
164	166	176	176	387	-1.0	-0.24	0.874
148	150	152	162	288	-18.0	-22.25	0.000
250	173	187	201	366	2.0	9.89	0.425
165	185	197	199	361	10.0	2.20	0.154
141	150	164	175	348	-20.0	-14.58	0.000
168	169	185	184	396	-2.0	1.68	0.706
175	175	189	158	392	4.0	3.80	0.241
168	168	184	175	377	-4.5	-5.86	0.234
173	170	170	173	354	-2.5	-15.88	0.416
176	170	193	199	359	0.0	13.13	0.598
170	168	173	183	295	-3.0	-11.80	0.270
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)
198	200	396	172	83	152
190	188	400	215	123	151
184	184	400	207	121	151
191	189	397	17	143	170
181	182	398	52	122	152
191	189	399	17	109	161
191	189	399	40	136	164
180	181	399	127	88	149
181	186	400	68	141	166
169	179	398	10	81	167
170	181	398	33	107	162
175	181	391	23	112	156
175	177	400	109	130	153
172	176	400	684	105	153
179	178	398	2946	100	138
175	178	399	30	121	165
187	186	400	63	140	155
181	184	400	4754	101	160
182	187	400	31	131	162
181	183	400	150	110	144
179	184	400	5290	95	159
181	186	400	140	101	155
187	190	397	20	92	141
190	192	400	8065	85	156
174	182	400	2586	101	147
185	188	400	2808	100	150
182	187	400	2227	100	154
176	183	396	8425	100	155
186	188	399	142	112	146
186	185	399	104	132	158
183	185	392	3462	101	160
182	183	399	25	94	140
177	181	399	3789	101	159
181	184	400	57	131	152
183	191	400	36	118	154
187	185	399	362	110	152
182	188	400	20	158	163
185	187	397	23	126	151
188	189	400	2980	100	158
183	163	391	2793	91	158
185	189	395	7357	100	158
184	184	398	5186	101	157
182	187	400	15595	64	159
186	185	400	6749	101	158
193	190	400	23	127	148

APPENDIX C-continued

Table 3. Targeted cfDNA fragment analyses in cancer patients

Table 3. Targeted cfDNA fragment analyses in cancer patients							
Mutant Fragments					Difference between Median Mutant	Difference between Mean Mutant	Adjusted P Value of Difference between
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)	and Wild type cfDNA Fragment Size (bp)	and Wild-type cfDNA Fragment Size (bp)	Mutant and Wild-type cfDNA Fragment Size
182	185	394	3901	101	160		
179	180	400	4633	100	158		
175	179	400	734	101	151		
175	180	394	4022	101	159		
184	182	400	117	116	156		
172	176	395	65	109	145		
160	166	193	226	396	-4.0	-4.93	0.490
159	163	188	196	365	-6.0	-1.72	0.735
157	161	181	179	365	-7.0	-3.01	0.571
217	214	198	217	294	43.0	7.08	0.000
167	164	179	173	372	-4.5	-2.07	0.137
173	171	181	174	392	-1.0	-9.24	0.576
166	171	185	185	335	-1.0	-5.86	0.571
131	162	168	178	311	-6.0	-11.80	0.005
175	176	198	207	387	4.0	17.11	0.184
167	167	159	176	182	1.0	-10.20	0.589
167	167	174	185	322	0.0	4.57	0.636
190	164	175	190	349	-4.0	-0.92	0.308
169	166	175	178	382	0.0	-0.09	0.987
167	166	172	175	385	1.0	0.00	0.999
157	155	172	174	398	-9.0	-7.28	0.000
165	176	198	219	325	12.0	22.37	0.007
154	167	201	215	372	-3.0	13.70	0.286
170	170	179	161	393	0.0	-1.72	0.154
162	174	180	185	352	2.0	2.26	0.494
166	162	176	173	385	-6.0	-5.86	0.314
167	169	179	164	400	-1.0	0.11	0.909
175	167	179	180	352	-4.5	-2.77	0.589
241	168	178	209	283	-3.0	-9.82	0.479
164	169	190	190	399	0.0	-0.08	0.942
165	165	169	179	386	-3.5	-4.59	0.000
158	167	189	200	399	-3.0	4.17	0.007
162	171	183	190	398	0.0	1.00	0.564
165	169	176	184	400	0.0	0.54	0.568
140	159	180	193	352	-13.0	-5.41	0.463
159	167	189	180	331	-2.0	3.05	0.657
173	172	184	167	396	1.0	0.82	0.576
140	158	159	163	341	-11.0	-23.47	0.027
168	169	176	161	395	0.0	-0.66	0.576
170	170	179	184	327	-1.0	-2.41	0.568
201	182	187	201	328	11.0	3.60	0.114
143	180	207	268	389	11.0	20.70	0.000
311	174	198	209	311	3.0	15.25	0.475
184	168	185	185	328	-1.0	-1.49	0.571
169	170	187	189	398	0.0	-0.84	0.637
167	170	161	182	389	1.0	-2.30	0.171
175	171	162	187	399	-1.0	-2.37	0.008
165	170	185	186	400	1.0	1.72	0.240
167	170	181	185	397	-1.0	-1.39	0.245
167	170	185	187	400	0.0	-0.52	0.702
148	194	222	292	378	24.0	29.58	0.027
167	171	182	155	398	2.0	0.32	0.821
169	170	185	157	400	1.0	6.16	0.000
155	165	176	178	366	-4.0	0.48	0.823
167	168	172	178	399	-1.0	-2.84	0.000
156	172	199	184	399	5.0	15.08	0.084
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	3081312000	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	7357346200	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	568043600	2.23
CGCRC307	Preoperative treatment naïve	WGS	Colorectal Cancer	100	8034720400	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 81	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	11710246400	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	6320133800	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	9346936200	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	5502597200	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

APPENDIX-D-continued

Table 4 Summary of whole genome cfDNA analyses

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGPLBR49	Preoperative treatment naïve	WGS	Breast Cancer	100	7311195000	4559460200	1.81
CGPLBR50	Preoperative treatment naïve	WGS	Breast Cancer	100	11107960600	7582776600	3.01
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	5059873200	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
CGPLBR63	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	18418841400	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
CGPLBR83	Preoperative treatment naïve	WGS	Breast Cancer	100	8665810400	5499893200	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	6493593000	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
CGP6H197	Preoperative treatment naïve	WGS	Healthy	100	11961841600	3052855200	3.20
CGPLH193	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	6208766806	4171843400	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	6696983600	2.66
CGPLH208	Preoperative treatment naïve	WGS	Healthy	100	12796300000	3272073400	3.28
CGPLH209	Preoperative treatment naïve	WGS	Healthy	100	13123035400	3531813600	3.39
CGPLH210	Preoperative treatment naïve	WGS	Healthy	100	10184218800	6832204600	2.71
CGPLH211	Preoperative treatment naïve	WGS	Healthy	100	14655260200	3887067600	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	6112544000	2.43
CGPLH327	Preoperative treatment naïve	WGS	Healthy	100	8239168800	5351280200	2.12
CGPLH328	Preoperative treatment naïve	WGS	Healthy	100	7197086300	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

APPENDIX-D-continued

Table 4 Summary of whole genome cfDNA analyses

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
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
CGPLH342	Preoperative treatment naïve	WGS	Healthy	100	8633413000	5701972400	2.26
CGPLH343	Preoperative treatment naïve	WGS	Healthy	100	6694769800	4410670860	1.75
CGPLH344	Preoperative treatment naïve	WGS	Healthy	100	7628192400	4961476600	1.97
CGPLH345	Preoperative treatment naïve	WGS	Healthy	100	7121569406	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	7059351600	4752309400	1.89
CGPLH353	Preoperative treatment naïve	WGS	Healthy	100	8435782400	5215098200	2.09
CGPLH354	Preoperative treatment naïve	WGS	Healthy	100	8018644000	4857577660	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	3914810400	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	6111382800	3965952400	1.57
CGPLH364	Preoperative treatment naïve	WGS	Healthy	100	10823490400	7195657000	2.86
CGPLH365	Preoperative treatment naïve	WGS	Healthy	100	5938367400	3954556200	1.57
CGPLH366	Preoperative treatment naïve	WGS	Healthy	100	7063168600	4731853060	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	9237170006	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	10767862800	4.27
CGPLH382	Preoperative treatment naïve	WGS	Healthy	100	18474025200	12276437200	4.87
CGPLH383	Preoperative treatment naïve	WGS	Healthy	100	13215954000	8430420600	3.36
CGPLH384	Preoperative treatment naïve	WGS	Healthy	100	8481814000	5463636260	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
CGPLH393	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	2912027800	1.18
CGPLH403	Preoperative treatment naïve	WGS	Healthy	100	6470913200	3549172600	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

APPENDIX-D-continued

Table 4 Summary of whole genome cfDNA analyses

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
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	70143072800	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
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	6965093800	2.76
CGPLH435	Preoperative treatment naïve	WGS	Healthy	100	6747793800	5677115290	2.29
CGPLH436	Preoperative treatment naïve	WGS	Healthy	100	7990589400	5228737800	2.07
GGPLH437	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	5795941660	2.26
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	4415186060	1.79
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	6692520006	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	6314830460	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	3853071400	6084059400	2.41
CGPLH475	Preoperative treatment naïve	WGS	Healthy	100	8115374000	5291718000	2.10
CGPLH476	Preoperative treatment naïve	WGS	Healthy	100	8163162000	5096869660	2.02
CGPLH477	Preoperative treatment naïve	WGS	Healthy	100	8350093206	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	7832983200	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

