

NCI Biospecimen Evidence-Based Practices		CELL-FREE DNA: BIOSPECIMEN COLLECTION AND PROCESSING			
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1.0 PURPOSE

The purpose of this document is to provide evidence-based guidance for the proper collection and processing of cell-free DNA (cfDNA) from human plasma¹. This guidance is intended to support the development and execution of evidence-based Standard Operating Procedures (SOPs) for human biospecimen collection, processing, and storage to be used in conjunction with properly validated analytical assays

2.0 SCOPE

This evidence-based best practice document is applicable to the collection, processing, storage and extraction of cfDNA from plasma for research and clinical analytical applications. Recommendations within this document pertain to the analysis of cfDNA of both tumor and fetal origin, and detection of both somatic and germline mutations.

3.0 DEFINITIONS

- 3.1 Anticoagulant:** A substance that is used to prevent and treat blood clots in blood vessels and the heart; also called blood thinner
- 3.2 Serum:** The clear liquid portion of the blood that remains after blood cells and clotting proteins have been removed
- 3.3 Plasma:** The clear, yellowish, fluid portion of the blood that carries the blood cells; the proteins that form blood clots are in plasma
- 3.4 Aliquot:** A portion of the total amount of the biospecimen collected
- 3.5 Cell-free DNA (cfDNA):** DNA found in the bloodstream, and generally measured in serum or plasma.
- 3.6 Circulating tumor DNA (ctDNA):** DNA found in the bloodstream that is derived from tumor cells
- 3.7 Cell-free fetal DNA (cffDNA):** DNA found in the bloodstream originating from a fetus

¹ While plasma is preferred for prospective studies, properly processed serum may be used for some applications. Proper processing of serum requires prompt centrifugation after clotting.

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- 3.8** **Freeze-thaw cycles**: The number of times a biospecimen or sample has been frozen and then thawed
- 3.9** **Plasma processing delay**: The time between venipuncture and centrifugation of blood to fractionate the sample and isolate plasma
- 3.10** **Interim plasma storage**: The duration between the transfer of plasma to new tube(s) and analysis
- 3.11** **Extraction delay**: The time between the completion of plasma processing and DNA extraction

4.0 ENVIRONMENTAL HEALTH & SAFETY

- 4.1** The Guideline for Isolation Precautions (CDC-2007) should be used for all phases of blood collection and processing and cfDNA processing to prevent the transmission of infectious agents in a Healthcare setting (Reference 9.1.1).
- 4.2** Infection Prevention and Control Recommendations for Hospitalized Patients Under Investigation for Ebola Virus Disease (EVD) in U.S. Hospitals (CDC, 2014) should be consulted prior to biospecimen procurement from patients with suspected or confirmed EVD (Reference 9.1.2).

5.0 RECOMMENDED MATERIALS/EQUIPMENT

- 5.1** Appropriate safety equipment as described in published guidelines (References 9.1.1, 9.1.2, 9.1.4)
- 5.2** Plastic-backed absorbent bench paper
- 5.3** K2 EDTA blood collection tubes (10 mL)(See 7.1) or stabilizing cfDNA blood collection tube of choice (See 7.2)
- 5.4** Antiseptic wipes
- 5.5** Vacutainer needle with hub or butterfly needle with Luer adapter
- 5.6** Tourniquet
- 5.7** Phlebotomy chair

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5.8 Refrigerator (4°C)

5.9 Hi-speed centrifuge

5.10 Falcon tubes

5.11 Storage tubes suitable for centrifugation and storage at -80°C

5.12 Pipettes and sterile DNase free tips for transfer

5.13 Freezer (-80°C or colder) for storage

6.0 PROCEDURAL GUIDELINES

6.1 Recording of biospecimen preacquisition data

6.1.1 Whenever possible, extensive data should be recorded relating to preacquisition conditions that may affect the integrity of the biospecimen. Such data may include patient information (including age, gender, fasting status, diagnosis, treatment, and date of last treatment received) as well as details relating to biospecimen acquisition (including number of venipuncture attempts, patient position, tourniquet usage, and date and time of blood collection) (Reference 9.1.3). Variability in all preacquisition and acquisition variables (including but not limited to sample collection, labeling, transport, and storage) should be minimized via strict accordance to a validated SOP (Reference 9.1.8) and all deviations from the SOP should be recorded for each sample.

6.1.2 Label each collection tube with unique unambiguous identifiers, such that the tube can be readily matched to all relevant patient and specimen handling data (Reference 9.1.3). Ensure that all labels are robust to all handling steps including but not limited to frozen storage, water, and commonly used solvents.

6.2 Collection tube considerations

6.2.1 Optimally, collection tubes containing EDTA should be used to prevent coagulation. Alternatively, acid citrate dextrose is also an acceptable anticoagulant. Heparin and citrate should be avoided (See 7.1 and 8.3.3).

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6.2.2 Streck Blood Collection Tubes (BCT) or other cfDNA stabilizing tubes are recommended when processing delays longer than 2 h are anticipated (See 7.2 and 8.3.3).

6.2.3 The required volume of blood collection is dependent on both the downstream analytical platform and endpoint measured, but generally one to two 10 mL tubes will ensure sufficient cfDNA yield (See 8.3.4); however, use of collection tubes between 2.7 and 10 mL is acceptable, depending on the downstream application (See 7.3).

6.3 Blood Collection

6.3.1 If using K2 EDTA tubes, optimally tubes should be pre-chilled on ice for a minimum of 5 minutes prior to collection, but this may not be necessary (Reference 9.1.4). If using a cfDNA stabilizing tube, tubes must remain at room temperature.

6.3.2 The patient must be seated for at least 5 minutes before venipuncture with the arm positioned on a slanting armrest such that there is a straight line from the shoulder to the wrist (Reference 9.1.4).

6.3.3 Apply a tourniquet 3-4 inches above the venipuncture site (Reference 9.1.3) with enough pressure to provide adequate vein visibility. Have the patient form a fist. Select the median, cubital, basilic, or cephalic veins for venipuncture (References 9.1.4 and 9.1.5). Collection from a port should be avoided (Reference 9.1.5).

6.3.4 Clean the venipuncture site with an antiseptic wipe in a circular motion beginning at the insertion site (References 9.1.4 and 9.1.5). Once dry, anchor the vein by placing your thumb 2 inches below the site and pulling the skin taut to prevent the vein from moving (References 9.1.4 and 9.1.5).

6.3.5 Insert the 21-23 gauge butterfly needle (See 8.3.2) with Luer adapter into the vein at a 30° angle and then push the evacuated tube into the hub or adapter (References 9.1.4 and 9.1.5). Alternatively, a vacutainer needle (with hub attached) may be used (References 9.1.4 and 9.1.5).

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6.3.6 Once blood flow is established, release the tourniquet (total elapsed tourniquet time should be < 1 min) (References 9.1.4 and 9.1.5) and ask patient to open hand.

