Center for Advanced Molecular Diagnostics
Translational Biomarker Core
Brigham and Women's Hospital
Boston, MA 02115

Brigham and Women's Hospital
Founding Member, Mass General Brigham

Clinical Laboratory Test Menu

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Rapid Heme Panel

Rapid Heme Panel (RHP) is a genomic assay that detects single nucleotide variants, small insertions and deletions, and a limited number of copy number changes in genes commonly mutated in myeloid and lymphoid malignancies; it cannot detect gene fusions. The RHP assay uses a New England Biolabs NextDirect custom panel targeting 88 genes. Samples are subjected to massively parallel sequencing on the Illumina NextSeq 550 Dx platform and variant analysis performed on a clinically validated custom pipeline.

Turnaround Time Estimates

- For 1–4 samples = 2–3 weeks
- For 5–20 samples = 2–5 weeks
- For projects exceeding 20 samples, longitudinal studies, or studies that require expedited processing, please contact BWHCAMDResearchCore@bwh.harvard.edu to set up a time to discuss study timelines and requirements

Assay Input Requirements

Optimal DNA Input: 500 ng by Qubit
Qubit Concentration: ≥ 13 ng/µL
DNA Input Volume: 40 µL

Acceptable Specimens and Requirements

WHOLE BLOOD/BONE MARROW

Minimum 1 mL whole blood or bone marrow collected in a K2EDTA (lavender/purple top) tube. Specimens may be submitted immediately after collection or stored at 4°C for **up to 6 days**, or frozen and stored at ≤ -20°C.

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Specimens at 4°C storage, transport with cold packs; -20°C to -80°C storage, transport on dry ice

CELLS

Freshly collected, refrigerated (<24 hours), or frozen cell pellet or suspension with a minimum of 5 X 10^5 cells. Please indicate the storage solution (e.g., culture medium, PBS).

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Specimens at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

GENOMIC DNA

Genomic DNA isolated with an appropriate commercially available kit (e.g., QIAGEN, Promega, Roche) from any acceptable specimen type may be submitted. DNA at a concentration ≥ 13 ng/µL by Qubit or other fluorescent detection method in up to 40 µL is recommended (≥ 520 ng total). Samples at lower concentrations may be accepted; please contact us at

BWHCAMDResearchCore@bwh.harvard.edu prior to opening a service request. All DNA samples are re-quantified upon receipt to confirm input requirements; requested volume accounts for quantification.

Storage and Transport Conditions
Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

Please note we **do accept select mouse PDX models**; contact us prior to submission to make appropriate arrangements.

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nCounter RNA Panel (formerly NanoString)

nCounter RNA Panel assays using the nCounter Analysis System provide a robust method for detecting and counting unique RNA transcripts. Gene expression is quantified via direct detection technology, which utilizes color-coded molecular barcodes that bind to specific targets, allowing for precise and simultaneous analysis of up to 800 genes.

TBC performs RNA isolation and sample processing on the nCounter platform. Prior to opening a service request, please work directly with Bruker to determine the appropriate nCounter RNA panel and order the reagents. Reagents may be shipped directly to TBC with appropriate arrangements or dropped off with the specimens.

TapeStation analysis is recommended for formalin-fixed paraffin-embedded (FFPE) specimens to obtain the DV200 score, which reflects the percentage of RNA fragments >200 nucleotides (nt) in length. DV200 is used to guide RNA input requirements for degraded samples. TapeStation must be added as a separate service in the requisition at 1 unit/sample.

Turnaround Time Estimates

- For 12–24 RNA samples = 1–3 weeks
- For 25–48 RNA samples = 3–5 weeks
- For projects exceeding 48 RNA samples or longitudinal studies, please contact BWHCAMDResearchCore@bwh.harvard.edu to discuss study timelines and requirements
- For projects requiring RNA isolation, please see the appropriate service pages to determine the additional time required for completion of the work

Assay Input Requirements

Optimal RNA Input: 100 ng by NanoDrop
TapeStation DV200 score: ≥ 70% recommended
NanoDrop Concentration: ≥ 20 ng/µL
260/280 ratio: 1.7–2.3
RNA Input Volume: 5 µL
NOTE: 100 ng RNA input is typically loaded. For RNA extracted from FFPE or degraded samples, DV200 is used to adjust the input to achieve ~100 ng of intact RNA in a final loading volume of 5 µL. Samples with DV200 scores between 15–70% may require concentration (e.g., via speedvac) prior to loading.

Acceptable Specimens and Requirements

FFPE

Slides

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 10 unstained slides (USS) cut at 5 µm, mounted onto positively charged slides (unbaked preferred). Macrodissection of tumor ROI is performed.

Scrolls

- 1 H&E; if tumor area and cellularity are *unknown*, pathology review will be performed.

- 2 scrolls cut at 50 µm supplied in a 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content or submission of non-cancerous specimens, all tissue will be utilized; for USS, please indicate "scrape all" in the service requisition.

Storage and Transport Conditions
Ambient temperature

FRESH FROZEN TISSUE

OCT-embedded

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 1 OCT block with embedded tissue. Macrodissection is available if the ROI may be discerned in the block, otherwise the entire tissue is processed.

Snap Frozen

- 1 H&E; if tumor area and cellularity are *unknown*, pathology review will be performed.
- Minimum 4 mm^2 tissue supplied in a biopsy tube or 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content or submission of non-cancerous specimens, all tissue will be utilized.