APPENDIX-D-continued

Table 4 Summary of whole genome cfDNA analyses

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGPLH485	Preoperative treatment naïve	WGS	Healthy	100	8371255406	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	545316000	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
CGPLH499	Preoperative treatment naïve	WGS	Healthy	100	10221293600	6951282800	2.76
CGPLH50	Preoperative treatment naïve	WGS	Healthy	100	41248860600	4073272890	10.78
CGPLH500	Preoperative treatment naïve	WGS	Healthy	100	9703168209	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	9019992209	6100383400	2.42
CGPLH504	Preoperative treatment naïve	WGS	Healthy	100	9320330200	6109750200	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	7105271400	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	0013937000	3.18
CGPLH518	Preoperative treatment naïve	WGS	Healthy	100	12804517400	3606661600	3.42
CGPLH519	Preoperative treatment naïve	WGS	Healthy	100	11513222200	7922798400	3.14
CGPLH52	Preoperative treatment naïve	WGS	Healthy	100	49247304200	4849531400	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
CGPLH51	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	9.26
CGPLH639	Preoperative treatment naïve	WGS	Healthy	100	8158965890	5216049600	2.07
CGPLH64	Preoperative treatment naïve	WGS	Healthy	100	34275506800	3264503000	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	251713861400	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	4856643600	1.93

APPENDIX-D-continued

Table 4 Summary of whole genome cfDNA analyses

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGPLLU14	Pre-treatment, Day-3	WGS	Lung Cancer	100	7653473000	4816193600	1.91
CGPLLU14	Pre-treatment, Day 0	WGS	Lung Cancer	100	7351997400	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	7102000000	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	32344959200	2218577200	5.86
CGPLLU202	Preoperative treatment naïve	WGS	Lung Cancer	100	21110128200	1831279400	4.84
CGPLLU203	Preoperative treatment naïve	WGS	Lung Cancer	100	4304235600	2806429000	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
CGPLLU944	Post-treatment, Day 6	WGS	Lung Cancer	100	9535898600	6452174000	2.56
CGPLLU244	Post-treatment, Day 62	WGS	Lung Cancer	100	6783628000	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	9143025000	6431013200	2.55
CGPLLU245	Post-treatment, Day 21	WGS	Lung Cancer	100	9072713800	6368533000	2.53
CGPLLU946	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	9012645000	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	2.49
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	3931976400	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	6227735060	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	3.09
CGPLLU269	Pre-treatment, Day 0	WGS	Lung Cancer	100	9170168000	5830454400	2.31
CGPLLU269	Post-treatment, Day 9	WGS	Lung Cancer	100	8905640400	5290461400	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	6407811200	5203486400	2.06
CGPLLU43	Post-treatment, Day 6	WGS	Lung Cancer	100	9964335200	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	5875064200	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	8505475400	2.18
CGPLLU88	Post-treatment, Day 7	WGS	Lung Cancer	100	0283192200	5784217600	2.30
CGPLLU88	Post-treatment, Day 297	WGS	Lung Cancer	100	9297110800	6407258000	2.54

APPENDIX-D-continued

Table 4 Summary of whole genome cfDNA analyses

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGPLLU89	Pre-treatment, Day 0	WGS	Lung Cancer	100	7042145200	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	8562142400	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	5605165800	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
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
CCPLOW48	Preoperative treatment naïve	WGS	Ovarian Cancer	100	9258552600	6380106400	2.53
CGPLOW49	Preoperative treatment naïve	WGS	Ovarian Cancer	100	8787025400	6134503600	2.43
CGFLOV50	Preoperative treatment naïve	WGS	Ovarian Cancer	100	10144154400	6984721400	2.77
CGPLPA2	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	8062012400	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	8750665600	5800613200	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	9345385800	6728653000	2.67
CGPLPA165	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	8356604600	0829895800	2.31
CGPLPA168	Preoperative treatment naïve	WGS	Bile Duct Cancer	100	10365661600	7048115600	2.80
CGPLPA17	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8073547400	4687803000	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	2.21
CGPLPA28	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8477461600	5688846800	2.26
CGPLPA33	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7287615600	4506723800	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

APPENDIX-D-continued

Table 4 Summary of whole genome cfDNA analyses

Patient	Timepoint	Analysis type	Patient Type	Read Length	Total Bases Sequenced	High Quality Bases Analyzed	Coverage
CGPLPA39	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	10502663600	6812333000	2.70
CGPLPA40	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9083670000	0394717800	2.14
CGPLPA42	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	5072126600	3800395200	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	1.90
CGPLPA52	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	5655875000	3551861600	1.41
COPLPA53	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	9617773600	3.82
CGPLPA67	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	8222177400	5351172000	2.12
CGPLPA69	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7899181400	5006114800	1.90
CGPLPA71	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	7340620400	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	10853223000	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	Pancreatic Cancer	100	6637004600	4545072600	1.80
CGST11	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9718427800	6259679600	2.48
CGST110	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9319661600	6359317400	2.52
CGST114	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	6865213000	4841171600	1.92
CGST13	Preoperative treatment naïve	WGS	Pancreatic Cancer	100	9284554800	6360843800	2.52
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	5494881200	5038064000	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 Profile of Healthy Individuals	Correlation of GC Corrected Fragment Ratio Profile to Median Profile of Healthy Individuals	Correlation of Fragment Ratio Profile to Median Profile of Lymphocytes	Correlation of Fragment Ratio Profile to 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

APPENDIX E-continued

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 of Healthy Individuals	Correlation of GC Corrected Fragment Ratio Profile to Median Fragment Ratio of Healthy Individuals	Correlation of Fragment Ratio Profile to Median Fragment Ratio of Lymphocytes	Correlation of Fragment Ratio Profile to Nucleosome Distances
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
CGPLH51	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	0.985	0.953	-0.923
CGPLH63	Healthy	WGS	Preoperative treatment naïve	NA	168	0.977	0.968	0.939	-0.920
CAPLH51	Healthy	WGS	Preoperative treatment naïve	NA	168	0.935	0.955	0.957	-0.914
CAPLH57	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	160	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)
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-38	IV	15.4
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-16	IV	15.4
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-3	IV	15.4
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	15.4
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 0.33	IV	15.4
CGPLLU14	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	15.4
CGPLLU88	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	18.0
CGPLLU88	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	18.0
CGPLLU88	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 297	IV	18.0

APPENDIX F-continued

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

CGPLLU244	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-7	IV	1.2
CGPLLU244	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-1	IV	1.2
CGPLLU244	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 6	IV	1.2
CGPLLU244	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 62	IV	1.2
CGPLLU245	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-32	IV	1.7
CGPLLU245	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	1.7
CGPLLU245	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	1.7
CGPLLU245	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 21	IV	1.7
CGPLLU246	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-21	IV	1.3
CGPLLU246	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	1.3
CGPLLU246	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 9	IV	1.3
CGPLLU246	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 42	IV	1.1
CGPLLU86	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	12.4
CGPLLU86	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 0.5	IV	12.4
CGPLLU86	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	12.4
CGPLLU86	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 17	IV	12.4
CGPLLU89	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	6.7
CGPLLU89	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	6.7
CGPLLU89	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 22	IV	6.7
CGLU316	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-53	IV	1.4
CGLU316	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-4	IV	1.4
CGLU316	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 18	IV	1.4
CGLU316	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 87	IV	1.4
CGLU344	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-21	IV	Ongoing
CGLU344	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	Ongoing
CGLU344	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 0.1675	IV	Ongoing
CGLU344	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 59	IV	Ongoing
CGLU369	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-2	IV	7.5
CGLU369	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 12	IV	7.5
CGLU369	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 68	IV	7.5
CGLU369	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 110	IV	7.5
CGLU373	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-2	IV	Ongoing
CGLU373	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 0.125	IV	Ongoing
CGLU373	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	Ongoing
CGLU373	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 47	IV	Ongoing
CGPLLU13	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-2	IV	1.5
CGPLLU13	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 5	IV	1.5
CGPLLU13	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 28	IV	1.5
CGPLLU13	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 91	IV	1.5
CGPLLU264	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-1	IV	Ongoing
CGPLLU264	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 6	IV	Ongoing
CGPLLU264	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 27	IV	Ongoing
CGPLLU264	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 69	IV	Ongoing
CGPLLU265	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	Ongoing
CGPLLU265	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 3	IV	Ongoing
CGPLLU265	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 7	IV	Ongoing
CGPLLU265	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 84	IV	Ongoing
CGPLLU266	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	9.6
CGPLLU266	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 16	IV	9.6
CGPLLU266	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 83	IV	9.6
CGPLLU266	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 328	IV	9.6
CGPLLU267	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-1	IV	3.9
CGPLLU267	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 34	IV	3.9
CGPLLU267	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 90	IV	3.9
CGPLLU269	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	Ongoing
CGPLLU269	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 9	IV	Ongoing
CGPLLU269	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 28	IV	Ongoing
CGPLLU271	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day 0	IV	8.2
CGPLLU271	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 6	IV	8.2
CGPLLU271	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 20	IV	8.2
CGPLLU271	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 104	IV	8.2
CGPLLU271	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 259	IV	8.2
CGPLLU43	Lung Cancer	Targeted Mutation Analysis and WGS	Pre-treatment, Day-1	IV	Ongoing
CGPLLU43	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 6	IV	Ongoing
CGPLLU43	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 27	IV	Ongoing
CGPLLU43	Lung Cancer	Targeted Mutation Analysis and WGS	Post-treatment, Day 83	IV	Ongoing