6.3.7 Make sure that tube additives do not touch the stopper or the end of the needle during venipuncture (Reference 9.1.5).

6.3.8 Optimally the first 0.5-3 mL of blood should be discarded prior to collecting the EDTA plasma (Reference 9.1.5). It may be acceptable to collect blood without discarding blood.

6.3.9 Immediately after completely filling the tube (See 8.3.4), remove the tube leaving the needle inserted until all tubes have been filled. Place gauze over the puncture site and remove the needle (Reference 9.1.4). Slowly and gently invert each tube 8-10 times (Reference 9.1.5).

6.3.10 If using K2 EDTA tubes, tubes containing blood specimens should be stored vertically on wet ice (Reference 9.1.5, See 8.3.5). If using Streck BCT tubes or other cfDNA stabilizing tubes, tubes containing blood specimens should be stored vertically at room temperature until processing (See 8.3.5).

6.4 Processing Delay

6.4.1 Optimally, EDTA blood should be centrifuged within 2 h of venipuncture, although a delay of up to 4 h at room temperature or 24 h at 4°C is acceptable (See 7.4 and 8.3.5). If blood is collected in a Streck BCT tube, then room temperature or ambient storage or transport for up to 3 days before processing is acceptable (See 7.2 and 8.3.5).

6.4.2 Regardless of tube type, agitation of blood after initial tube inversion should be minimized during a processing delay (See 7.5).

6.5 Blood Processing

6.5.1 To separate cells from the remaining plasma, centrifuge blood collection tubes at 800-1600 *g* for 20 min at 4°C or room temperature (See 8.3.6). See 7.6 for alternative speeds and durations.

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6.5.2 Transfer plasma to a new Lo-Bind (See 8.3.6) (or an equivalent container), carefully leaving the buffy coat behind.²

6.5.3 To separate cell debris and organelles as well as to ensure cell removal from plasma, a second centrifugation at 14000-16000 *g* for 10-20 min at room temperature or 4°C is preferred (See 7.8 and 8.3.6), but filtration is an acceptable alternative (See 7.8).

6.5.4 Plasma should be aliquoted into new tubes suitable for -80°C storage (See 7.8 and 8.3.7). The required volume ranges from 400 µl to more than 10 mL of plasma depending on the extraction method and analytical platform.

6.6 Interim Plasma Storage

6.6.1 Optimally, storage of plasma post-centrifugation but prior to cfDNA extraction should be limited to 3 h or less at 4°C, up to 3 months at -20°C, or 9 months at -80°C (See 7.9). However, the expert panel has found that long term storage at -80°C is acceptable for most analyses (See 8.3.7). For noninvasive prenatal testing (NIPT), refrigerated storage of Streck plasma for 3-4 days is acceptable (See 8.3.7).

6.6.2 cfDNA should be extracted from frozen plasma immediately after thawing at room temperature (See 8.3.7). DNA should be extracted after the first thaw (See 7.10 and 8.3.7).

6.7 cfDNA Extraction and Quantification

6.7.1 Optimally, cfDNA should be extracted using a circulating nucleic acid kit or an equivalent kit (See 8.3.8). See 7.11 and 8.3.8 for acceptable alternatives.

6.7.2 cfDNA should be quantified by real-time or digital PCR using multiple amplicons but use of fluorometry is also acceptable (See 7.12 and 8.3.10). PCR-based methods are preferred when evaluating fragment size, but electrophoretic methods are also acceptable (See 7.12 and 8.3.10).

² Plasma may be stored in liquid nitrogen between centrifugations (See 7.7).

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- 6.7.3** cfDNA suitability for subsequent analysis should be evaluated by real-time PCR (See 7.13).
- 6.7.4** Extracted cfDNA may be stored as aliquots at -20°C (See 7.14). Optimally, cfDNA should only be used after the first thaw (See 8.3.9).
- 6.7.5** Each analytical assay should be validated for accuracy, precision, specificity, and sensitivity using suitable reference material (Reference 9.1.7) (See 7.15).

7.0 SUMMARIES OF LITERATURE EVIDENCE

- 7.1 Collection tube choice.** Plasma is preferred over serum for cfDNA analysis due to a higher incidence of cellular genomic DNA contamination in serum (reviewed in [1, 2]). The anticoagulants EDTA, heparin, citrate and acid-citrate dextrose are acceptable when blood is processed immediately (<2 h) [3, 4], but cfDNA concentrations differ among anticoagulants [5]. For processing delays of 6 h or longer at room temperature, EDTA performed superiorly, with significantly smaller changes in cfDNA concentration over time than heparin or citrate (1.6-fold vs. 7.6- and 8.0-fold, respectively) [4]. However, when specimens were refrigerated during the delay cfDNA concentrations were stable longer among specimens collected in tubes containing sodium citrate than EDTA [6]. EDTA has also been shown to inhibit DNase activity in plasma specimens compared to serum controls, although other anticoagulants were not examined [7]. While heparin has been shown to inhibit Taq DNA polymerase at concentrations below those used during blood collection [8, 9], a recent study reported comparable real-time PCR efficiencies for plasma collected using heparin, EDTA, and citrate [4]. Comparable cfDNA concentrations were reported when blood was collected in Monovette and Vacutainer tubes, but data was not shown [10].
- 7.2 Stabilized collection tubes.** When immediate plasma separation is not possible, the use of Streck BCT [11-28], PAXgene cfDNA [14, 21, 27, 29, 30], Roche cfDNA [21, 26, 31, 32], CellSave [15, 33], or Blood Exo DNA ProTeck tube [34] collection tubes may extend cfDNA stability. In the majority of articles surveyed, comparable levels of cfDNA [18], low molecular weight cfDNA fraction or mutant allele fraction [22] were observed among whole blood collected in Streck BCT tubes subjected to ambient shipping or processing delays of 2 days [11], 3 days [12, 13], 4 days [14, 15], 5 days [16-18, 25, 35], 7 days [19, 21, 22, 31, 36, 37]; or according to research published by Streck, 14 days [20,

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38] and immediately processed controls. Similarly, comparable cfDNA yields were reported among whole blood specimens collected in PAXgene cfDNA tubes when subjected to a processing delay at room temperature of 4 days [14] or 7 days [21, 29] and immediately processed controls. While use of Roche cfDNA tubes largely prevented release of genomic DNA during a processing delay of 14 days at room temperature [31] or 5 h at 39°C followed by 19 h at 22°C [21], increased genomic DNA was evident after 7 days at room temperature [21, 26] and hemolysis was reported after as little as 24 h at room temperature or 4°C [32]. When stabilized collection tubes were experimentally compared, equivalent cfDNA levels were obtained for Streck BCT and PAXgene cfDNA tubes when processing delays were limited to 3 days or less [6]; but while the prevalence of genomic contamination and hemolysis were similar in some studies among Streck BCT, Roche cfDNA tubes [31], and PAXgene cfDNA tubes [21] when processing delays were limited to 7 days or less, one study observed an increase in both the degree and frequency of hemolysis after 72 h (or 24 h with agitation) among plasma collected in Roche tubes compared to Streck BCT or PAXgene cfDNA tubes, although genomic DNA contamination occurred more frequently in PAXgene cfDNA tubes than Streck BCT or Roche cfDNA tubes [28]. Notably, several studies have reported processing delay-induced effects in BCT tubes, including a 0.4-fold increase in genomic DNA yield after a room temperature delay of 3 days [39], increased genomic DNA release and hemolysis after a room temperature delay of 14 days [31] and altered levels of β -actin [20] and fetal Y chromosome [23] after 3 h and 24 h at room temperature, respectively.