Storage and Transport Conditions
Specimens at -20°C to -80°C storage, transport on dry ice

WHOLE BLOOD/BONE MARROW

Minimum 5 mL whole blood or 500 µL bone marrow collected in a K2EDTA (lavender/purple top) tube. Specimens may be submitted immediately after collection or stored at 4°C for **up to 3 days**, or frozen and stored at ≤ -80°C. PaxGene RNA or Streck tubes are accepted as well, following manufacturer's recommendations for storage.

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Specimens at 4°C storage, transport with cold packs; -20°C to -80°C storage, transport on dry ice

ISOLATED RNA

RNA isolated with an appropriate commercially available kit (e.g., QIAGEN, Promega, Roche) from any acceptable specimen type may be submitted. RNA at a concentration ≥ 20 ng/µL by NanoDrop in up to 15 µL is recommended (≥ 300 ng total); minimum of 20 ng/µL in 10 µL (200 ng total) is required. All RNA samples are re-quantified upon receipt and TapeStation is recommended for FFPE primary specimens to confirm input requirements; requested volumes account for quantification and analysis.

Storage and Transport Conditions
Samples at -20°C to -80°C storage, transport on dry ice

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BCR::ABL (p190 or p210)

BCR::ABL fusion transcripts can be detected in RNA isolated from human whole blood or bone marrow using qPCR methods developed by Asuragen. Please select the appropriate test from the **Services** below.

Turnaround Time Estimates

- For 1–4 samples = up to 7 days
- For 5–20 samples = 7–21 days
- For projects exceeding 20 samples or longitudinal studies, please contact BWHCAMDResearchCore@bwh.harvard.edu to discuss study timelines and requirements

Services

***BCR::ABL* p190 – Asuragen** *BCR::ABL* Minor Kit detects p190 (minor fusion transcripts e1a2)
***BCR::ABL* p210 – Asuragen** *BCR::ABL* IS Kit detects p210 (fusion transcripts e13a2 and/or e14a2)

Assay Input Requirements

Optimal RNA Input: 1000–4000 ng by NanoDrop
NanoDrop Concentration: ≥ 100–400 ng/µL
RNA Input Volume: 10 µL

Acceptable Specimens and Requirements

WHOLE BLOOD/BONE MARROW

Minimum 5 mL whole blood or 500 µL bone marrow collected in a K2EDTA (lavender/purple top) tube. Specimens may be submitted immediately after collection or stored at 4°C for **up to 3 days**.

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Specimens at 4°C storage, transport with cold packs

ISOLATED RNA

RNA isolated with an appropriate commercially available kit (e.g., QIAGEN, Promega, Roche) from any acceptable specimen type may be submitted. RNA at a concentration ≥ 100–400 ng/µL by NanoDrop in up to 15 µL is recommended (≥ 1500–6000 ng total). Samples at lower concentrations may be accepted; please contact us at BWHCAMDResearchCore@bwh.harvard.edu prior to opening a service request. All RNA samples are re-quantified upon receipt to confirm input requirements; requested volume accounts for quantification.

Storage and Transport Conditions
Samples at -20°C to -80°C storage, transport on dry ice

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BRAF ddPCR

***BRAF* p.V600E** or **p.V600K** variant alleles are detected using BioRad's **droplet digital PCR (ddPCR)** platform in DNA extracted from human FFPE, fresh frozen, or aspirate smear specimens containing a minimum of 20% tumor nuclei.

Turnaround Time Estimates

- For 1–4 samples = 1–2 weeks
- For 5–20 samples = 2–4 weeks
- For projects exceeding 20 samples or longitudinal studies, please contact BWHCAMDResearchCore@bwh.harvard.edu to discuss study timelines and requirements

Assay Input Requirements

Optimal DNA Input: 30 ng by Qubit
Qubit Concentration: ≥ 3 ng/µL
DNA Input Volume: 10 µL

Acceptable Specimens and Requirements

FFPE

Slides

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 10 unstained slides (USS) cut at 5 µm, mounted onto positively charged slides (unbaked preferred). Macrodissection of tumor ROI is performed.

Scrolls

- 1 H&E; if tumor area and cellularity are *unknown*, pathology review will be performed.
- 2 scrolls cut at 50 µm supplied in a 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content, all tissue will be utilized; for USS, please indicate "scrape all" in the service requisition.

Storage and Transport Conditions
Ambient temperature

FRESH FROZEN TISSUE

OCT-embedded

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 1 OCT block with embedded tissue. Macrodissection is available if the ROI may be discerned in the block, otherwise the entire tissue is processed.

Snap Frozen

- 1 H&E if tumor area and cellularity are *unknown*, pathology review will be performed.
- Minimum 4 mm^2 tissue supplied in a biopsy tube or 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content, all tissue will be utilized.

Storage and Transport Conditions
Specimens at -20°C to -80°C storage, transport on dry ice

ASPIRATE SMEARS

2–5 unstained smear slides with ≥ 20% malignant cells; if a differential cell count was not performed on the specimen, please submit 1 stained aspirate smear slide for pathology review.

Storage and Transport Conditions
Ambient temperature

GENOMIC DNA

Genomic DNA isolated with an appropriate commercially available kit (e.g., QIAGEN, Promega, Roche) from any acceptable specimen type may be submitted. DNA at a concentration ≥ 3 ng/µL by Qubit or other fluorescent detection method in 15 µL (≥ 45 ng total) is required. All DNA samples are re-quantified upon receipt to confirm input requirements; requested volume accounts for quantification.