APPENDIX F-continued

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

Patient	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	0.941	-0.841	EGFR 861L > Q	0.89%
CGPLLU14	0.933	-0.833	EGFR 861L > Q	0.18%
CGPLLU14	0.908	-0.814	EGFR 719G > S	0.49%
CGPLLU14	0.883	-0.752	EGFR 861L > Q	1.39%
CGPLLU14	0.820	-0.692	EGFR 719G > S	1.05%
CGPLLU14	0.927	-0.887	EGFR 861L > Q	0.00%
CGPLLU88	0.657	-0.584	EGFR 7459ELREA > T	9.06%
CGPLLU88	0.939	-0.799	EGFR 790T > M	0.15%
CGPLLU88	0.946	-0.869	EGFR 7459ELREA > T	0.93%
CGPLLU244	0.850	-0.706	EGFR 858L > R	4.98%
CGPLLU244	0.867	-0.764	EGFR 62L > R	3.41%
CGPLLU244	0.703	-0.639	EGFR 858L > R	5.57%
CGPLLU244	0.659	-0.660	EGFR 858L > R	11.80%
CGPLLU245	0.871	-0.724	EGFR 745KELREA > K	10.60%
CGPLLU245	0.736	-0.608	EGFR 745KELREA > K	14.10%
CGPLLU245	0.731	-0.559	EGFR 745KELREA > K	8.56%
CGPLLU245	0.613	-0.426	EGFR 745KELREA > K	10.69%
CGPLLU246	0.897	-0.757	EGFR 790T > M	0.49%
CGPLLU246	0.469	-0.376	EGFR 858L > R	6.17%
CGPLLU246	0.874	-0.746	EGFR 858L > R	1.72%
CGPLLU246	0.775	-0.665	EGFR 858L > R	5.29%
CGPLLU86	0.817	-0.630	EGFR 746ELREATS > D	0.00%
CGPLLU86	0.916	-0.811	EGFR 746ELREATS > D	0.19%
CGPLLU86	0.859	-0.694	EGFR 746ELREATS > D	0.00%
CGPLLU86	0.932	-0.848	EGFR 746ELREATS > D	0.00%
CGPLLU89	0.864	-0.729	EGFR 747LREATS > -	0.42%
CGPLLU89	0.908	-0.803	EGFR 747LREATS > -	0.20%
CGPLLU89	0.853	-0.881	EGFR 747LREATS > -	0.00%
CGLU316	0.331	-0.351	EGFR L861Q	15.72%
CGLU316	0.225	-0.253	EGFR L861Q	45.67%
CGLU316	0.336	-0.364	EGFR G719A	33.38%
CGLU316	0.340	-0.364	EGFR L861Q	66.01%
CGLU344	0.935	-0.818	EGFR E746_A75Cdel	0.00%
CGLU344	0.919	-0.774	EGFR E746_A75Cdel	0.22%
CGLU344	0.953	-0.860	EGFR E746_A75Cdel	0.40%
CGLU344	0.944	-0.832	EGFR E746_A75Cdel	0.00%
CGLU369	0.825	-0.826	EGFR L858R	20.61%
CGLU369	0.950	-0.903	EGFR L858R	0.22%
CGLU369	0.945	-0.889	EGFR L858R	0.16%
CGLU369	0.886	-0.883	EGFR L858R	0.10%
CGLU373	0.922	-0.804	EGFR E746_A75Cdel	0.82%
CGLU373	0.959	-0.853	EGFR E746_A75Cdel	0.00%
CGLU373	0.967	-0.886	EGFR E746_A75Cdel	0.15%
CGLU373	0.951	-0.890	EGFR E746_A75Cdel	0.00%
CGPLLU13	0.425	-0.400	EGFR E746_A75Cdel	7.66%
CGPLLU13	0.272	-0.257	EGFR E746_A75Cdel	13.10%
CGPLLU13	0.584	-0.536	EGFR E746_A75Cdel	6.09%
CGPLLU13	0.530	-0.513	EGFR E746_A75Cdel	9.28%
CGPLLU264	0.946	-0.824	EGFR D761N	0.00%
CGPLLU264	0.927	-0.788	EGFR D761N	0.16%
CGPLLU264	0.962	-0.856	EGFR D761N	0.00%
CGPLLU264	0.960	-0.894	EGFR D761N	0.00%
CGPLLU265	0.953	-0.859	EGFR L858R	0.21%
CGPLLU265	0.949	-0.842	EGFR L858R	0.21%
CGPLLU265	0.955	-0.844	EGFR T790M	0.21%
CGPLLU265	0.946	-0.825	EGFR L858R	0.00%
CGPLLU266	0.951	-0.904	NA	0.00%
CGPLLU266	0.959	-0.886	NA	0.00%
CGPLLU266	0.961	-0.880	NA	0.00%
CGPLLU266	0.958	-0.855	NA	0.00%
CGPLLU267	0.919	-0.863	EGFR L858R	1.93%
CGPLLU267	0.863	-0.889	EGFR L858R	0.14%
CGPLLU267	0.962	-0.876	EGFR L858R	0.38%

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

CGPLLU269	0.951	-0.864	EGFR L858R	0.10%
CGPLLU269	0.941	-0.694	EGFR L858R	0.00%
CGPLLU269	0.957	-0.676	EGFR L858R	0.00%
CGPLLU271	0.871	-0.284	EGFR E746_A75Cdel	3.36%
CGPLLU271	0.947	-0.826	EGFR E746_A75Cdel	0.17%
CGPLLU271	0.952	-0.839	EGFR E746_A75Cdel	0.00%
CGPLLU271	0.944	-0.810	EGFR E746_A75Cdel	0.00%
CGPLLU271	0.950	-0.831	EGFR E746_A75Cdel	0.44%
CGPLLU43	0.944	-0.903	NA	0.00%
CGPLLU43	0.956	-0.899	NA	0.00%
CGPLLU43	0.959	-0.901	NA	0.00%
CGPLLU43	0.965	-0.896	NA	0.00%

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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
CGCRC291	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	163	0.1972
CGCRC292	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	166	0.7604
CGCRC293	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	166	0.9335
CGCRC294	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.6531
CGCRC296	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.8161
CGCRC299	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	162	0.7325
CGCRC300	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.9382
CGCRC301	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	165	0.8252
CGCRC302	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	163	0.7499
CGCRC304	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	162	0.4642
CGCRC305	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.8909
CGCRC306	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.8523
CGCRC307	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.9140
CGCRC308	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	165	0.8734
CGCRC311	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.8535
CGCRC315	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	167	0.6083
CGCRC316	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	161	0.1546
CGCRC317	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	163	0.6242
CGCRC318	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.8824
CGCRC319	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	160	0.5979
CGCRC320	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.7949
CGCRC321	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	164	0.7804
CGCRC333	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	163	0.4263
CGCRC335	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	162	0.6466
CGCRC338	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	162	0.7740
CGCRC341	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	164	0.8995
CGCRC342	Colorectal Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	158	0.2524
CGPLBR100	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	166	0.9440
CGPLBR101	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.8864
CGPLBR102	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	168	0.9617
CGPLBR103	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.9498
CGPLBR104	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	164	0.8490
CGPLBR12	Breast Cancer	WGS	Preoperative treatment naïve	III	163	0.8350
CGPLBR18	Breast Cancer	WGS	Preoperative treatment naïve	II	166	0.8411
CGPLBR23	Breast Cancer	WGS	Preoperative treatment naïve	II	156	0.9714
CGPLBR24	Breast Cancer	WGS	Preoperative treatment naïve	III	166	0.8402
CGPLBR28	Breast Cancer	WGS	Preoperative treatment naïve	II	161	0.9584
CGPLBR30	Breast Cancer	WGS	Preoperative treatment naïve	II	167	0.6951
CGPLBR31	Breast Cancer	WGS	Preoperative treatment naïve	II	166	0.9719
CGPLBR32	Breast Cancer	WGS	Preoperative treatment naïve	II	166	0.9590
CGPLBR33	Breast Cancer	WGS	Preoperative treatment naïve	II	163	0.9706
CGPLBR34	Breast Cancer	WGS	Preoperative treatment naïve	II	168	0.8735
CGPLBR35	Breast Cancer	WGS	Preoperative treatment naïve	II	169	0.9655

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CGPLBR36	Breast Cancer	WGS	Preoperative treatment naïve	II	167	0.9394
CGPLBR37	Breast Cancer	WGS	Preoperative treatment naïve	I	165	0.9691
CGPLBR38	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	167	0.9105
CGPLBR40	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	168	0.9273
CGPLBR41	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.9626
CGPLBR45	Breast Cancer	WGS	Preoperative treatment naïve	III	168	0.9615
CGPLBR46	Breast Cancer	WGS	Preoperative treatment naïve	I	166	0.9322
CGPLBR47	Breast Cancer	WGS	Preoperative treatment naïve	II	169	0.9461
CGPLBR48	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	171	0.7686
CGPLBR49	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	160	0.8867
CGPLBR50	Breast Cancer	WGS	Preoperative treatment naïve	II	165	0.8593
CGPLBR51	Breast Cancer	WGS	Preoperative treatment naïve	III	164	0.9359
CGPLBR52	Breast Cancer	WGS	Preoperative treatment naïve	III	165	0.8688
CGPLBR55	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	163	0.9634
CGPLBR56	Breast Cancer	WGS	Preoperative treatment naïve	III	166	0.9459
CGPLBR57	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.9672
CGPLBR59	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.9438
CGPLBR60	Breast Cancer	WGS	Preoperative treatment naïve	II	163	0.9479
CGPLBR61	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.9611
CGPLBR63	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	168	0.9555
CGPLBR65	Breast Cancer	WGS	Preoperative treatment naïve	II	167	0.9506
CGPLBR68	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	163	0.9154
CGPLBR69	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.9460
CGPLBR70	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	168	0.9651
CGPLBR71	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.9577
CGPLBR72	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.9786
CGPLBR73	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.9576
CGPLBR76	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	170	0.9410
CGPLBR81	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	170	0.9643
CGPLBR82	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.9254
CGPLBR83	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9451
CGPLBR84	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	169	0.9315
CGPLBR87	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9154
CGPLBR88	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9370
CGPLBR90	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9002
CGPLBR91	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	164	0.7955
CGPLBR92	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	162	0.6774
CGPLBR93	Breast Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.8773
CGPLH189	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9325
CGPLH190	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9403
CGPLH192	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9646
CGPLH193	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9423
CGPLH194	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9567
CGPLH196	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9709
CGPLH197	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9605
CGPLH198	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9238
CGPLH199	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9618
CGPLH200	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9183
CGPLH201	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9548
CGPLH202	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9471
CGPLH203	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9534
CGPLH205	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9075
CGPLH208	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9422
CGPLH209	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9556
CGPLH210	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9447
CGPLH211	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9538
CGPLH300	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9019
CGPLH307	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9576
CGPLH308	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9481
CGPLH309	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9672
CGPLH310	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9547
CGPLH311	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9302
CGPLH314	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9482
CGPLH315	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8659
CGPLH316	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9374
CGPLH317	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9542
CGPLH319	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9578
CGPLH320	Healthy	WGS	Preoperative treatment naïve	NA	164	0.8913
CGPLH322	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8751
CGPLH324	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9519
CGPLH325	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9124
CGPLH326	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9574
CGPLH327	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9533
CGPLH328	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9643
CGPLH329	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9609
CGPLH330	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9118
CGPLH331	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9679