- 7.3 Blood collection volume.** There is no consensus in the literature on an optimal blood collection volume. Use of 2.7 mL [40], 3.0 mL [41], 5 mL [12, 23], 6 mL [42], and 10 mL [20, 23, 24, 36, 38, 43] tubes have been reported for cfDNA analysis in the literature. Blood collection volume is dependent on the volume of plasma required for downstream applications. The volume of plasma used is correlated with the cfDNA yield, and cfDNA input into next generation sequencing (NGS) assays is inversely correlated with the limit of detection for variant alleles [44].
- 7.4 Processing delay for EDTA blood.** Effects attributable to a delay in plasma processing have been reported after as short as 4 h [45], with storage temperature [18, 23, 45-47], fragment size [13], anticoagulant (See 7.1) and cfDNA source [5, 12, 19, 38] identified as confounding factors. Increases in genomic DNA yield have been reported after storage

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for 4 h [45], 6 h [1, 48], 24 h [4, 22, 23, 38, 46], or 48 h [1, 11, 19, 36, 48]. The low molecular weight DNA fraction decreased when EDTA blood was stored 8 h prior to centrifugation compared to 0 h [21], and when retrospective EDTA specimens that experienced a processing delay of up to 24 h were compared to prospectively collected EDTA specimens processed within 1-3 h [13]. Mutational frequencies were altered after a processing delay of 3 [22] or 4 days [15, 47] and the percentage of genomic wildtype (wt) DNA was higher in 3 of 6 specimens when processing was delayed by 48 h [11]. Conversely, several studies report cfDNA concentrations were unaffected by room temperature storage of whole blood for up to 24 h and the mutant tumor-derived cfDNA (ctDNA) fraction copy numbers were unaffected by storage for up to 48 h in EDTA or BCT tubes [17]. Reducing the temperature of the EDTA tube during the delay by placement in refrigeration or incubation on wet ice did not prevent the alterations in cfDNA concentration observed among EDTA plasma specimens after a 2 h processing delay [23, 45, 46], but did partially attenuate effects observed after 24 h or longer [1, 22, 47]. Further, incubation on wet ice prevented an increase in the ratio of long to short PCR amplicons that was observed following a 24 h delay at room temperature [46]. Similarly, shipping blood collected in EDTA tubes when the ambient temperature was less than 0°C, rather than 0 to 10 or 30°C, resulted in smaller changes to the levels of fetal or total cfDNA, indicating shipping on ice may provide stabilization [18]. Delayed centrifugation resulted in a decline in the percentage of fetal cfDNA relative to maternal cfDNA after 24 h [23, 38, 49], 48 h [19], or 72 h [12], but not after 48 h [24], indicating cfDNA source may be a confounding factor.

- 7.5 Specimen agitation.** When EDTA or K3EDTA tubes were agitated during a processing delay, statistically significant increases in cfDNA fragmentation and concentrations were reported after 3 h [1] or 6 h [20], respectively, in comparison to controls that were processed within 40 min; but, similar increases did not occur among the same tube types when stored for the same duration without agitation or in BCT tubes with agitation [16].
- 7.6 First centrifugation.** Levels of cfDNA in plasma were not affected by the speed of initial centrifugation. Comparable cfDNA levels were found in plasma obtained by initial centrifugation at 820 versus 1600 *g* [47] or at speeds between 400-16000 *g* [50, 51], but in all studies cellular contamination was further decreased by subsequent processing steps before analysis. Levels of cfDNA were also not affected by refrigeration during

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centrifugation [43, 51] or brake speed [43]. While not experimentally compared, initial centrifugation at 1200-1900 *g* for 10 min was common in the literature [1, 12, 23, 24, 36, 38, 40-42, 46, 48, 52-55].

7.7 Interim specimen storage. Storage of plasma at -20°C between centrifugation steps did not affect albumin cfDNA levels [56] or multiplexed cfDNA copies per mL [5]. Similarly, storage of plasma at -80°C for up to 2 weeks, 4°C for up to 72 h, or for up to 1 week at room temperature prior to a second centrifugation step did not affect total, long or fetal cfDNA copy numbers, but unfavorable effects were noted after 2 weeks at room temperature [52]. While experimental comparisons were not investigated, frozen storage at either -20°C or -80°C between centrifugation steps has been reported elsewhere [1, 48].

7.8 Second centrifugation. Microcentrifugation of separated plasma at 16,000 *g* for 10 min served to minimize cellular DNA contamination [55, 56], producing cfDNA concentrations comparable to those of control specimens filtered through a 0.2 μm membrane after initial separation [55]. There was no effect found of centrifuging at 3000 *g* versus 14000 [47] or 16,000 *g* [57] or of centrifuging at 360, 6000 or 16000 *g* on cfDNA yield and genomic contamination [51]. However, centrifugation speed has been shown *in situ* to influence the expected recovery of cfDNA and plasma components [58]. Comparable results were also obtained when separated plasma underwent microcentrifugation immediately or after a period of frozen storage [5, 56, 57]. While different speeds, duration, and temperatures of a second centrifugation have not been compared experimentally, several studies also report successful cfDNA analysis after microcentrifugation of separated plasma at 6,000 [16], 14,000 [47] and 16,000 *g* for 10 min [1, 12, 23, 24, 36, 38, 40, 41, 46, 52, 53, 55, 59].

7.9 Interim and long-term plasma storage. Storage of plasma before cfDNA extraction for 4 h [1] or up to 172 h [60] at room temperature did not significantly alter cfDNA concentration in plasma specimens. When temperatures of a delay to extraction were compared experimentally, 3 h at -80°C, -20°C, 4°C, and room temperature resulted in comparable cfDNA concentrations but specimens stored at -80°C or -20°C had a slightly higher DNA integrity index (the ratio of long to short PCR amplicons) than specimens stored at higher temperatures [1]. Similarly, genotyping results were comparable among specimens sent to different laboratories and stored for 2-23 days at 4, -20 or -80°C [61].