Storage and Transport Conditions
Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

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EGFR ddPCR

***EGFR* p.T790M**, **p.L858R**, and **exon 19 deletion** variant alleles are detected using BioRad's **droplet digital PCR (ddPCR)** platform in DNA extracted from human FFPE specimens containing a minimum of 20% tumor nuclei or cfDNA isolated from fresh or frozen plasma.

Turnaround Time Estimates

- For 1–4 samples = 1–2 weeks
- For 5–20 samples = 2–4 weeks
- For projects exceeding 20 samples or longitudinal studies, please contact BWHCAMDResearchCore@bwh.harvard.edu to discuss study timelines and requirements

Assay Input Requirements

Optimal DNA Input: 150 ng by Qubit
Qubit Concentration: ≥ 3 ng/µL
DNA Input Volume: 50 µL

Acceptable Specimens and Requirements

FFPE

Slides

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 10 unstained slides (USS) cut at 5 µm, mounted onto positively charged slides (unbaked preferred). Macrodissection of tumor ROI is performed.

Scrolls

- 1 H&E; if tumor area and cellularity are *unknown*, pathology review will be performed.
- 2 scrolls cut at 50 µm supplied in a 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content, all tissue will be utilized; for USS, please indicate "scrape all" in the service requisition.

Storage and Transport Conditions
Ambient temperature

FRESH OR FROZEN PLASMA

Minimum 2–3 mL of fresh or frozen plasma must be provided for cfDNA isolation.

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Samples at 4°C storage, transport with cold packs; -20°C to -80°C storage, transport on dry ice

GENOMIC DNA

Genomic DNA isolated with an appropriate commercially available kit (e.g., QIAGEN, Promega, Roche) from any acceptable specimen type may be submitted. DNA at a concentration ≥ 3 ng/µL by Qubit or other fluorescent detection method in 55 µL is recommended (≥ 165 ng total). Samples at lower concentrations may be accepted; please contact us at BWHCAMDResearchCore@bwh.harvard.edu prior to opening a service request. All DNA samples are re-quantified upon receipt to confirm input requirements; requested volume accounts for quantification.

Storage and Transport Conditions

Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

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HPV PCR Genotyping

HPV PCR Genotyping is performed on DNA extracted from human formalin-fixed paraffin-embedded (FFPE) specimens. The assay entails amplification of an HPV-specific DNA sequence that, when detected in positive samples, is subjected to restriction enzyme digestion and gel electrophoresis to determine the HPV subtype (aka. Restriction Fragment Length Polymorphism [RFLP] analysis).

Turnaround Time Estimates

- For 1–4 samples = 1–2 weeks
- For 5–20 samples = 2–6 weeks
- For projects exceeding 20 samples or longitudinal studies, please contact BWHCAMDResearchCore@bwh.harvard.edu to discuss study timelines and requirements

Assay Input Requirements

Optimal DNA Input: 850 ng by NanoDrop
NanoDrop Concentration: ≥ 100 ng/µL
DNA Input Volume: 8.5 µL

Acceptable Specimens and Requirements

FFPE

Slides

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 10 unstained slides (USS) cut at 5 µm, mounted onto positively charged slides (unbaked preferred). Macrodissection of tumor ROI is performed.

Scrolls

- 1 H&E; if tumor area and cellularity are *unknown*, pathology review will be performed.
- 2 scrolls cut at 50 µm supplied in a 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content, all tissue will be utilized; for USS, please indicate “scrape all” in the service requisition.

Storage and Transport Conditions
Ambient temperature

GENOMIC DNA

Genomic DNA isolated with an appropriate commercially available kit (e.g., QIAGEN, Promega, Roche) from any acceptable specimen type may be submitted. DNA at a concentration ≥ 100 ng/µL by NanoDrop in 10 µL is recommended (≥ 1000 ng total). Samples at lower concentrations may be accepted; please contact us at BWHCAMDResearchCore@bwh.harvard.edu prior to opening a service request. All DNA samples are re-quantified upon receipt to confirm input requirements; requested volume accounts for quantification.

Storage and Transport Conditions

Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

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Microsatellite Instability (MSI)

Microsatellite Instability (MSI) testing is performed on DNA extracted from human formalin-fixed paraffin-embedded (FFPE) specimens. The assay typically entails amplification of 5 genomic microsatellite loci from tumor cells and adjacent normal tissue, followed by capillary electrophoresis (CE) to compare PCR fragment sizes. If no normal tissue is available, tumor-only MSI analysis may be performed.

Turnaround Time Estimates

- For 1–4 samples = 1–2 weeks
- For 5–20 samples = 2–6 weeks
- For projects exceeding 20 samples or longitudinal studies, please contact BWHCAMDResearchCore@bwh.harvard.edu to discuss study timelines and requirements

Assay Input Requirements

Optimal DNA Input: 400 ng by NanoDrop
NanoDrop Concentration: ≥ 20 ng/µL
DNA Input Volume: 20 µL

Acceptable Specimens and Requirements

FFPE

Slides

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 10 unstained slides (USS) cut at 5 µm, mounted onto positively charged slides (unbaked preferred). Macrodissection of tumor ROI is performed.

Scrolls

- 1 H&E; if tumor area and cellularity are *unknown*, pathology review will be performed.
- 2 scrolls cut at 50 µm supplied in a 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content, all tissue will be utilized; for USS, please indicate “scrape all” in the service requisition.