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CGPLH333	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9474
CGPLH335	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8909
CGPLH336	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9248
CGPLH337	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9533
CGPLH338	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9388
CGPLH339	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9396
CGPLH340	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9488
CGPLH341	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9533
CGPLH342	Healthy	WGS	Preoperative treatment naïve	NA	166	0.7858
CGPLH343	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9421
CGPLH344	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9192
CGPLH345	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9345
CGPLH346	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9475
CGPLH350	Healthy	WGS	Preoperative treatment naïve	NA	171	0.9570
CGPLH351	Healthy	WGS	Preoperative treatment naïve	NA	168	0.8176
CGPLH352	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9521
CGPLH353	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9435
CGPLH354	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9481
CGPLH355	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9613
CGPLH356	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9474
CGPLH357	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9255
CGPLH358	Healthy	WGS	Preoperative treatment naïve	NA	167	0.7777
CGPLH360	Healthy	WGS	Preoperative treatment naïve	NA	168	0.8500
CGPLH361	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9261
CGPLH362	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9236
CGPLH363	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9488
CGPLH364	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9311
CGPLH365	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9371
CGPLH366	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9536
CGPLH367	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8748
CGPLH368	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9490
CGPLH369	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9428
CGPLH370	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9642
CGPLH371	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9621
CGPLH380	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9652
CGPLH381	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9541
CGPLH382	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9380
CGPLH383	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9700
CGPLH384	Healthy	WGS	Preoperative treatment naïve	NA	169	0.8061
CGPLH385	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8856
CGPLH386	Healthy	WGS	Preoperative treatment naïve	NA	167	0.6920
CGPLH387	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9583
CGPLH388	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9348
CGPLH389	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9409
CGPLH390	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9216
CGPLH391	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9334
CGPLH392	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9165
CGPLH393	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9256
CGPLH394	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9257
CGPLH395	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8611
CGPLH396	Healthy	WGS	Preoperative treatment naïve	NA	167	0.7884
CGPLH398	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9463
CGPLH399	Healthy	WGS	Preoperative treatment naïve	NA	169	0.8780
CGPLH400	Healthy	WGS	Preoperative treatment naïve	NA	168	0.6662
CGPLH401	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9428
CGPLH402	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9353
CGPLH403	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9329
CGPLH404	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9402
CGPLH405	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9579
CGPLH406	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8188
CGPLH407	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9527
CGPLH408	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9584
CGPLH049	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9220
CGPLH410	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9102
CGPLH411	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9392
CGPLH412	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9561
CGPLH413	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9451
CGPLH414	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9258
CGPLH415	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9217
CGPLH416	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9672
CGPLH417	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9578
CGPLH418	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9376
CGPLH419	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9228
CGPLH420	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9164
CGPLH422	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9069
CGPLH423	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9606
CGPLH424	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9553

APPENDIX-G-continued

CGPLH425	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9722
CGPLH426	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9560
CGPLH427	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9594
CGPLH428	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9591
CGPLH429	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9358
CGPLH430	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9639
CGPLH431	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9570
CGPLH432	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9485
CGPLH434	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9671
CGPLH435	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9133
CGPLH436	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9360
CGPLH437	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9445
CGPLH438	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9537
CGPLH439	Healthy	WGS	Preoperative treatment naïve	NA	171	0.9547
CGPLH440	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9562
CGPLH441	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9660
CGPLH442	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9569
CGPLH443	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9431
CGPLH444	Healthy	WGS	Preoperative treatment naïve	NA	171	0.9429
CGPLH445	Healthy	WGS	Preoperative treatment naïve	NA	171	0.9446
CGPLH446	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9502
CGPLH447	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9421
CGPLH448	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9553
CGPLH449	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9550
CGPLH450	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9572
CGPLH451	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9548
CGPLH452	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9498
CGPLH453	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9572
CGPLH455	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9626
CGPLH456	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9537
CGPLH457	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9429
CGPLH458	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9511
CGPLH459	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9609
CGPLH460	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9331
CGPLH463	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9506
CGPLH464	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9133
CGPLH465	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9251
CGPLH466	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9679
CGPLH467	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9273
CGPLH468	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8353
CGPLH469	Healthy	WGS	Preoperative treatment naïve	NA	169	0.8225
CGPLH470	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9073
CGPLH471	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9354
CGPLH472	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8509
CGPLH473	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9206
CGPLH474	Healthy	WGS	Preoperative treatment naïve	NA	168	0.8474
CGPLH475	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9155
CGPLH476	Healthy	WGS	Preoperative treatment naïve	NA	169	0.8807
CGPLH477	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9129
CGPLH478	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9588
CGPLH479	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9303
CGPLH480	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9522
CGPLH481	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9558
CGPLH482	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9379
CGPLH483	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9518
CGPLH484	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9630
CGPLH485	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9547
CGPLH486	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9199
CGPLH487	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9575
CGPLH488	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9618
CGPLH490	Healthy	WGS	Preoperative treatment naïve	NA	167	0.8950
CGPLH491	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9631
CGPLH492	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9335
CGPLH493	Healthy	WGS	Preoperative treatment naïve	NA	168	0.8718
CGPLH494	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9623
CGPLH495	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8777
CGPLH496	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8788
CGPLH497	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9576
CGPLH498	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9526
CGPLH499	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9733
CGPLH500	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9542
CGPLH501	Healthy	WGS	Preoperative treatment naïve	NA	169	0.9526
CGPLH052	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9512
CGPLH503	Healthy	WGS	Preoperative treatment naïve	NA	169	0.8947
CGPLH504	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9561
CGPLH505	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9554
CGPLH506	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9733

APPENDIX-G-continued

CGPLH507	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9222
CGPLH508	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9674
CGPLH509	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9475
CGPLH510	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9459
CGPLH511	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9714
CGPLH512	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9442
CGPLH513	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9705
CGPLH514	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9690
CGPLH515	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9568
CGPLH516	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9508
CGPLH517	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9635
CGPLH518	Healthy	WGS	Preoperative treatment naïve	NA	168	0.9647
CGPLH519	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9366
CGPLH520	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9649
CGPLH625	Healthy	WGS	Preoperative treatment naïve	NA	166	0.8766
CGPLH626	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9011
CGPLH639	Healthy	WGS	Preoperative treatment naïve	NA	165	0.9482
CGPLH640	Healthy	WGS	Preoperative treatment naïve	NA	166	0.9131
CGPLH642	Healthy	WGS	Preoperative treatment naïve	NA	167	0.9641
CGPLH643	Healthy	WGS	Preoperative treatment naïve	NA	169	0.8450
CGPLH644	Healthy	WGS	Preoperative treatment naïve	NA	170	0.9398
CGPLH646	Healthy	WGS	Preoperative treatment naïve	NA	172	0.296
CGLLU141	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.8702
CGLLU161	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.9128
CGLLU162	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.7753
CGLLU163	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.4770
CGLLU168	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	163	0.9164
CGLLU169	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	163	0.9326
CGLLU176	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.9572
CGLLU177	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.8472
CGLLU203	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.9119
CGLLU205	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	163	0.9518
CGLLU207	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9344
CGLLU208	Lung Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.9091
CGPLOW11	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	166	0.8902
CGPLOW12	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.8779
CGPLOW13	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	166	0.7560
CGPLOW15	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	165	0.8585
CGPLOW16	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	165	0.9052
CGPLOW19	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.7854
CGPLOW20	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.8711
CGPLOW21	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	167	0.8942
CGPLOW22	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	164	0.8944
CGPLOW23	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	169	0.8510
CGPLOW24	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.9449
CGPLOW25	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.9590
CGPLOW26	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	161	0.8148
CGPLOW28	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.9635
CGPLOW31	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	167	0.9461
CGPLOW32	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.9582
CGPLOW37	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	170	0.9397
CGPLOW38	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.5779
CGPLOW40	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	170	0.6097
CGPLOW41	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	V	167	0.9403
CGPLOW42	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.9265
CGPLOW43	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.9626
CGPLOW44	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	164	0.9536
CGPLOW46	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	166	0.9622
CGPLOW47	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	165	0.9704
CGPLOW48	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.9675
CGPLOW49	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	164	0.8998
CGPLOW50	Ovarian Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	III	165	0.9682
CGPLPA112	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	164	0.8914
CGPLPA113	Doudenal Cancer	WGS	Preoperative treatment naïve	I	170	0.8751
CGPLPA114	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	166	0.9098
CGPLPA115	Bile Duct Cancer	WGS	Preoperative treatment naïve	V	165	0.8053
CGPLPA117	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	165	0.9395
CGPLPA118	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	167	0.9406
CGPLPA122	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.8231
CGPLPA124	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9108
CGPLPA125	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	166	0.9675
CGPLPA126	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9155
CGPLPA127	Bile Duct Cancer	WGS	Preoperative treatment naïve	V	167	0.8916
CGPLPA128	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.9262
CGPLPA129	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9220
CGPLPA130	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.8586
CGPLPA131	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	165	0.7707