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Frozen storage of processed plasma at -80°C for longer durations did not significantly alter cfDNA concentration as determined by real-time PCR when durations were limited to 2 weeks [46] or 9 months [1], but after 7 years there was an extraction method-dependent reduction in detection of an EGFR mutation [6]. When assessed by real-time PCR, storage of plasma at -20°C led to small but significant declines in cfDNA concentration beginning after 3-5 months [1], with an estimated decline of 30% per year by one study, although only two timepoints were examined 4-24 months post-collection [62]. Conversely, no difference in sequencing metrics were observed between matched fresh and frozen (9-24 days at -80°C) plasma specimens [63] and no such alteration in cfDNA concentration was detected using a semi-quantitative colorimetric method after plasma storage for 3.5 months at -20°C [64].

7.10 Freeze-thaw cycling. Plasma subjected to three freeze-thaw cycles exhibited evidence of cfDNA degradation in the form of significant declines in the ratio of long to short PCR amplicons when compared to controls that underwent one freeze-thaw cycle [1] or remained unfrozen [46]. Freeze-thaw cycling was shown to have an effect on the size distribution of cfDNA fragments, but the significance depended on cfDNA extraction method [65]. Potential effects of thaw duration and temperature on plasma cfDNA have not been investigated to date.

7.11 cfDNA extraction. While, a comparison of DNA integrity among 44 laboratories that extracted cfDNA from the same plasma specimen found cfDNA to be more intact when a cfDNA-specific extraction kit was used rather than a general DNA isolation kit [66], when commercially available fragmented tumor and wildtype DNA was used cfDNA size was comparable among five different extraction kits [67]. However, the literature supports the use of the QIAamp Circulating nucleic acid (CNA) kit [23, 27, 52, 68-75], QIASymphony circulating DNA kit [27], QIAamp MinElute ccfDNA kit [27], QIAamp DSP virus kit [69], Norgen Plasma/Serum Cell-Free Circulating DNA Purification Midi Kit [13, 73], Maxwell RSC cfDNA Plasma Kit [6, 72, 74], Norgen Plasma/Serum Cell-Free Circulating DNA purification kit [13, 76], Zymo Research Quick-cfDNA Serum and Plasma kit [76], MagNaPure isolation kit [77], and the NucleoSpin kit [77]. Extraction verification should involve use of real-time PCR-based amplification or electrophoretic analysis of different sized fragments of a spike-in control as extraction kit choice may introduce fragment size bias [73, 78].

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- 7.12 cfDNA quantification.** While fluorometry overestimated the number of amplifiable copies of cfDNA compared to real-time PCR [79-82] and automated capillary electrophoresis [65], cfDNA yields determined by fluorometric methods and real-time PCR were modestly to strongly correlated [80] or strongly to very strongly correlated [81, 82] and PicoGreen was shown in one study to result in lower correlations of variance (CVs) than real-time PCR [61]. cfDNA yields as determined by fluorometric methods and droplet digital PCR (ddPCR) were very strongly correlated [13]. The magnitude of the differences between quantification methods was influenced by the extraction kit used [27, 65, 76]. Also, use of TapeStation to quantify cfDNA resulted in overestimation in some specimens compared to fluorometry or real-time PCR [76]. Differences among reference gene levels were larger when quantified by real-time PCR than by digital PCR, but reliable yield determination was possible using real-time PCR when three targets were amplified [78]. Finally, the ddPCR-determined input of low molecular weight cfDNA was strongly correlated with NGS library diversity [13].
- 7.13 Sample qualification.** Genomic contamination of isolated cfDNA samples can be assessed by examining either the ratio of long to short real-time PCR generated amplicons [21, 83] or the electropherogram trace [83], although real-time PCR displayed greater sensitivity and also revealed the presence of PCR inhibitors [83].
- 7.14 Storage of extracted cfDNA.** A decline in amplifiable copies of cfDNA was observed when isolated cfDNA was stored at -20°C, although freshly isolated cfDNA was not included as a control [62]. We were unable to locate additional studies investigating effects of isolated cfDNA storage duration or temperature.
- 7.15 Assay validation and analysis.** Appropriate control material for cfDNA assay validation to determine accuracy, precision, specificity, and range includes commercially available reference materials that are fragmented to mirror the size range of cfDNA and contain somatic mutations or the target of interest at differing levels [67, 84]. Importantly, quality assessment data based on real-time PCR amplicon length differed slightly between sonicated genomic DNA and true cfDNA [83], highlighting the importance of the appropriate material for assay validation and using sonication parameters to obtain an accurate fragmentation size.

A recent review found that the sensitivity, specificity, requirements, cost, and limitations of assays used for cfDNA analysis were highly variable, and that the majority

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of differences were attributable to the NGS strategies applied and the real-time PCR, digital PCR, and mass spectrometry platforms employed [85]. Using synthetic cfDNA quality control materials, comparable detection rates of variants were achieved using NGS [67, 84], ARMS and ddPCR [84] in different laboratories; however, even when the same control material was used differences were encountered, including an approximately 10% higher variant allele frequency using ddPCR than NGS [67].

8.0 EXPERT-VETTING

8.1 Details of Expert Review

Eight experts were identified and invited to review the document based on their contributions to the literature regarding the isolation of cfDNA from whole blood specimens (See 8.2). Feedback from participants was collected and documented following initial review of the draft BEBP. Final thoughts and recommendations were captured from the expert panel during a scheduled teleconference after review of the BEBP document. Participating individuals did so voluntarily and without compensation.

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8.3 Expert Recommendations:

- 8.3.1 Scope:** The expert panel agreed that cfDNA obtained using an SOP in accordance with these recommendations should be of suitable quality for the study of cfDNA and cell-free fetal DNA.
- 8.3.2 Biospecimen Acquisition:** An expert stated that when selecting a needle gauge, it is critical to consider the pressure the cfDNA is exposed to, thus use of a butterfly needle for collection is preferred. When selecting the optimal needle size and type, an expert noted the importance of considering patient discomfort. One expert finds that use of a 23 gauge butterfly needle minimizes pain for the patient while permitting the collection of multiple tubes and use of 20-23 gauge needles is usually specified for NIPT. Two experts noted that it is not usually necessary to discard any blood.
- 8.3.3 Tube Type:** The experts panel unanimously agreed that EDTA collection tubes are preferred if immediate processing is possible. When processing delays are necessary and anticipated, each panel member reported using Streck BCT tubes. However, individual experts each shared that based on preliminary comparisons, they observed no differences in cfDNA endpoints when specimens were collected and shipped in Streck versus PAXgene tubes, or PAXgene and Roche cfDNA tubes versus Streck BCT tubes. The experts agreed that blood collection tubes containing heparin and citrate should be avoided when possible.
- 8.3.4 Tube volume:** The majority of the expert panel agreed that underfilling tubes must be avoided to ensure the proper concentration of stabilizers and/or anticoagulants. However, one expert routinely processes 7-10 mL specimens for NIPT and, while not recommended, noted that smaller volumes (4-7 mL) may be acceptable for this application. The panel unanimously agreed that the volume of blood necessary for cfDNA analysis is dependent on the intended analytical platform and the requirements for detection. For example, a smaller volume may be necessary if only a limited number of real-time PCR or digital PCR assays are anticipated and the target occurs at a higher frequency, while a larger volume (one or two 10 mL tubes) is required when detecting low frequency mutations on platforms such as NGS.