Storage and Transport Conditions
Ambient temperature

GENOMIC DNA

Genomic DNA isolated with an appropriate commercially available kit (e.g., QIAGEN, Promega, Roche) from any acceptable specimen type may be submitted. DNA at a concentration ≥ 20 ng/µL by NanoDrop in 25 µL is recommended (≥ 500 ng total). Samples at lower concentrations may be accepted; please contact us at BWHCAMDResearchCore@bwh.harvard.edu prior to opening a service request. All DNA samples are re-quantified upon receipt to confirm input requirements; requested volume accounts for quantification.

Storage and Transport Conditions

Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

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IGH Gene Rearrangement

***IGH* Gene Rearrangement** testing is performed on DNA extracted from human formalin-fixed paraffin-embedded (FFPE) specimens. The assay entails amplification of the immunoglobulin heavy chain (IGH) conserved framework (FR), diversity (D), and joining (J) regions to identify V–D–J rearrangements, followed by capillary electrophoresis (CE) to determine PCR amplicon sizes. Samples containing a clonal population yield one or two prominent amplicons within a diminished polyclonal background, whereas polyclonal populations produce a Gaussian distribution (bell-shaped curve).

Turnaround Time Estimates

- For 1–4 samples = 1–2 weeks
- For 5–20 samples = 2–6 weeks
- For projects exceeding 20 samples or longitudinal studies, please contact BWHCAMDResearchCore@bwh.harvard.edu to discuss study timelines and requirements

Assay Input Requirements

Optimal DNA Input: 2500 ng by NanoDrop
NanoDrop Concentration: ≥ 100 ng/µL
DNA Input Volume: 25 µL

Acceptable Specimens and Requirements

FFPE

Slides

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 10 unstained slides (USS) cut at 5 µm, mounted onto positively charged slides (unbaked preferred). Macrodissection of tumor ROI is performed.

Scrolls

- 1 H&E; if tumor area and cellularity are *unknown*, pathology review will be performed.
- 2 scrolls cut at 50 µm supplied in a 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content, all tissue will be utilized; for USS, please indicate “scrape all” in the service requisition.

Storage and Transport Conditions
Ambient temperature

GENOMIC DNA

Genomic DNA isolated with an appropriate commercially available kit (e.g., QIAGEN, Promega, Roche) from any acceptable specimen type may be submitted. DNA at a concentration ≥ 100 ng/µL by NanoDrop in 30 µL is recommended (≥ 3000 ng total). Samples at lower concentrations may be accepted; please contact us at BWHCAMDResearchCore@bwh.harvard.edu prior to opening a service request. All DNA samples are re-quantified upon receipt to confirm input requirements; requested volumes account for quantification.

Storage and Transport Conditions

Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

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TCR Gene Rearrangement

***TCR* Gene Rearrangement** testing is performed on DNA extracted from human formalin-fixed paraffin-embedded (FFPE) specimens. The assay entails amplification of the conserved *TCR-gamma (γ)* variable (V) and joining (J) regions to identify V–J rearrangements, followed by capillary electrophoresis (CE) to determine PCR amplicon sizes. Samples containing a clonal population yield one or two prominent amplicons within a diminished polyclonal background, whereas polyclonal populations produce a Gaussian distribution (bell-shaped curve).

Turnaround Time Estimates

- For 1–4 samples = 1–2 weeks
- For 5–20 samples = 2–6 weeks
- For projects exceeding 20 samples or longitudinal studies, please contact BWHCAMDResearchCore@bwh.harvard.edu to discuss study timelines and requirements

Assay Input Requirements

Optimal DNA Input: 2000 ng by NanoDrop
NanoDrop Concentration: ≥ 100 ng/µL
DNA Input Volume: 20 µL

Acceptable Specimens and Requirements

WHOLE BLOOD/BONE MARROW

Minimum 1 mL whole blood or bone marrow collected in a K2EDTA (lavender/purple top) tube. Specimens may be submitted immediately after collection or stored at 4°C for **up to 6 days**, or frozen and stored at ≤ -20°C.

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Specimens at 4°C storage, transport with cold packs; -20°C to -80°C storage, transport on dry ice

FFPE

Slides

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 10 unstained slides (USS) cut at 5 µm, mounted onto positively charged slides (unbaked preferred). Macrodissection of tumor ROI is performed.

Scrolls

- 1 H&E; if tumor area and cellularity are *unknown*, pathology review will be performed.
- 2 scrolls cut at 50 µm supplied in a 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content, all tissue will be utilized; for USS, please indicate “scrape all” in the service requisition.

Storage and Transport Conditions
Ambient temperature

FRESH FROZEN TISSUE

OCT-embedded

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 1 OCT block with embedded tissue. Macrodissection is available if the ROI may be discerned in the block, otherwise the entire tissue is processed.

Snap Frozen

- 1 H&E if tumor area and cellularity are *unknown*, pathology review will be performed.
- Minimum 4 mm^2 tissue supplied in a biopsy tube or 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content, all tissue will be utilized.

Storage and Transport Conditions
Specimens at -20°C to -80°C storage, transport on dry ice

CELLS

Freshly collected, refrigerated (<24 hours), or frozen cell pellet or suspension with a minimum of 5 X 10^5 cells. Please indicate the cell type (e.g., patient-derived tumor cells or cell lines, PBMC, iPSC) and storage solution (e.g., culture medium, DMSO, PBS).

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Specimens at 4°C storage, transport with cold packs; -20°C to -80°C storage, transport on dry ice

FLUIDS

Cerebrospinal Fluid (CSF)

- Minimum 1 mL freshly collected, refrigerated (<24 hours) or frozen CSF.