APPENDIX-G-continued

CGPLPA134	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	160	0.7502
CGPLPA135	Bile Duct Cancer	WGS	Preoperative treatment naïve	I	165	0.9495
CGPLPA136	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.9289
CGPLPA137	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	166	0.9588
CGPLPA139	Bile Duct Cancer	WGS	Preoperative treatment naïve	V	166	0.9511
CGPLPA14	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.8718
CGPLPA140	Bile Duct Cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9215
CGPLPA141	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	165	0.9172
CGPLPA15	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9111
CGPLPA155	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	165	0.9496
CGPLPA156	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9479
CGPLPA165	Bile Duct Cancer	WGS	Preoperative treatment naïve	I	168	0.9596
CGPLPA168	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	162	0.7838
CGPLPA17	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.8624
CGPLPA184	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	165	0.9100
CGPLPA187	Bile Duct Cancer	WGS	Preoperative treatment naïve	II	165	0.8577
CGPLPA23	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.7887
CGPLPA25	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.9549
CGPLPA26	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.9598
CGPLPA28	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.9069
CGPLPA33	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.8361
CGPLPA34	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	168	0.8946
CGPLPA37	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.8840
CGPLPA38	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.8746
CGPLPA39	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.8562
CGPLPA40	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.8563
CGPLPA42	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9126
CGPLPA46	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	169	0.8274
CGPLPA47	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.8376
CGPLPA48	Pancreatic Cancer	WGS	Preoperative treatment naïve	I	167	0.9391
CGPLPA52	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9452
CGPLPA53	Pancreatic Cancer	WGS	Preoperative treatment naïve	I	163	0.9175
CGPLPA58	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.9587
CGPLPA59	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	163	0.9230
CGPLPA67	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.9574
CGPLPA69	Pancreatic Cancer	WGS	Preoperative treatment naïve	I	168	0.9172
CGPLPA71	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9424
CGPLPA74	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.9688
CGPLPA76	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	163	0.9681
CGPLPA85	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.9137
CGPLPA86	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	165	0.8875
CGPLPA92	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	167	0.9389
CGPLPA93	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	166	0.8585
CGPLPA94	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	162	0.9365
CGPLPA95	Pancreatic Cancer	WGS	Preoperative treatment naïve	II	163	0.8542
CGST102	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.9496
CGST11	Gastric cancer	WGS	Preoperative treatment naïve	IV	169	0.9419
CGST110	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	167	0.9626
CGST114	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	164	0.9535
CGST13	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.9369
CGST131	Gastric cancer	WGS	Preoperative treatment naïve	II	171	0.9428
CGST141	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	168	0.9621
CGST16	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	166	0.7804
CGST18	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9523
CGST21	Gastric cancer	WGS	Preoperative treatment naïve	II	165	-0.4778
CGST26	Gastric cancer	WGS	Preoperative treatment naïve	IV	166	0.9554
CGST28	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	X	169	0.9076
CGST30	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9246
CGST32	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9431
CGST33	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.7999
CGST38	Gastric cancer	WGS	Preoperative treatment naïve	0	168	0.9368
CGST39	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	164	0.8742
CGST41	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	168	0.8194
CGST45	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	168	0.9576
CGST47	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.9641
CGST48	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	IV	167	0.7469
CGST53	Gastric cancer	WGS	Preoperative treatment naïve	0	173	0.0019
CGST58	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	169	0.9470
CGST67	Gastric cancer	WGS	Preoperative treatment naïve	I	170	0.9352
CGST77	Gastric cancer	WGS	Preoperative treatment naïve	IV	170	0.0043
CGST80	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	II	168	0.9313
CGST81	Gastric cancer	Targeted Mutation Analysis and WGS	Preoperative treatment naïve	I	168	0.9480

APPENDIX-G-continued

Patient	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*
CGCRC291	0.5268	0.0484%	0.9976	Y	Y	22.85%
CGCRC292	0.8835	0.0270%	0.7299	Y	N	1.41%
CGCRC293	0.9206	0.0748%	0.5234	N	N	3.35%
CGCRC294	0.8904	0.0135%	0.8757	Y	Y	0.17%
CGCRC296	0.8395	0.0369%	0.9951	Y	Y	ND
CGCRC299	0.9268	0.0392%	0.9648	Y	Y	ND
CGCRC300	0.9303	0.0235%	0.4447	N	N	ND
CGCRC301	0.9151	0.0310%	0.2190	N	N	3.21%
CGCRC302	0.9243	0.0112%	0.9897	Y	Y	3.12%
CGCRC304	0.9360	0.0093%	0.9358	Y	Y	3.27%
CGCRC305	0.9250	0.0120%	0.8988	Y	Y	3.19%
CGCRC306	0.8186	0.0781%	0.9466	Y	Y	8.02%
CGCRC307	0.9342	0.0781%	0.7042	Y	N	0.56%
CGCRC308	0.9324	0.0078%	0.9082	Y	Y	0.11%
CGCRC311	0.9156	0.0173%	0.1867	N	N	ND
CGCRC315	0.8846	0.0241%	0.6422	Y	N	0.27%
CGCRC316	0.5879	0.0315%	0.9971	Y	Y	5.52%
CGCRC317	0.8944	0.0184%	0.9855	Y	Y	0.36%
CGCRC318	0.9140	0.0156%	0.5615	N	N	ND
CGCRC319	0.8230	0.1259%	0.9925	Y	Y	0.11%
CGCRC320	0.9101	0.0383%	0.8019	Y	Y	0.64%
CGCRC321	0.9091	0.0829%	0.9759	Y	Y	3.20%
CGCRC333	0.4355	0.4264%	0.9974	Y	Y	43.03%
CGCRC335	0.6858	0.1154%	0.9887	Y	Y	81.61%
CGCRC338	0.7573	0.1436%	0.9976	Y	Y	36.00%
CGCRC341	0.9181	0.0197%	0.9670	Y	Y	ND
CGCRC342	0.1845	0.1732%	0.9987	Y	Y	30.72%
CGPLBR100	0.8946	0.1234%	0.8664	Y	Y	ND
CGPLBR101	0.9304	0.0709%	0.9385	Y	Y	ND
CGPLBR102	0.9345	0.4742%	0.9052	Y	Y	0.25%
CGPLBR103	0.9251	0.0775%	0.5994	N	N	ND
CGPLBR104	0.9192	0.0532%	0.9950	Y	Y	0.13%
CGPLBR12	0.7760	0.1407%	0.7598	Y	Y	—
CGPLBR18	0.9534	0.0267%	0.3886	N	N	—
CGPLBR23	0.9312	0.0144%	0.1235	N	N	—
CGPLBR24	0.8766	0.0210%	0.7480	Y	Y	—
CGPLBR28	0.8120	0.1456%	0.9630	Y	Y	—
CGPLBR30	0.6611	0.0952%	0.9956	Y	Y	—
CGPLBR31	0.9556	0.0427%	0.2227	N	N	—
CGPLBR32	0.9229	0.0308%	0.9815	Y	Y	—
CGPLBR33	0.9432	0.0617%	0.2863	N	N	—
CGPLBR34	0.9425	0.0115%	0.1637	N	N	—
CGPLBR35	0.9348	0.1371%	0.5057	N	N	—
CGPLBR36	0.8884	0.0813%	0.4017	N	N	—
CGPLBR37	0.9496	0.0518%	0.0314	N	N	—
CGPLBR38	0.0349	0.1352%	0.8983	Y	Y	0.53%
CGPLBR40	0.9244	0.0929%	0.9046	Y	Y	ND
CGPLBR41	0.9346	0.0544%	0.9416	Y	Y	0.32%
CGPLBR45	0.9285	0.0296%	0.3860	N	N	—
CGPLBR46	0.9005	0.0345%	0.7270	Y	N	—
CGPLBR47	0.9028	0.0591%	0.6247	Y	Y	—
CGPLBR48	0.8246	0.0504%	0.9973	Y	Y	0.18%
CGPLBR49	0.7887	0.0377%	0.9946	Y	Y	ND
CGPLBR50	0.9332	0.0137%	0.6820	Y	N	—
CGPLBR51	0.9160	0.0863%	0.6915	Y	N	—
CGPLBR52	0.9196	0.0165%	0.6390	Y	N	—
CGPLBR55	0.9341	0.0356%	0.9494	Y	Y	0.68%
CGPLBR56	0.9428	0.2025%	0.4700	N	N	—
CGPLBR57	0.9416	0.0902%	0.9090	Y	Y	ND
CGPLBR59	0.9130	0.0761%	0.5828	N	N	ND
CGPLBR60	0.8916	0.0626%	0.8779	Y	Y	—
CGPLBR61	0.9422	0.0601%	0.4417	N	N	0.44%
CGPLBR63	0.9132	0.0514%	0.8788	Y	Y	ND
CGPLBR65	0.8970	0.0264%	0.9048	Y	Y	—