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8.3.5 Processing delays: Experts stressed that effects of a processing delay are observed rapidly when blood is stored in EDTA tubes, particularly at room temperature, before centrifugation. The experts minimize storage of EDTA blood at room temperature, processing blood specimens within 1-3 h of collection. However, one expert noted that this window may be extended to 6 h for high frequency mutation detection, if necessary. The panel agreed that EDTA blood may be stored at 4°C for up to 24 h before processing. There was also a consensus among the panel that use of stabilizing tubes extends cfDNA stability at room temperature, but tube types differed slightly in maximum allowable storage duration (3-4 days versus 5-7 days). Two experts cautioned that the volume of plasma obtained decreases with storage in Streck tubes beyond 3 days. Two experts reported detrimental effects of storing blood in Streck BCT tubes at 4°C. Regardless of tube type, one expert cautioned that tubes must be stored in a vertical position.

8.3.6 Centrifugation: The experts agreed that centrifugation and speed must be considered together and are dependent on tube type. Three experts found no effect of initial centrifugation speed for EDTA collection tubes, as all were sufficient in the elimination of cellular contamination, but three experts have found it necessary to centrifuge Streck tubes for at least 20 min. For the first centrifugation, all the experts on the panel perform an initial centrifugation at 800-1600 *g* for 10-20 min with the majority using 1600 *g*. The panel agreed that a second centrifugation at 14000-16000 *g* is necessary to eliminate genomic contamination from cells and cellular debris. Three experts advised against storage between centrifugation steps as it can lead to genomic contamination. Further, two experts noted that Lo-Bind tubes should be considered for the second centrifugation step.

8.3.7 Plasma storage: The expert panel agreed that plasma should be stored at -80°C. The experts have not identified a maximum duration of -80°C storage but note that plasma stored for as long as 3 years was successfully analyzed. If cfDNA is only being used for detection of a high frequency mutation, then storage at -20°C may be acceptable. Refrigerated storage of plasma from Streck tubes for 3-4 days is acceptable for NIPT. Experts advised that the volume and number of plasma aliquots should be governed by cfDNA extraction method and analytical

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platform. It was stressed that freeze-thaw cycling of plasma aliquots should be avoided. While one expert noted that there has not been a well-controlled study on potential effects due to thaw temperature, all experts participating on the panel noted they thaw plasma aliquots at room temperature.

- 8.3.8 Extraction:** One expert cautioned that some extraction kits may favor nucleic acids of a specific size, thus bias in cfDNA length can be introduced through the extraction method chosen/used. Therefore, a series of internally spiked controls of different fragment lengths should be used to verify differences are not due to extraction method. Regarding specific commercial extraction kits, two experts recommended the QIAamp CNA method over bead-based methods, while another noted that QIAamp blood and CNA kits are identical. If convenience is a priority, experts reported sufficient yields and consistent findings with the magnetic-based MagMAX kit and MAXwell kits. Finally, if a large plasma volume is used, it is recommended that a vacuum manifold and pump-based method be applied. The use of two high-speed centrifugations of plasma will decrease the potential for clogs in the vacuum-based method.
- 8.3.9 cfDNA storage:** All of the experts surveyed store extracted cfDNA at -20°C, although one expert also noted storage at -80°C. Three of the experts stressed that freeze-thaw cycling of cfDNA samples is detrimental and should be avoided, while another expert stated that cfDNA is always freshly extracted from stored plasma to avoid cfDNA frozen storage. Two experts recommended that extracted cfDNA be stored in Lo-Bind tubes.
- 8.3.10 Quantification:** Quantifying isolated DNA by real-time PCR or digital PCR were considered superior methods by the expert panel, as each also evaluates integrity and size distribution. All of the experts recommended using both long (>150 bp) and short (<80 bp) amplicons for this analysis and one expert suggested normalization to multiple (two or more) reference genes. One expert cautioned that shorter cfDNA fragments (50-166) may be missed by real-time PCR so a second quantification method should be considered. One expert stated the InviQuant GeneCount 40 assay can be used for this purpose. For assays such as NGS where input quantity is more flexible, fluorometric methods were deemed sufficient by the panel and may be superior for quantification of short

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cfDNA. An expert suggested that electrophoretic methods can be used to quantify extracted cfDNA and verify it is of the appropriate size prior to analysis.

9.0 REFERENCES

9.1 Laboratory Guidelines

9.1.1 2007 Guideline for Isolation Precautions: Preventing Transmission of Infectious Agents in Healthcare Settings (CDC, 2007):

<http://www.cdc.gov/hicpac/2007IP/2007isolationPrecautions.html>

9.1.2 *Infection Prevention and Control Recommendations for Hospitalized Patients Under Investigation (PUIs) for Ebola Virus Disease (EVD) in U.S. Hospitals* (CDC, 2014):

<http://www.cdc.gov/vhf/ebola/healthcare-us/hospitals/infection-control.html>

9.1.3 Biorepositories and Biospecimen Research Branch (formerly Office of Biorepositories and Biospecimen Research), National Cancer Institute, National Institutes of Health. NCI Best Practices for Biospecimen Resources. 2016

<https://biospecimens.cancer.gov/bestpractices/2016-NCIBestPractices.pdf>

9.1.4 CLSI (formerly NCCLS): Procedures for the collection of diagnostic blood specimens by venipuncture; Approved Standard - Sixth Edition. CLSI document GP41-A6 (ISBN 1-56238-650-6). Clinical and Laboratory Standards Institute, 940 West Valley Road, Suite 1400, Wayne, Pennsylvania 19087-1898 USA, 2007.

9.1.5 Clinical Proteomic Tumor Analysis Consortium, Office of Cancer Clinical Proteomics Research, National Cancer Institute. Prospective Biospecimen Collection Protocol, Blood Collection and Processing for Plasma and Whole Cell Components. v 2.0. 2013.