Vitreous Fluid

- Minimum 1 mL freshly collected, refrigerated (<24 hours) or frozen vitreous fluid.

Storage and Transport Conditions
Specimens at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

GENOMIC DNA

Genomic DNA isolated with an appropriate commercially available kit (e.g., QIAGEN, Promega, Roche) from any acceptable specimen type may be submitted. DNA at a concentration ≥ 100 ng/µL by NanoDrop in 25 µL is recommended (≥ 2500 ng total). Samples at lower concentrations may be accepted; please contact us at BWHCAMDResearchCore@bwh.harvard.edu prior to opening a service request. All DNA samples are re-quantified upon receipt to confirm input requirements; requested volumes account for quantification.

Storage and Transport Conditions
Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

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Optical Genome Mapping (OGM)

Optical Genome Mapping (OGM) on the Bionano Saphyr platform is a whole genome cytogenomic assay that detects all classes of structural variants in ultra-high molecular weight (UHMW) DNA isolated from a variety of human specimen types, including blood, bone marrow, and enriched cell populations or cultured cells. Structural variants including indels, gene fusions, and copy number alterations are identified down to 500 base pair (bp) resolution and 5% variant allele frequency.

Turnaround Time Estimates

- For 1–3 samples = 2–3 weeks
- For 4–18 samples = 3–8 weeks
- For projects exceeding 18 samples, longitudinal studies, or studies that require expedited processing, please contact BWHCAMDResearchCore@bwh.harvard.edu to set up a time to discuss study timelines and requirements

Assay Input Requirements

Optimal Specimen Input: 1.5 million viable cells (pelleted cells) or 200–600 µL whole blood or bone marrow containing approximately 1.5 million white blood cells (WBCs).
UHMW DNA Input: 750 ng (39 ng/µL–150 ng/µL)

Acceptable Specimens and Requirements

WHOLE BLOOD/BONE MARROW

Minimum 1 mL whole blood or bone marrow collected in a K2EDTA (lavender/purple top) tube is preferred; specimens collected in sodium heparin (green top) tubes will be accepted. Specimens may be submitted immediately after collection or stored at 4°C for **up to 3 days**, or frozen and stored at ≤ −20°C.

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Specimens at 4°C storage, transport with cold packs; -20°C to -80°C storage, transport on dry ice

CELLS

Freshly collected specimens with a minimum of 1.5 X 10^6 cells resuspended in 500 µL of chilled PBS, stored at 4°C, and submitted within 24 hours of harvest, or frozen cell pellets.

Storage and Transport Conditions
Specimens at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

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Simoa (COVID-19, Biomarker kits)

The Quanterix **Simoa HD-X Analyzer is** a digital immunoassay platform designed for ultrasensitive biomarker detection down to the femtomolar range in a variety of human specimen types including blood, serum, plasma, cerebrospinal fluid (CSF), and urine. Quanterix has developed over 50 readily available Simoa assays for the detection of immunology, neurology, oncology, cardiology, and infectious disease biomarkers.

Because each Simoa assay varies, project-specific consultation is required. Please contact BWHCAMDResearchCore@bwh.harvard.edu to discuss your project needs.

Turnaround Time Estimates

Based on the size and scope of each project, independent turnaround time estimates will be provided.

Assay Input, Acceptable Specimens, and Requirements

Optimal inputs and accepted specimens will be determined for each project, based upon the recommendations provided by Quanterix for the required assay.

For a complete list of available assays, please refer to: https://www.quanterix.com/simoa-assay-kits-and-reagents/

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FISH

Prior to opening a service request, please email BWHCAMDResearchCore@bwh.harvard.edu with a brief description of the project, including the assay required, number of specimens, and specimen type. Projects must be reviewed and approved based on feasibility and confirmation that the required probes are validated. Upon approval, investigators will be notified with a timeframe in which the specimens may be submitted.

Fluorescent In Situ Hybridization (FISH) is performed on human formalin-fixed paraffin-embedded (FFPE) or cellular specimens. Fluorescently labeled antibody probes are hybridized to samples to assess specific genetic events, including gene duplications, amplifications, deletions, or chromosomal rearrangements.

Turnaround Time Estimates

- For 1–4 samples = 1–2 weeks
- For 5–10 samples = 2–6 weeks
- For projects exceeding 10 samples or longitudinal studies, please contact BWHCAMDResearchCore@bwh.harvard.edu to discuss study timelines and requirements

Acceptable Specimens and Requirements

Please note: Arrangements must be made with TBC (BWHCAMDResearchCore@bwh.harvard.edu) **at least 48 hours in advance** of specimen delivery to confirm an appropriate delivery time.

FFPE

Slides

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 2 unstained slides (USS) cut at 5 µm mounted onto **positively charged, unbaked** slides.

Storage and Transport Conditions
Ambient temperature

WHOLE BLOOD/BONE MARROW

Minimum 3 mL whole blood or bone marrow collected in a heparin (green top) tube is preferred; a K2EDTA (lavender/purple top) tube is accepted. Specimens may be submitted immediately after collection or stored at 4°C for **up to 4 days**.

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Samples at 4°C storage, transport with cold packs

FRESH CELLS

Cells at 75–80% confluence in a minimum T-25 flask or equivalent, fed the night before.

Storage and Transport Conditions
Ambient temperature transport and delivery within 4 hours of removal from the incubator, or shipped priority overnight

FIXED CELL PELLET

Cells at 75–80% confluence in a minimum T-25 flask or equivalent, harvested and fixed in 3:1 methanol:acetic acid. Specimens may be submitted immediately after collection or stored at 4°C.