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CGPLBR68	0.9532	0.0164%	0.7883	Y	Y	ND
CGPLBR69	0.9474	0.0279%	0.0600	N	N	ND
CGPLBR70	0.9388	0.0171%	0.6447	Y	N	0.36%
CGPLBR71	0.9368	0.0271%	0.6706	Y	N	0.10%
CGPLBR72	0.9640	0.0263%	0.6129	N	N	ND
CGPLBR73	0.9421	0.0142%	0.0746	N	N	0.27%
CGPLBR76	0.9254	0.0775%	0.9334	Y	Y	0.12%
CGPLBR81	0.8193	0.0241%	0.9899	Y	Y	—
CGPLBR82	0.9288	0.1640%	0.9834	Y	Y	0.12%
CGPLBR83	0.9138	0.0419%	0.9810	Y	Y	0.28%
CGPLBR84	0.8659	0.0274%	0.9901	Y	Y	—
CGPLBR87	0.8797	0.0294%	0.9968	Y	Y	0.45%
CGPLBR88	0.8547	0.0181%	0.9958	Y	Y	0.38%
CGPLBR90	0.8330	0.0417%	0.9667	Y	Y	—
CGPLBR91	0.9408	0.0799%	0.8710	Y	Y	ND
CGPLBR92	0.8835	0.1042%	0.9856	Y	Y	0.20%
CGPLBR93	0.9072	0.0352%	0.7253	Y	N	ND
CGPLH189	0.8947	0.0591%	0.1748	N	N	—
CGPLH190	0.9369	0.1193%	0.5168	N	N	—
CGPLH192	0.9487	0.0276%	0.0178	N	N	—
CGPLH193	0.9442	0.0420%	0.5794	N	N	—
CGPLH194	0.9289	0.0407%	0.1616	N	N	—
CGPLH196	0.9512	0.0266%	0.0999	N	N	—
CGPLH197	0.9416	0.0334%	0.4699	N	N	—
CGPLH198	0.9457	0.0302%	0.6571	Y	N	—
CGPLH199	0.9439	0.0170%	0.5584	N	N	—
CGPLH200	0.9391	0.0362%	0.3833	N	N	—
CGPLH201	0.9180	0.0470%	0.8395	Y	Y	—
CGPLH202	0.9436	0.0501%	0.1088	N	N	—
CGPLH203	0.9575	0.0455%	0.2485	N	N	—
CGPLH205	0.9283	0.0409%	0.4401	N	N	—
CGPLH208	0.9409	0.0371%	0.2706	N	N	—
CGPLH209	0.9367	0.0427%	0.2213	N	N	—
CGPLH210	0.9181	0.0279%	0.3500	N	N	—
CGPLH211	0.9410	0.0317%	0.1752	N	N	—
CGPLH300	0.9200	0.0397%	0.0226	N	N	—
CGPLH307	0.9167	0.0388%	0.1789	N	N	—
CGPLH308	0.8352	0.0311%	0.0155	N	N	—
CGPLH309	0.9451	0.0226%	0.0441	N	N	—
CGPLH310	0.9527	0.0145%	0.7135	Y	N	—
CGPLH311	0.9348	0.0202%	0.2589	N	N	—
CGPLH314	0.9491	0.0212%	0.1632	N	N	—
CGPLH315	0.9427	0.0071%	0.3450	N	N	—
CGPLH316	0.9552	0.0191%	0.4697	N	N	—
CGPLH317	0.9352	0.0232%	0.4330	N	N	—
CGPLH319	0.9189	0.0263%	0.2232	N	N	—
CGPLH320	0.9165	0.0222%	0.1095	N	N	—
CGPLH322	0.9411	0.0248%	0.0749	N	N	—
CGPLH324	0.9133	0.0402%	0.0128	N	N	—
CGPLH325	0.9202	0.0711%	0.0102	N	N	—
CGPLH326	0.9408	0.0213%	0.0475	N	N	—
CGPLH327	0.9071	0.1275%	0.4891	N	N	—
CGPLH328	0.9332	0.0256%	0.0234	N	N	—
CGPLH329	0.8396	0.0269%	0.0139	N	N	—
CGPLH330	0.9403	0.0203%	0.2642	N	N	—
CGPLH331	0.9377	0.0314%	0.0304	N	N	—
CGPLH333	0.9132	0.0350%	0.1633	N	N	—
CGPLH335	0.9333	0.0285%	0.0096	N	N	—
CGPLH336	0.9159	0.0158%	0.3872	N	N	—
CGPLH337	0.9262	0.0367%	0.2976	N	N	—
CGPLH338	0.9303	0.0103%	0.0431	N	N	—
CGPLH339	0.9338	0.0280%	0.0379	N	N	—
CGPLH340	0.9321	0.0210%	0.0379	N	N	—
CGPLH341	0.9187	0.0448%	0.1775	N	N	—
CGPLH342	0.8986	0.0283%	0.0904	N	N	—
CGPLH343	0.9067	0.0632%	0.0160	N	N	—
CGPLH344	0.8998	0.0257%	0.0120	N	N	—
CGPLH345	0.9107	0.0445%	0.0031	N	N	—
CGPLH346	0.9074	0.0208%	0.0686	N	N	—
CGPLH350	0.9388	0.0284%	0.0071	N	N	—
CGPLH351	0.9294	0.0223%	0.0207	N	N	—
CGPLH352	0.9190	0.0613%	0.0512	N	N	—
CGPLH353	0.9130	0.0408%	0.0132	N	N	—
CGPLH354	0.9121	0.0318%	0.0082	N	N	—
CGPLH355	0.9308	0.0400%	0.6407	Y	N	—
CGPLH356	0.8312	0.0427%	0.2437	N	N	—
CGPLH357	0.9540	0.0217%	0.0070	N	N	—

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CGPLH358	0.9372	0.0174%	0.1451	N	N	—
CGPLH360	0.8775	0.0395%	0.0048	N	N	—
CGPLH361	0.9283	0.0268%	0.1524	N	N	—
CGPLH362	0.9503	0.0309%	0.4832	N	N	—
CGPLH363	0.9187	0.0620%	0.0199	N	N	—
CGPLH364	0.9480	0.0282%	0.8719	Y	Y	—
CGPLH365	0.9051	0.1740%	0.9638	Y	Y	—
CGPLH366	0.9170	0.0344%	0.0952	N	N	—
CGPLH367	0.9181	0.0353%	0.1235	N	N	—
CGPLH368	0.9076	0.1073%	0.1252	N	N	—
CGPLH369	0.9541	0.0246%	0.2821	N	N	—
CGPLH370	0.9423	0.0410%	0.0989	N	N	—
CGPLH371	0.9414	0.0734%	0.2173	N	N	—
CGPLH380	0.9424	0.0523%	0.0128	N	N	—
CGPLH381	0.9501	0.0435%	0.0152	N	N	—
CGPLH382	0.9584	0.0340%	0.0326	N	N	—
CGPLH383	0.9407	0.0389%	0.0035	N	N	—
CGPLH384	0.9043	0.0207%	0.0258	N	N	—
CGPLH385	0.9246	0.0165%	0.0566	N	N	—
CGPLH386	0.8859	0.0502%	0.2677	N	N	—
CGPLH387	0.9223	0.0375%	0.0081	N	N	—
CGPLH388	0.9266	0.0527%	0.0499	N	N	—
CGPLH389	0.9035	0.0667%	0.6585	Y	N	—
CGPLH390	0.9182	0.0229%	0.0837	N	N	—
CGPLH391	0.9162	0.0223%	0.0716	N	N	—
CGPLH392	0.9014	0.0424%	0.1305	N	N	—
CGPLH393	0.9045	0.0407%	0.0037	N	N	—
CGPLH394	0.9292	0.0522%	0.1073	N	N	—
CGPLH395	0.9254	0.0424%	0.0171	N	N	—
CGPLH396	0.8928	0.0393%	0.0303	N	N	—
CGPLH398	0.9578	0.0242%	0.3195	N	N	—
CGPLH399	0.9195	0.0579%	0.0685	N	N	—
CGPLH400	0.9047	0.0300%	0.2103	N	N	—
CGPLH401	0.9339	0.0146%	0.0620	N	N	—
CGPLH402	0.8800	0.1516%	0.0395	N	N	—
CGPLH403	0.8829	0.0515%	0.0223	N	N	—
CGPLH404	0.8948	0.0528%	0.0027	N	N	—
CGPLH405	0.9204	0.0358%	0.0188	N	N	—
CGPLH406	0.8592	0.0667%	0.0206	N	N	—
CGPLH407	0.9099	0.0229%	0.0040	N	N	—
CGPLH408	0.9192	0.0415%	0.1257	N	N	—
CGPLH409	0.8950	0.0302%	0.0056	N	N	—
CGPLH410	0.9006	0.0453%	0.0019	N	N	—
CGPLH411	0.8857	0.0621%	0.0188	N	N	—
CGPLH412	0.9191	0.0140%	0.0417	N	N	—
CGPLH413	0.9145	0.0355%	0.0084	N	N	—
CGPLH414	0.9127	0.0290%	0.0294	N	N	—
CGPLH415	0.9025	0.0296%	0.0131	N	N	—
CGPLH416	0.9388	0.0198%	0.0645	N	N	—
CGPLH417	0.9192	0.0241%	0.0836	N	N	—
CGPLH418	0.9234	0.0306%	0.0052	N	N	—
CGPLH419	0.9295	0.0280%	0.0489	N	N	—
CGPLH420	0.9109	0.0187%	0.0420	N	N	—
CGPLH422	0.9006	0.0208%	0.0324	N	N	—
CGPLH423	0.8288	0.0532%	0.0139	N	N	—
CGPLH424	0.9265	0.1119%	0.0864	N	N	—
CGPLH425	0.9488	0.0722%	0.0156	N	N	—
CGPLH426	0.9080	0.0548%	0.1075	N	N	—
CGPLH427	0.9257	0.0182%	0.0470	N	N	—
CGPLH428	0.9272	0.0346%	0.0182	N	N	—
CGPLH429	0.8757	0.0593%	0.8143	Y	Y	—
CGPLH430	0.9307	0.0258%	0.0389	N	N	—
CGPLH431	0.9185	0.0234%	0.0174	N	N	—
CGPLH432	0.9082	0.0433%	0.0181	N	N	—
CGPLH434	0.9442	0.0297%	0.0050	N	N	—
CGPLH435	0.9097	0.0179%	0.0441	N	N	—
CGPLH436	0.9158	0.0290%	0.0958	N	N	—
CGPLH437	0.9245	0.0156%	0.0136	N	N	—
CGPLH438	0.9138	0.0169%	0.1041	N	N	—
CGPLH439	0.9028	0.0226%	0.0078	N	N	—
CGPLH440	0.8295	0.0330%	0.0687	N	N	—
CGPLH441	0.9430	0.0178%	0.0085	N	N	—
CGPLH442	0.9405	0.0169%	0.0582	N	N	—
CGPLH443	0.8801	0.0207%	0.0578	N	N	—
CGPLH444	0.8068	0.0464%	0.0097	N	N	—
CGPLH445	0.8750	0.0267%	0.1939	N	N	—
CGPLH446	0.9257	0.0281%	0.0340	N	N	—