9.1.6 Qiagen. QIAamp Circulating Nucleic Acid Handbook. Second Edition, January 2011.

<https://www.qiagen.com/us/resources/resourcedetail?id=0c4b31ab-f4fb-425f-99bf-10ab9538c061&lang=en>

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9.1.7 International Council for Harmonisation of Technical Requirements for Pharmaceuticals for Human Use. Validation of Analytical Procedure: Text and Methodology Q2(R1) 2005

9.1.8 International Council for Harmonisation of Technical Requirements for Pharmaceuticals for Human Use. ICH guideline E18 on genomic sampling and management 13 of genomic data 2016

9.2 Literature References

1. El Messaoudi, S., et al., *Circulating cell free DNA: Preanalytical considerations*. Clin Chim Acta, 2013. 424C: p. 222-230.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
2. Bronkhorst, A.J., J. Aucamp, and P.J. Pretorius, *Cell-free DNA: Preanalytical variables*. Clin Chim Acta, 2015. 450: p. 243-53.
[PubMed Abstract](#)
3. Lee, T.H., et al., *Quantitation of genomic DNA in plasma and serum samples: higher concentrations of genomic DNA found in serum than in plasma*. Transfusion, 2001. 41(2): p. 276-82.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
4. Lam, N.Y., et al., *EDTA is a better anticoagulant than heparin or citrate for delayed blood processing for plasma DNA analysis*. Clin Chem, 2004. 50(1): p. 256-7.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
5. van Ginkel, J.H., et al., *Preanalytical blood sample workup for cell-free DNA analysis using Droplet Digital PCR for future molecular cancer diagnostics*. Cancer Med, 2017. 6(10): p. 2297-2307.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
6. Sato, A., et al., *Investigation of appropriate pre-analytical procedure for circulating free DNA from liquid biopsy*. Oncotarget, 2018. 9(61): p. 31904-31914.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
7. Barra, G.B., et al., *EDTA-mediated inhibition of DNases protects circulating cell-free DNA from ex vivo degradation in blood samples*. Clin Biochem, 2015. 48(15): p. 976-81.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)

NCI Biospecimen Evidence-Based Practices		CELL-FREE DNA: BIOSPECIMEN COLLECTION AND PROCESSING			
Author	Biorepositories and Biospecimen Research Branch			Revision #	
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8. Holodniy, M., et al., *Inhibition of human immunodeficiency virus gene amplification by heparin*. J Clin Microbiol, 1991. 29(4): p. 676-9.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
9. Yokota, M., et al., *Effects of heparin on polymerase chain reaction for blood white cells*. J Clin Lab Anal, 1999. 13(3): p. 133-40.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
10. Gautschi, O., et al., *Circulating deoxyribonucleic Acid as prognostic marker in non-small-cell lung cancer patients undergoing chemotherapy*. J Clin Oncol, 2004. 22(20): p. 4157-64.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
11. Kang, Q., et al., *Comparative analysis of circulating tumor DNA stability In K3EDTA, Streck, and CellSave blood collection tubes*. Clin Biochem, 2016. 49(18): p. 1354-1360.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
12. Hidestrand, M., et al., *Influence of temperature during transportation on cell-free DNA analysis*. Fetal Diagn Ther, 2012. 31(2): p. 122-8.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
13. Markus, H., et al., *Evaluation of pre-analytical factors affecting plasma DNA analysis*. Sci Rep, 2018. 8(1): p. 7375.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
14. Warton, K., et al., *Evaluation of Streck BCT and PAXgene Stabilised Blood Collection Tubes for Cell-Free Circulating DNA Studies in Plasma*. Mol Diagn Ther, 2017.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
15. van Dessel, L.F., et al., *Application of circulating tumor DNA in prospective clinical oncology trials - standardization of preanalytical conditions*. Mol Oncol, 2017. 11(3): p. 295-304.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
16. Medina Diaz, I., et al., *Performance of Streck cfDNA Blood Collection Tubes for Liquid Biopsy Testing*. PLoS One, 2016. 11(11): p. e0166354.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
17. Henao Diaz, E., et al., *The In Vitro Stability of Circulating Tumour DNA*. PLoS One, 2016. 11(12): p. e0168153.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)

NCI Biospecimen Evidence-Based Practices		CELL-FREE DNA: BIOSPECIMEN COLLECTION AND PROCESSING			
Author	Biorepositories and Biospecimen Research Branch			Revision #	
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18. Wang, Q., et al., *Real-time PCR evaluation of cell-free DNA subjected to various storage and shipping conditions*. Genet Mol Res, 2015. 14(4): p. 12797-804.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
19. Wong, D., et al., *Optimizing blood collection, transport and storage conditions for cell free DNA increases access to prenatal testing*. Clin Biochem, 2013. 46(12): p. 1099-104.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
20. Norton, S.E., et al., *A new blood collection device minimizes cellular DNA release during sample storage and shipping when compared to a standard device*. J Clin Lab Anal, 2013. 27(4): p. 305-11.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
21. Nikolaev, S., et al., *Circulating tumoral DNA: Preanalytical validation and quality control in a diagnostic laboratory*. Anal Biochem, 2017.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
22. Parpart-Li, S., et al., *The Effect of Preservative and Temperature on the Analysis of Circulating Tumor DNA*. Clin Cancer Res, 2017. 23(10): p. 2471-2477.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
23. Barrett, A.N., et al., *Implementing prenatal diagnosis based on cell-free fetal DNA: accurate identification of factors affecting fetal DNA yield*. PLoS One, 2011. 6(10): p. e25202.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
24. Buysse, K., et al., *Reliable noninvasive prenatal testing by massively parallel sequencing of circulating cell-free DNA from maternal plasma processed up to 24h after venipuncture*. Clin Biochem, 2013. 46(18): p. 1783-6.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
25. Meddeb, R., E. Pisareva, and A.R. Thierry, *Guidelines for the Preanalytical Conditions for Analyzing Circulating Cell-Free DNA*. Clin Chem, 2019.
[PubMed Abstract](#)
26. Parackal, S., et al., *Comparison of Roche Cell-Free DNA collection Tubes*. Pract Lab Med, 2019. 16: p. e00125.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
27. Lampignano, R., et al., *Multicenter Evaluation of Circulating Cell-Free DNA Extraction and Downstream Analyses for the Development of Standardized (Pre)analytical Work Flows*. Clin

NCI Biospecimen Evidence-Based Practices		CELL-FREE DNA: BIOSPECIMEN COLLECTION AND PROCESSING			
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Page #	Page 22 of 28	Initial Release Date	1/30/2020	Revision Date	