Storage and Transport Conditions
Freshly fixed, ambient temperature
Samples at 4°C storage, transport on ice

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OncoScan CNV Assay

Prior to opening a service request, please email BWHCAMDResearchCore@bwh.harvard.edu with a brief description of the project, including the number of samples and specimen type. Projects must be reviewed and approved based on feasibility. Upon approval, investigators will be notified with a timeframe in which the samples may be submitted.

The **OncoScan CNV Assay** is a cancer genomic microarray assay that provides accurate analysis of copy number changes and allelic imbalances across the entire genome in DNA extracted from human specimens containing a minimum of 50% tumor nuclei in formalin-fixed paraffin-embedded (FFPE) tissue or fresh cells. OncoScan utilizes molecular inversion probe (MIP) technology to identify copy number alterations, loss of heterozygosity (LOH), copy neutral LOH (cnLOH) with high-density copy number coverage across 900 cancer research genes and standard coverage across the whole genome.

Turnaround Time Estimates

- For 1–4 samples = 4–8 weeks
- For 5–10 samples = 8–12 weeks
- For projects exceeding 10 samples, please contact BWHCAMDResearchCore@bwh.harvard.edu

Assay Input Requirements

Minimum tumor cellularity: 50% per pathologist review
Recommended tumor area: ≥ 1 cm^2
Optimal DNA Input: 120 ng by Qubit
Qubit Concentration: ≥ 12 ng/µL
Volume: 10 µL

Acceptable Specimens and Requirements

FFPE

Slides

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 10 unstained slides (USS) cut at 5 µm, mounted onto positively charged slides (unbaked preferred). Macrodissection of tumor ROI is performed.

Scrolls

- 1 H&E; if tumor area and cellularity are *unknown*, pathology review will be performed.
- 2 scrolls cut at 50 µm supplied in a 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content, all tissue will be utilized; for USS, please indicate “scrape all” in the service requisition.

Storage and Transport Conditions
Ambient temperature

FIXED CELL PELLET

- Cells at 75–80% confluence in a minimum T-25 flask or equivalent, harvested and fixed in 3:1 methanol:acetic acid.

Storage and Transport Conditions
Freshly fixed, ambient temperature
Specimens at 4°C storage, transport on ice

GENOMIC DNA

Genomic DNA isolated with an appropriate commercially available kit (e.g., QIAGEN, Promega, Roche) from any acceptable specimen type may be submitted. DNA at a concentration ≥ 12 ng/µL by Qubit or other fluorescent detection method in up to 15 µL is required (≥ 180 ng total). All DNA samples are re-quantified upon receipt to confirm input requirements; requested volumes account for quantification.

Storage and Transport Conditions
Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

Please note we **do not accept mouse PDX models or cells co-cultured with mouse fibroblasts** for OncoScan at CAMD.

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CytoScan HD Accel Array

Prior to opening a service request, please email BWHCAMDResearchCore@bwh.harvard.edu with a brief description of the project, including the number of samples and specimen type. Projects must be reviewed and approved based on feasibility. Upon approval, investigators will be notified with a timeframe in which the samples may be submitted.

The **CytoScan HD Accel Array** is a genomic assay that provides accurate detection of chromosomal aberrations across the entire genome in DNA extracted from human specimens, including blood, tissue, or fresh cells. CytoScan enables low-level mosaicism visualization, absence of heterozygosity (AOH) and acquired UPD (aUPD) detection, copy number change confirmation, triploidy detection, allelic imbalance pattern visualization, and genomic contamination identification due to the dense tiling of more than 2.6 million copy number marker probes.

Turnaround Time Estimates

- For 1–4 samples = 4–8 weeks
- For 5–10 samples = 8–12 weeks
- For projects exceeding 10 samples, please contact BWHCAMDResearchCore@bwh.harvard.edu

Assay Input Requirements

Optimal DNA Input: 100 ng by Qubit
Qubit Concentration: ≥ 20 ng/µL
DNA Input Volume: 5 µL

Acceptable Specimens and Requirements

WHOLE BLOOD/BONE MARROW

Minimum 1 mL whole blood or bone marrow collected in a sodium heparin (green top) tube is preferred; a K2EDTA (lavender/purple top) tube is accepted. Specimens may be submitted immediately after or **within 7 days** of collection.

Storage and Transport Conditions
Ambient temperature

FRESH FROZEN TISSUE

OCT-embedded

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 1 OCT block with embedded tissue. Macrodissection is available if the ROI may be discerned in the block, otherwise the entire tissue is processed.

Snap Frozen

- 1 H&E if tumor area and cellularity are *unknown*, pathology review will be performed.
- Minimum 4 mm^2 tissue supplied in a biopsy tube or 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content or submission of non-cancerous material, all tissue will be utilized.

Storage and Transport Conditions
Specimens at -20°C to -80°C storage, transport on dry ice

CELLS

Freshly collected, refrigerated (<24 hours), or frozen cell pellet or suspension with a minimum of 5 X 10^5 cells. Please indicate the cell type (e.g., patient-derived tumor cells or cell lines, PBMC, iPSC) and storage solution (e.g., culture medium, DMSO, PBS).

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

GENOMIC DNA

Genomic DNA isolated with an appropriate commercially available kit (e.g., QIAGEN, Promega, Roche) from any acceptable specimen type may be submitted. DNA at a concentration ≥ 20 ng/µL by Qubit or other fluorescent detection method in up to 10 µL is required (≥ 200 ng total). All DNA samples are re-quantified upon receipt to confirm input requirements; requested volumes account for quantification.