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CGPLH447	0.8968	0.0167%	0.0017	N	N	—
CGPLH448	0.9191	0.0401%	0.0389	N	N	—
CGPLH449	0.9254	0.0236%	0.0116	N	N	—
CGPLH450	0.9195	0.0331%	0.0597	N	N	—
CGPLH451	0.9167	0.0262%	0.0104	N	N	—
CGPLH452	0.8948	0.0480%	0.4722	N	N	—
CGPLH453	0.9339	0.0186%	0.3419	N	N	—
CGPLH455	0.9322	0.0455%	0.4536	N	N	—
CGPLH456	0.9098	0.0207%	0.0385	N	N	—
CGPLH457	0.9022	0.0298%	0.0384	N	N	—
CGPLH458	0.9275	0.0298%	0.1891	N	N	—
CGPLH459	0.9209	0.0281%	0.0371	N	N	—
CGPLH460	0.8863	0.0227%	0.1157	N	N	—
CGPLH463	0.9372	0.0130%	0.0865	N	N	—
CGPLH464	0.8511	0.0659%	0.2040	N	N	—
CGPLH465	0.9164	0.0325%	0.0124	N	N	—
CGPLH466	0.9408	0.0155%	0.1733	N	N	—
CGPLH467	0.9024	0.0229%	0.2303	N	N	—
CGPLH468	0.9345	0.0247%	0.5427	N	N	—
CGPLH469	0.8799	0.0201%	0.5351	N	N	—
CGPLH470	0.9228	0.0715%	0.0327	N	N	—
CGPLH471	0.9333	0.0150%	0.0406	N	N	—
CGPLH472	0.8915	0.0481%	0.6152	N	N	—
CGPLH473	0.9128	0.0443%	0.2995	N	N	—
CGPLH474	0.9245	0.0316%	0.8246	Y	N	—
CGPLH475	0.9233	0.0269%	0.0736	N	N	—
CGPLH476	0.9059	0.0236%	0.0143	N	N	—
CGPLH477	0.9376	0.0382%	0.1111	N	N	—
CGPLH478	0.9344	0.0256%	0.0628	N	N	—
CGPLH479	0.9207	0.0221%	0.0648	N	N	—
CGPLH480	0.9046	0.0672%	0.7473	Y	N	—
CGPLH481	0.9113	0.0311%	0.0282	N	N	—
CGPLH482	0.9336	0.0162%	0.0058	N	N	—
CGPLH483	0.9275	0.0251%	0.0495	N	N	—
CGPLH484	0.9366	0.0261%	0.0048	N	N	—
CGPLH485	0.9128	0.0291%	0.1084	N	N	—
CGPLH486	0.9042	0.0220%	0.0820	N	N	—
CGPLH487	0.9098	0.0594%	0.2154	N	N	—
CGPLH488	0.8299	0.0409%	0.0903	N	N	—
CGPLH490	0.8794	0.0432%	0.0424	N	N	—
CGPLH491	0.8332	0.0144%	0.0223	N	N	—
CGPLH492	0.8799	0.0322%	0.0311	N	N	—
CGPLH493	0.9330	0.0065%	0.0280	N	N	—
CGPLH494	0.9303	0.0232%	0.0824	N	N	—
CGPLH495	0.8908	0.0513%	0.0465	N	N	—
CGPLH496	0.8398	0.0208%	0.0572	N	N	—
CGPLH497	0.9330	0.0335%	0.0404	N	N	—
CGPLH498	0.9315	0.0403%	0.0752	N	N	—
CGPLH499	0.9442	0.0198%	0.0149	N	N	—
CGPLH500	0.9240	0.0433%	0.0754	N	N	—
CGPLH501	0.9308	0.0300%	0.0159	N	N	—
CGPLH052	0.9200	0.0351%	0.0841	N	N	—
CGPLH503	0.8939	0.0398%	0.0649	N	N	—
CGPLH504	0.9324	0.0440%	0.1231	N	N	—
CGPLH505	0.9243	0.0605%	0.1869	N	N	—
CGPLH506	0.9498	0.0284%	0.0180	N	N	—
CGPLH507	0.9192	0.0186%	0.0848	N	N	—
CGPLH508	0.9410	0.0150%	0.1077	N	N	—
CGPLH509	0.9323	0.0163%	0.0828	N	N	—
CGPLH510	0.9548	0.0128%	0.0376	N	N	—
CGPLH511	0.9493	0.0224%	0.1779	N	N	—
CGPLH512	0.9244	0.0094%	0.0076	N	N	—
CGPLH513	0.9595	0.0441%	0.5250	N	N	—
CGPLH514	0.9369	0.0114%	0.3131	N	N	—
CGPLH515	0.9283	0.0352%	0.4936	N	N	—
CGPLH516	0.8298	0.0175%	0.0916	N	N	—
CGPLH517	0.9494	0.0161%	0.0059	N	N	—
CGPLH518	0.9432	0.0274%	0.0130	N	N	—
CGPLH519	0.9351	0.0171%	0.0949	N	N	—
CGPLH520	0.9476	0.0241%	0.0844	N	N	—
CGPLH625	0.9231	0.0697%	0.4977	N	N	—
CGPLH626	0.9269	0.0231%	0.3100	N	N	—
CGPLH639	0.9410	0.0549%	0.0773	N	N	—
CGPLH640	0.9264	0.0232%	0.0327	N	N	—
CGPLH642	0.8376	0.0768%	0.0555	N	N	—
CGPLH643	0.9271	0.0579%	0.1325	N	N	—
CGPLH644	0.8948	0.0621%	0.3819	N	N	—

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CGPLH646	0.8691	0.0462%	0.2423	N	N	—
CGPLLU144	0.6861	0.0423%	0.9892	Y	Y	5.10%
CGPLLU161	0.9187	0.0273%	0.9955	Y	Y	0.20%
CGPLLU162	0.0836	0.1410%	0.9966	Y	Y	0.22%
CGPLLU163	0.3033	0.0724%	0.9940	Y	Y	0.21%
CGPLLU168	0.6842	0.0712%	0.9861	Y	Y	0.07%
CGPLLU169	0.9189	0.0846%	0.9856	Y	Y	0.13%
CGPLLU176	0.9081	0.0626%	0.8769	Y	Y	ND
CGPLLU177	0.6790	0.0564%	0.9924	Y	Y	3.22%
CGPLLU203	0.8741	0.0568%	0.9178	Y	Y	0.11%
CGPLLU205	0.9476	0.0495%	0.9877	Y	Y	ND
CGPLLU207	0.9379	0.0421%	0.9908	Y	Y	0.32%
CGPLLU208	0.8942	0.0815%	0.9273	Y	Y	1.33%
CGPLOV11	0.8872	0.0469%	0.9343	Y	Y	0.87%
CGPLOV12	0.8973	0.2767%	0.9764	Y	Y	ND
CGPLOV13	0.9146	0.1017%	0.9690	Y	Y	0.35%
CGPLOV15	0.8552	0.0876%	0.9945	Y	Y	3.54%
CGPLOV16	0.9046	0.0400%	0.9683	Y	Y	1.12%
CGPLOV19	0.7578	0.1089%	0.9989	Y	Y	46.35%
CGPLOV20	0.9154	0.0581%	0.9749	Y	Y	0.21%
CGPLOV21	0.8889	0.0677%	0.9961	Y	Y	14.36%
CGPLOV22	0.9355	0.0251%	0.9775	Y	Y	0.49%
CGPLOV23	0.8850	0.1520%	0.9910	Y	Y	1.39%
CGPLOV24	0.8995	0.0303%	0.9856	Y	Y	ND
CGPLOV25	0.9228	0.0141%	0.8544	Y	Y	ND
CGPLOV26	0.9351	0.0646%	0.9946	Y	Y	ND
CGPLOV28	0.9378	0.0547%	0.8160	Y	Y	ND
CGPLOV31	0.9283	0.1605%	0.9795	Y	Y	ND
CGPLOV32	0.9338	0.1351%	0.8609	Y	Y	ND
CGPLOV37	0.8831	0.0985%	0.9849	Y	Y	0.29%
CGPLOV38	0.6502	0.0490%	0.9990	Y	Y	4.89%
CGPLOV40	0.8127	0.6145%	0.9963	Y	Y	6.73%
CGPLOV41	0.8929	0.1110%	0.9484	Y	Y	0.60%
CGPLOV42	0.9086	0.0489%	0.9979	Y	Y	1.24%
CGPLOV43	0.9342	0.0432%	0.6042	N	N	ND
CGPLOV44	0.9173	0.1946%	0.9962	Y	Y	0.37%
CGPLOV46	0.9291	0.0801%	0.9128	Y	Y	ND
CGPLOV47	0.9461	0.0270%	0.3410	N	N	3.20%
CGPLOV48	0.9429	0.0422%	0.4874	N	N	10.70%
CGPLOV49	0.8083	0.1527%	0.9897	Y	Y	2.03%
CGPLOV50	0.9382	0.0907%	0.9955	Y	Y	ND
CGPLPA112	0.9429	0.0268%	0.0856	N	N	—
CGPLPA113	0.7674	1.0116%	0.9935	Y	Y	—
CGPLPA114	0.9246	0.0836%	0.7598	Y	Y	—
CGPLPA115	0.8810	0.0763%	0.9974	Y	Y	—
CGPLPA117	0.8767	0.1084%	0.9049	Y	Y	—
CGPLPA118	0.9001	0.1842%	0.9859	Y	Y	0.14%
CGPLPA122	0.8058	0.2047%	0.9983	Y	Y	37.22%
CGPLPA124	0.9238	0.1542%	0.8791	Y	Y	0.62%
CGPLPA125	0.9373	0.0273%	0.0228	N	N	—
CGPLPA126	0.9139	0.4349%	0.9908	Y	Y	ND
CGPLPA127	0.8117	0.4371%	0.9789	Y	Y	—
CGPLPA128	0.9003	0.1317%	0.9812	Y	Y	ND
CGPLPA129	0.9155	0.0642%	0.9839	Y	Y	ND
CGPLPA130	0.8499	0.1055%	0.9895	Y	Y	ND
CGPLPA131	0.9195	0.0760%	0.9685	Y	Y	0.21%
CGPLPA134	0.8847	0.0260%	0.9896	Y	Y	0.93%
CGPLPA135	0.9184	0.0558%	0.6594	Y	N	—
CGPLPA136	0.9050	0.0769%	0.9596	Y	Y	0.10%
CGPLPA137	0.9320	0.0499%	0.7282	Y	N	—
CGPLPA139	0.9374	0.0465%	0.0743	N	N	—
CGPLPA14	0.9069	0.0515%	0.9824	Y	Y	—
CGPLPA140	0.9548	0.0330%	0.9751	Y	Y	3.21%
CGPLPA141	0.9381	0.0920%	0.9388	Y	Y	—
CGPLPA15	0.8927	0.0160%	0.8737	Y	Y	—
CGPLPA155	0.9313	0.0260%	0.8013	Y	Y	—
CGPLPA156	0.9432	0.0290%	0.0159	N	N	—
CCPLPA165	0.9309	0.0558%	0.2158	N	N	—
CGPLPA168	0.7757	0.3123%	0.9878	Y	Y	—
CGPLPA17	0.6771	1.2600%	0.9956	Y	Y	—
CGPLPA184	0.9203	0.0897%	0.9926	Y	Y	—
CGPLPA187	0.8968	0.0658%	0.9875	Y	Y	—
CGPLPA23	0.6938	0.5785%	0.9984	Y	Y	—
CGPLPA25	0.9239	0.0380%	0.8103	Y	Y	—
CGPLPA26	0.9356	0.0247%	0.8231	Y	Y	—
CGPLPA28	0.8930	0.0546%	0.9036	Y	Y	—
CGPLPA33	0.8553	0.0894%	0.9967	Y	Y	—