- Chem, 2019.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
28. Sorber, L., et al., *Specialized Blood Collection Tubes for Liquid Biopsy: Improving the Pre-analytical Conditions*. Mol Diagn Ther, 2019.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
29. Schmidt, B., et al., *Liquid biopsy - Performance of the PAXgene® Blood ccfDNA Tubes for the isolation and characterization of cell-free plasma DNA from tumor patients*. Clin Chim Acta, 2017. 469: p. 94-98.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
30. Denis, M.G., et al., *Efficient Detection of BRAF Mutation in Plasma of Patients after Long-term Storage of Blood in Cell-Free DNA Blood Collection Tubes*. Clin Chem, 2015. 61(6): p. 886-8.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
31. Zhao, Y., et al., *Performance comparison of blood collection tubes as liquid biopsy storage system for minimizing cfDNA contamination from genomic DNA*. J Clin Lab Anal, 2018: p. e22670.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
32. Enko, D., G. Halwachs-Baumann, and G. Kriegshäuser, *Plasma free DNA: Evaluation of temperature-associated storage effects observed for Roche Cell-Free DNA collection tubes*. Biochem Med (Zagreb), 2019. 29(1): p. 010904.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
33. van Dessel, L.F., et al., *High-throughput isolation of circulating tumor DNA: a comparison of automated platforms*. Mol Oncol, 2018.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
34. Fernando, M.R., et al., *A novel approach to stabilize fetal cell-free DNA fraction in maternal blood samples for extended period of time*. PLoS One, 2018. 13(12): p. e0208508.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
35. Hyland, C.A., et al., *Non-invasive fetal RHD genotyping for RhD negative women stratified into RHD gene deletion or variant groups: comparative accuracy using two blood collection tube types*. Pathology, 2017.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
36. Norton, S.E., et al., *A stabilizing reagent prevents cell-free DNA contamination by cellular DNA in plasma during blood sample storage and shipping as determined by digital PCR*. Clin Biochem,

NCI Biospecimen Evidence-Based Practices		CELL-FREE DNA: BIOSPECIMEN COLLECTION AND PROCESSING			
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Page #	Page 23 of 28	Initial Release Date	1/30/2020	Revision Date	

2013. 46: p. 1561-5.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
37. Toro, P.V., et al., *Comparison of cell stabilizing blood collection tubes for circulating plasma tumor DNA*. Clin Biochem, 2015. 48(15): p. 993-8.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
38. Fernando, M.R., et al., *A new methodology to preserve the original proportion and integrity of cell-free fetal DNA in maternal plasma during sample processing and storage*. Prenat Diagn, 2010. 30(5): p. 418-24.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
39. Sherwood, J.L., et al., *Optimised Pre-Analytical Methods Improve KRAS Mutation Detection in Circulating Tumour DNA (ctDNA) from Patients with Non-Small Cell Lung Cancer (NSCLC)*. PLoS One, 2016. 11(2): p. e0150197.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
40. Jung, M., et al., *Changes in concentration of DNA in serum and plasma during storage of blood samples*. Clin Chem, 2003. 49(6 Pt 1): p. 1028-9.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
41. Ordoñez, E., et al., *Evaluation of sample stability and automated DNA extraction for fetal sex determination using cell-free fetal DNA in maternal plasma*. Biomed Res Int, 2013. 2013: p. 195363.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
42. Clausen, F.B., et al., *Pre-analytical conditions in non-invasive prenatal testing of cell-free fetal RHD*. PLoS One, 2013. 8(10): p. e76990.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
43. Ammerlaan, W., et al., *Method validation for preparing serum and plasma samples from human blood for downstream proteomic, metabolomic, and circulating nucleic acid-based applications*. Biopreserv Biobank, 2014. 12(4): p. 269-80.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
44. Alborelli, I., et al., *Cell-free DNA analysis in healthy individuals by next-generation sequencing: a proof of concept and technical validation study*. Cell Death Dis, 2019. 10(7): p. 534.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)

NCI Biospecimen Evidence-Based Practices		CELL-FREE DNA: BIOSPECIMEN COLLECTION AND PROCESSING			
Author	Biorepositories and Biospecimen Research Branch			Revision #	
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45. Xue, X., et al., *Optimizing the yield and utility of circulating cell-free DNA from plasma and serum*. Clin Chim Acta, 2009. 404(2): p. 100-4.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
46. Chan, K.C., et al., *Effects of preanalytical factors on the molecular size of cell-free DNA in blood*. Clin Chem, 2005. 51(4): p. 781-4.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
47. Risberg, B., et al., *Effects of Collection and Processing Procedures on Plasma Circulating Cell-Free DNA from Cancer Patients*. J Mol Diagn, 2018.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
48. Angert, R.M., et al., *Fetal cell-free plasma DNA concentrations in maternal blood are stable 24 hours after collection: analysis of first- and third-trimester samples*. Clin Chem, 2003. 49(1): p. 195-8.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
49. Zhang, Y., et al., *Effect of formaldehyde treatment on the recovery of cell-free fetal DNA from maternal plasma at different processing times*. Clin Chim Acta, 2008. 397(1-2): p. 60-4.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
50. Lui, Y.Y., K.W. Chik, and Y.M. Lo, *Does centrifugation cause the ex vivo release of DNA from blood cells?* Clin Chem, 2002. 48(11): p. 2074-6.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
51. Sorber, L., et al., *Circulating Cell-Free DNA and RNA Analysis as Liquid Biopsy: Optimal Centrifugation Protocol*. Cancers (Basel), 2019. 11(4).
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
52. Barrett, A.N., et al., *Stability of cell-free DNA from maternal plasma isolated following a single centrifugation step*. Prenat Diagn, 2014. 34(13): p. 1283-8.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
53. Chen, W., et al., *Strategies of reducing input sample volume for extracting circulating cell-free nuclear DNA and mitochondrial DNA in plasma*. Clin Chem Lab Med, 2012. 50(2): p. 261-5.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
54. Jing, R.R., et al., *A sensitive method to quantify human cell-free circulating DNA in blood: Relevance to myocardial infarction screening*. Clin Biochem, 2011. 44(13): p. 1074-9.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)

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Page #	Page 25 of 28	Initial Release Date	1/30/2020	Revision Date	

55. Chiu, R.W., et al., *Effects of blood-processing protocols on fetal and total DNA quantification in maternal plasma*. Clin Chem, 2001. 47(9): p. 1607-13.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
56. Swinkels, D.W., et al., *Effects of blood-processing protocols on cell-free DNA quantification in plasma*. Clin Chem, 2003. 49(3): p. 525-6.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
57. Cavallone, L., et al., *A Study of Pre-Analytical Variables and Optimization of Extraction Method for Circulating Tumor DNA Measurements by Digital Droplet PCR*. Cancer Epidemiol Biomarkers Prev, 2019.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
58. Rikkert, L.G., et al., *Centrifugation affects the purity of liquid biopsy-based tumor biomarkers*. Cytometry A, 2018. 93(12): p. 1207-1212.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
59. Lui, Y.Y., et al., *Predominant hematopoietic origin of cell-free DNA in plasma and serum after sex-mismatched bone marrow transplantation*. Clin Chem, 2002. 48(3): p. 421-7.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
60. Raymond, C.K., et al., *Collection of cell-free DNA for genomic analysis of solid tumors in a clinical laboratory setting*. PLoS One, 2017. 12(4): p. e0176241.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
61. Haselmann, V., et al., *Results of the first external quality assessment scheme (EQA) for isolation and analysis of circulating tumour DNA (ctDNA)*. Clin Chem Lab Med, 2018. 56(2): p. 220-228.
[PubMed Abstract](#)
62. Sozzi, G., et al., *Effects of prolonged storage of whole plasma or isolated plasma DNA on the results of circulating DNA quantification assays*. J Natl Cancer Inst, 2005. 97(24): p. 1848-50.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
63. Shishido, S.N., et al., *Pre-analytical variables for the genomic assessment of the cellular and acellular fractions of the liquid biopsy in a cohort of breast cancer patients*. J Mol Diagn, 2020.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
64. Frattini, M., et al., *Reproducibility of a semiquantitative measurement of circulating DNA in plasma from neoplastic patients*. J Clin Oncol, 2005. 23(13): p. 3163-4; author reply 3164-5.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)