Storage and Transport Conditions
Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

Please note we **do not accept mouse PDX models or cells co-cultured with mouse fibroblasts** for CytoScan at CAMD.

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DNA Isolation from Blood or Bone Marrow

DNA Isolation from Blood or Bone Marrow is performed with the Promega Maxwell RSC Whole Blood DNA Isolation Kit (AS1520). Quantification with NanoDrop is provided at no extra charge. Quantification with Qubit must be ordered separately at one unit per sample.

Turnaround Time Estimates

The turnaround time depends upon the number of samples pending across all nucleic acid extraction services.

- For 1–20 samples = 2–4 weeks
- For projects exceeding 20 samples, please contact BWHCAMDResearchCore@bwh.harvard.edu

Acceptable Specimens and Requirements

WHOLE BLOOD/BONE MARROW

Minimum 1 mL whole blood or bone marrow collected in a K2EDTA (lavender/purple top) tube. Specimens may be submitted immediately after collection or stored at 4°C for **up to 6 days**, or frozen and stored at ≤ -20°C.

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Samples at 4°C storage, transport with cold packs; -20°C to -80°C storage, transport on dry ice

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DNA Isolation from FFPE, Fresh Frozen Tissue, Cells or CSF

DNA Isolation from FFPE or Fresh Frozen tissue is performed with the QIAamp DNA Mini Kit (51304). DNA isolation from fresh or frozen **Cells or CSF** is performed with a manual extraction validated for CAMD clinical assays. Quantification with NanoDrop is provided at no extra charge. Quantification with Qubit must be ordered separately at one unit per sample.

Turnaround Time Estimates

The turnaround time depends upon the number of samples pending across all nucleic acid extraction services.

- For 1–20 samples = 2–4 weeks
- For projects exceeding 20 samples, please contact BWHCAMDResearchCore@bwh.harvard.edu

Acceptable Specimens and Requirements

FFPE

Slides

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 10 unstained slides (USS) cut at 5 µm, mounted onto positively charged slides (unbaked preferred). Macrodissection of tumor ROI is performed.

Scrolls

- 1 H&E; if tumor area and cellularity are *unknown*, pathology review will be performed.
- 2 scrolls cut at 50 µm supplied in a 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content or submission of non-cancerous specimens, all tissue will be utilized; for USS, please indicate “scrape all” in the service requisition.

Storage and Transport Conditions
Ambient temperature

FRESH FROZEN TISSUE

OCT-embedded

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 1 OCT block with embedded tissue. Macrodissection is available if the ROI may be discerned in the block, otherwise the entire tissue is processed.

Snap Frozen

- 1 H&E (if tumor area and cellularity are *unknown*, pathology review will be performed).
- Minimum 4 mm^2 tissue supplied in a biopsy tube or 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content or submission of non-cancerous material, all tissue will be utilized.

Storage and Transport Conditions
-20°C to -80°C storage, transport on dry ice

CELLS

Freshly collected, refrigerated (<24 hours), or frozen cell pellet or suspension with a minimum of 5 X 10^5 cells. Please indicate the cell type (e.g., patient-derived tumor cells or cell lines, PBMC, iPSC) and storage solution (e.g., culture medium, DMSO, PBS).

Storage and Transport Conditions

Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

CEREBROSPINAL FLUID (CSF)

Minimum 1 mL freshly collected, refrigerated (<24 hours), or frozen CSF.

Storage and Transport Conditions

Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Samples at 4°C storage, transport on ice; -20°C to -80°C storage, transport on dry ice

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RNA Isolation from Blood or Bone Marrow

RNA Isolation from Blood or Bone Marrow is performed with the Promega Maxwell RSC simplyRNA Blood Kit (AS1380). Quantification with NanoDrop is provided at no extra charge. Quantification with Qubit must be ordered separately at one unit per sample.

Turnaround Time Estimates

The turnaround time depends upon the number of samples pending across all nucleic acid extraction services.

- For 1–20 samples = 2–4 weeks
- For projects exceeding 20 samples, please contact BWHCAMDResearchCore@bwh.harvard.edu

Acceptable Specimens and Requirements

WHOLE BLOOD/BONE MARROW

Minimum 1 mL whole blood or bone marrow collected in a K2EDTA (lavender/purple top) tube. Specimens may be submitted immediately after collection or stored at 4°C for **up to 3 days**, or frozen and stored at ≤ −20°C.

Storage and Transport Conditions
Fresh specimens may be delivered at ambient temperature within 4 hours of collection
Samples at 4°C storage, transport with cold packs; -20°C to -80°C storage, transport on dry ice

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RNA Isolation from FFPE or Fresh Frozen Tissue

RNA Isolation from FFPE is performed with the ReliaPrep RNA Miniprep (Z6010). **RNA Isolation from Fresh Frozen Tissue** is performed with the Maxwell RSC simplyRNA Tissue Kit (AS1340). Quantification with NanoDrop is provided at no extra charge. Quantification with Qubit must be ordered separately at one unit per sample.

Turnaround Time Estimates

The turnaround time depends upon the number of samples pending across all nucleic acid extraction services and will be determined upon submission.

- For 1–20 samples = 2–4 weeks
- For projects exceeding 20 samples, please contact BWHCAMDResearchCore@bwh.harvard.edu

Acceptable Specimens and Requirements

FFPE

Slides

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 10 unstained slides (USS) cut at 5 µm, mounted onto positively charged slides (unbaked preferred). Macrodissection of tumor ROI is performed.