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CGPLPA34	0.8885	0.0438%	0.7977	Y	Y	—
CGPLPA37	0.9294	0.0410%	0.9924	Y	Y	—
CGPLPA38	0.8941	0.0372%	0.9851	Y	Y	—
CGPLPA39	0.7972	0.5058%	0.9951	Y	Y	—
CGPLPA40	0.8865	0.2268%	0.9920	Y	Y	—
CGPLPA42	0.8863	0.0283%	0.3544	N	N	—
CGPLPA46	0.7525	1.0982%	0.9952	Y	Y	—
CGPLPA47	0.8439	0.1598%	0.9946	Y	Y	—
CGPLPA48	0.9207	1.0232%	0.2251	N	N	—
CGPLPA52	0.8863	0.0154%	0.0963	N	N	—
CGPLPA53	0.8776	0.1824%	0.8946	Y	Y	—
CGPLPA58	0.9224	0.0803%	0.9056	Y	Y	—
CGPLPA59	0.9193	0.1479%	0.9759	Y	Y	—
CGPLPA67	0.9248	0.0329%	0.6716	Y	N	—
CGPLPA69	0.8592	0.0458%	0.1245	Y	Y	—
CGPLPA71	0.8888	0.0479%	0.0524	Y	Y	—
CGPLPA74	0.9372	0.0292%	0.0108	Y	Y	—
CGPLPA76	0.9441	0.0345%	0.0897	Y	Y	—
CGPLPA85	0.9337	0.0363%	0.0508	Y	Y	—
CGPLPA86	0.8042	0.7564%	0.9864	Y	Y	—
CGPLPA92	0.9003	0.1458%	0.7061	N	N	—
CGPLPA93	0.8023	0.6250%	0.9978	Y	Y	—
CGPLPA94	0.9433	0.0180%	0.9025	Y	Y	—
CGPLPA95	0.8571	0.0815%	0.9941	Y	Y	—
CGST102	0.9057	0.0704%	0.8581	Y	Y	0.43%
CGST11	0.9161	0.0651%	0.1435	N	N	—
CGST110	0.9232	0.0817%	0.8900	Y	Y	ND
CGST114	0.9038	0.0317%	0.5893	N	N	ND
CGST13	0.9156	0.0321%	0.9754	Y	Y	ND
CGST131	0.8886	0.2752%	0.9409	Y	Y	—
CGST141	0.9205	0.0388%	0.2008	N	N	ND
CGST16	0.8355	0.1744%	0.9974	Y	Y	0.93%
CGST18	0.9111	0.0298%	0.3842	N	N	0.14%
CGST21	0.2687	0.2295%	0.9910	Y	Y	—
CGST26	0.9140	0.0399%	0.5009	N	N	—
CGST28	0.7832	0.1295%	0.9955	Y	Y	1.62%
CGST30	0.9121	0.0338%	0.9183	Y	Y	0.42%
CGST32	0.8639	0.0247%	0.9512	Y	Y	2.99%
CGST33	0.7770	0.0798%	0.9805	Y	Y	2.32%
CGST38	0.8758	0.0540%	0.9416	Y	Y	—
CGST39	0.9401	0.0287%	0.8480	Y	Y	ND
CGST41	0.9284	0.0398%	0.9253	Y	Y	ND
CGST45	0.9036	0.0220%	0.9713	Y	Y	ND
CGST47	0.9096	0.0157%	0.9687	Y	Y	0.45%
CGST48	0.5445	0.0220%	0.9975	Y	Y	4.21%
CGST53	0.7888	0.1140%	0.9914	Y	Y	—
CGST58	0.9094	0.0696%	0.9705	Y	Y	ND
CGST67	0.8853	0.3245%	0.9002	Y	Y	—
CGST77	0.8295	0.1851%	0.9981	Y	Y	—
CGST80	0.8845	0.0490%	0.9513	Y	Y	1.04%
CGST81	0.8851	0.0138%	0.9748	Y	Y	0.21%

*NO indicates not detected, please see reference 10 for additional information on targeted sequencing analyses. DELFI cancer detection at 95% and 98% specificity is based on scores greater than 0.6200 and 0.7500 respectively.

1-67. (canceled)

68. A system for determining a cell free DNA (cfDNA) fragmentation profile of a subject comprising:

- processing cfDNA fragments obtained from a sample obtained from the subject into sequencing libraries;
- subjecting the sequencing libraries to whole genome sequencing to obtain sequenced fragments, wherein genome coverage is from about 0.1x to 9x;
- mapping the sequenced fragments to a genome to obtain genomic intervals of mapped sequences;
- analyzing the genomic intervals of mapped sequences to determine cfDNA fragment lengths; and
- determining a cfDNA fragmentation profile for the subject.

69. The system of claim **68**, wherein the system is a machine learning system.

70. The system of claim **69**, wherein the machine learning system is a gradient tree boosting machine learning system.

71. The system of claim **68**, wherein a cfDNA fragmentation profile in the subject that is more variable than a reference cfDNA fragmentation profile is indicative of the subject as having or at risk of having cancer.

72. The system of claim **68**, wherein a cfDNA fragmentation profile in the subject that is less or equally variable than a reference cfDNA fragmentation profile is indicative of the subject as being healthy.

73. The system of claim **71**, wherein the reference cfDNA fragmentation profile is a reference nucleosome cfDNA fragmentation profile.

74. The system of claim **68**, wherein determining the cfDNA fragmentation profile distinguishes circulating tumor DNA (ctDNA) from non-cancer-associated white blood cell DNA in the blood.

75. The system of claim **68**, wherein the mapped sequences comprise tens or hundreds to thousands of genomic intervals.

76. The system of claim 68, wherein the genomic intervals are non-overlapping.

77. The system of claim 68, wherein the genomic intervals each comprise thousands to millions of base pairs.

78. The system of claim 68, wherein a cfDNA fragmentation profile is determined within each genomic interval.

79. The system of claim 68, wherein a cfDNA fragmentation profile comprises a median fragment size.

80. The system of claim 68, wherein a cfDNA fragmentation profile comprises a fragment size distribution.

81. The system of claim 68, wherein a cfDNA fragmentation profile is determined over the whole genome or a subgenomic interval.

82. The system of claim 68, wherein cfDNA fragmentation profiles provide over 20,000 reads per genomic intervals.

83. The system of claim 68, wherein the genomic coverage is about 0.1×, 0.2×, 0.5×, 1× or 2×.

84. The system of claim 68, wherein the cfDNA fragmentation profile further predicts the tissue of origin of the cancer in a subject having or at risk of having cancer.

85. The system of claim 68, wherein the cancer is selected from the group consisting of: colorectal cancer, lung cancer, breast cancer, gastric cancer, pancreatic cancer, bile duct cancer, and ovarian cancer.

86. The system of claim 68, wherein the cancer is treated with or has previously been treated with a treatment comprising administering to the subject 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 combination thereof.

87. The system of claim 68, wherein cfDNA fragments are nucleosome protected DNA fragments.

88. The system of claim 68, wherein the sample is a blood, serum, plasma, amnion, tissue, urine, cerebrospinal fluid, saliva, sputum, broncho-alveolar lavage, bile, lymphatic fluid, cyst fluid, stool, ascites, pap smear, breast milk or exhaled breath condensate sample.

89. A method of predicting a cell free DNA (cfDNA) fragmentation profile of a subject comprising:

determining a cfDNA fragmentation profile prediction for the subject based on a DNA evaluation of fragments for early interception (DELFI) classifier score, using the

system of claim 68, thereby predicting a cfDNA fragmentation profile of the subject.

90. A method of predicting a cancer status in a subject comprising:

determining a cfDNA fragmentation profile prediction for the subject using the system of claim 68; and classifying the subject as a healthy subject or a subject having or at risk of having cancer based on variability of the cfDNA fragmentation profile in the subject, thereby predicting a cancer status in the subject.

91. A method of detecting and/or monitoring the status of cancer in a subject comprising:

determining a first cfDNA fragmentation profile of the subject at a first time using the system of claim 68; and classifying the subject as a healthy subject or a subject having or at risk of having cancer based on the cfDNA fragmentation profile of the subject, thereby detecting cancer in the subject.

92. The method of claim 91, further comprising determining a second cfDNA fragmentation profile of the subject at a second time and comparing the first cfDNA fragmentation profile to the second cfDNA fragmentation profile to monitor the status of cancer in the subject.

93. The method of claim 92, wherein the first and/or the second cfDNA fragmentation profiles are determined before, during and/or after the course of a cancer treatment.

94. The method of claim 93, wherein determining the first and/or the second cfDNA fragmentation profiles over the course of a cancer treatment indicates responsiveness to the cancer treatment.

95. The method of claim 92, wherein a second cfDNA fragmentation profile that is less or equally variable than a reference cfDNA fragmentation profile obtained in a healthy subject indicates a response to the cancer treatment in the subject.

96. The method of claim 92, wherein a second cfDNA fragmentation profile that is more variable than a reference cfDNA fragmentation profile obtained in a healthy subject indicates an absence of response to the cancer treatment in the subject.

97. The method of claim 91, wherein determining the cfDNA fragmentation profile is indicative of a change in tumor size, and/or change in tumor localization.

* * * * *