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Page #	Page 26 of 28	Initial Release Date	1/30/2020	Revision Date	

65. Streleckiene, G., et al., *Effects of Quantification Methods, Isolation Kits, Plasma Biobanking, and Hemolysis on Cell-Free DNA Analysis in Plasma*. Biopreserv Biobank, 2019.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
66. Malentacchi, F., et al., *Influence of pre-analytical procedures on genomic DNA integrity in blood samples: the SPIDIA experience*. Clin Chim Acta, 2015. 440: p. 205-10.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
67. He, H.J., et al., *Multilaboratory Assessment of a New Reference Material for Quality Assurance of Cell-Free Tumor DNA Measurements*. J Mol Diagn, 2019. 21(4): p. 658-676.
[PubMed Abstract](#)
68. Page, K., et al., *Influence of plasma processing on recovery and analysis of circulating nucleic acids*. PLoS One, 2013. 8(10): p. e77963.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
69. Repiská, G., et al., *Selection of the optimal manual method of cell free fetal DNA isolation from maternal plasma*. Clin Chem Lab Med, 2013. 51(6): p. 1185-9.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
70. Legler, T.J., et al., *Workshop report on the extraction of foetal DNA from maternal plasma*. Prenat Diagn, 2007. 27(9): p. 824-9.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
71. Clausen, F.B., et al., *Improvement in fetal DNA extraction from maternal plasma. Evaluation of the NucliSens Magnetic Extraction system and the QIAamp DSP Virus Kit in comparison with the QIAamp DNA Blood Mini Kit*. Prenat Diagn, 2007. 27(1): p. 6-10.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
72. Sorber, L., et al., *A Comparison of Cell-Free DNA Isolation Kits: Isolation and Quantification of Cell-Free DNA in Plasma*. J Mol Diagn, 2017. 19(1): p. 162-168.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
73. Diefenbach, R.J., et al., *Evaluation of commercial kits for purification of circulating free DNA*. Cancer Genet, 2018. 228-229: p. 21-27.
[PubMed Abstract](#) [NCI Biospecimen Research Database Curation](#)
74. Pérez-Barrios, C., et al., *Comparison of methods for circulating cell-free DNA isolation using blood from cancer patients: impact on biomarker testing*. Transl Lung Cancer Res, 2016. 5(6): p.

NCI Biospecimen Evidence-Based Practices		CELL-FREE DNA: BIOSPECIMEN COLLECTION AND PROCESSING			
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665-672.

[PubMed Abstract](#)

[NCI Biospecimen Research Database Curation](#)

75. Jain, M., et al., *Direct comparison of QIAamp DSP Virus Kit and QIAamp Circulating Nucleic Acid Kit regarding cell-free fetal DNA isolation from maternal peripheral blood*. Mol Cell Probes, 2019. 43: p. 13-19.

[PubMed Abstract](#)

[NCI Biospecimen Research Database Curation](#)

76. Solassol, J., et al., *Comparison of five cell-free DNA isolation methods to detect the EGFR T790M mutation in plasma samples of patients with lung cancer*. Clin Chem Lab Med, 2018.

[PubMed Abstract](#)

[NCI Biospecimen Research Database Curation](#)

77. Fleischhacker, M., et al., *Methods for isolation of cell-free plasma DNA strongly affect DNA yield*. Clin Chim Acta, 2011. 412(23-24): p. 2085-8.

[PubMed Abstract](#)

[NCI Biospecimen Research Database Curation](#)

78. Devonshire, A.S., et al., *Towards standardisation of cell-free DNA measurement in plasma: controls for extraction efficiency, fragment size bias and quantification*. Anal Bioanal Chem, 2014. 406(26): p. 6499-512.

[PubMed Abstract](#)

[NCI Biospecimen Research Database Curation](#)

79. Mehrotra, M., et al., *Study of Preanalytic and Analytic Variables for Clinical Next-Generation Sequencing of Circulating Cell-Free Nucleic Acid*. J Mol Diagn, 2017. 19(4): p. 514-24.

[PubMed Abstract](#)

[NCI Biospecimen Research Database Curation](#)

80. Ponti, G., et al., *The value of fluorimetry (Qubit) and spectrophotometry (NanoDrop) in the quantification of cell-free DNA (cfDNA) in malignant melanoma and prostate cancer patients*. Clin Chim Acta, 2018. 479: p. 14-19.

[PubMed Abstract](#)

[NCI Biospecimen Research Database Curation](#)

81. Chiminqi, M., et al., *Specific real-time PCR vs. fluorescent dyes for serum free DNA quantification*. Clin Chem Lab Med, 2007. 45(8): p. 993-5.

[PubMed Abstract](#)

[NCI Biospecimen Research Database Curation](#)

82. Szepechcinski, A., et al., *Evaluation of fluorescence-based methods for total vs. amplifiable DNA quantification in plasma of lung cancer patients*. J Physiol Pharmacol, 2008. 59 Suppl 6: p. 675-81.

[PubMed Abstract](#)

[NCI Biospecimen Research Database Curation](#)

NCI Biospecimen Evidence-Based Practices		CELL-FREE DNA: BIOSPECIMEN COLLECTION AND PROCESSING			
Author	Biorepositories and Biospecimen Research Branch			Revision #	
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83. Johansson, G., et al., *Considerations and quality controls when analyzing cell-free tumor DNA*. *Biomol Detect Quantif*, 2019. 17: p. 100078.
[PubMed Abstract](#)
 84. Zhang, R., et al., *Synthetic Circulating Cell-free DNA as Quality Control Materials for Somatic Mutation Detection in Liquid Biopsy for Cancer*. *Clin Chem*, 2017. 63(9): p. 1465-1475.
[PubMed Abstract](#)
 85. Elazezy, M. and S.A. Joosse, *Techniques of using circulating tumor DNA as a liquid biopsy component in cancer management*. *Comput Struct Biotechnol J*, 2018. 16: p. 370-378.
[PubMed Abstract](#)
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