Scrolls

- 1 H&E; if tumor area and cellularity are *unknown*, pathology review will be performed.
- 2 scrolls cut at 50 µm supplied in a 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content or submission of non-cancerous specimens, all tissue will be utilized; for USS, please indicate “scrape all” in the service requisition.

Storage and Transport Conditions
Ambient temperature

FRESH FROZEN TISSUE

OCT-embedded

- 1 H&E with tumor regions of interest (ROI) circled and tumor cellularity indicated on the submission form; if ROI and cellularity are not indicated, pathology review will be performed.
- 1 OCT block with embedded tissue. Macrodissection is available if the ROI may be discerned in the block, otherwise the entire tissue is processed.

Snap Frozen

- 1 H&E if tumor area and cellularity are *unknown*, pathology review will be performed.
- Minimum 4 mm^2 tissue supplied in a biopsy tube or 1.5 mL microcentrifuge tube. Macrodissection is NOT available.

NOTE: If no H&E is provided due to known high tumor content or submission of non-cancerous material, all tissue will be utilized.

Storage and Transport Conditions
Samples at -20°C to -80°C storage, transport on dry ice

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NanoDrop Quantification

NanoDrop quantification of **DNA** or **RNA** samples is available as a standalone service for users who provide extracted nucleic acids, and it is included at no additional charge when performed with a nucleic acid extraction order. The **Thermo Scientific NanoDrop** instrument measures UV absorbance at three analytical wavelengths: 230 nm, 260 nm, and 280 nm. The intensity of the maximum absorbance peak at 260 nm is proportional to the nucleic acid concentration, and the sample purity is indicated by 260/280 and 260/230 ratios.

260/280 ratio
- A 260/280 ratio of ~ 1.8 is generally accepted as “pure” for DNA
- A 260/280 ratio of ~ 2.0 is generally accepted as “pure” for RNA

260/230 ratio
- The 260/230 ratio for “pure” nucleic acid is typically ~2.0–2.2; lower values (e.g., 1.8–2.0) may be observed depending on specimen type and extraction method.

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Qubit Quantification

The **Invitrogen Qubit** platform available from Thermo Fisher Scientific provides fluorescence-based nucleic acid quantification. **Qubit Quantification** of **DNA** or **RNA** is available for the products listed below.

Double stranded (ds) DNA kits:

- High Sensitivity dsDNA Assay (detection range of 0.1–120 ng)
- Broad Range dsDNA Assay (detection range of 4–4,000 ng)

RNA kits:

- High Sensitivity RNA Assay (detection range of 4−200 ng)
- Broad Range RNA Assay (detection range of 10−1,200 ng)
- microRNA Assay Kits (detection range of 0.5−150 ng)

NOTE: RNA Qubit kits are not kept in stock. Please contact BWHCAMDResearchCore@bwh.harvard.edu if your project requires fluorescence-based RNA quantification.

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TapeStation Nucleic Acid Analysis

The **Agilent TapeStation** system is an automated electrophoresis solution for quality control of DNA and RNA samples. Applications include:

DNA QC

- Analyze DNA fragments and smears for objective quantification, sizing, and purity determination
- Obtain the DNA Integrity Number (DIN) quality metric, calculated by the TapeStation software for genomic DNA samples: a DIN value of 1 is highly degraded and 10 is fully intact
- Determine accurate sizing over a broad range from 35 – 60,000 base pairs, depending on the ScreenTape assay

RNA QC

- Analyze RNA fragments and smears for objective quantification, sizing, and purity determination
- Obtain the RNA integrity number equivalent (RINe) quality metric, calculated by the TapeStation software: a RINe value of 1 is highly degraded and 10 is fully intact
- Obtain the DV200 (the percentage of fragments of >200 nucleotides), a reliable metric to classify degraded RNA based on fragment size and guide input into downstream workflows

NOTE: TapeStation analysis to obtain the DV200 is highly recommended for users ordering **nCounter** services for FFPE samples.

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Specimen Aliquoting

The **Specimen Aliquoting** service is utilized for projects that require multiple aliquots of a specimen to be prepared and/or distributed, or for plating samples (e.g., transferring nucleic acid from tubes to 96-well plates). Fees are determined based upon the needs of the project. Please contact BWHCAMDResearchCore@bwh.harvard.edu for a quote.

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Specimen Retrieval

Specimen Retrieval requests may be submitted to obtain aliquots of leftover DNA for samples processed in CAMD diagnostic assays, such as OncoPanel, RHP, or OncoScan. Before ordering specimen retrieval, please send a complete list of sample identifiers (e.g., BL, CG, or BWL numbers) to BWHCAMDResearchCore@bwh.harvard.edu (Excel format preferred). Please do not include patient names or medical record numbers. Sample concentration data will be reviewed to determine whether sufficient material is available for distribution.

For OncoPanel DNA requests, samples previously run as part of the DFCI Profile Program must be cleared with the DFCI User Committee. Profile cases will be identified in the submitted sample lists and returned to investigators with the concentration data. The OP Profile Specimen Request Form will be provided and must be completed only for confirmed Profile cases with sufficient material remaining and emailed to the DFCI User Committee.

Upon confirmation of sufficient material and DFCI User Committee approval (when applicable), a service request must be opened to receive the specimens.

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Bioinformatics and Data Transfer

The **Bioinformatics and Data Transfer** service is available for investigators to request custom formatted, structured, signed out data for samples processed through the CAMD TBC (e.g., OncoPanel or RHP variants). To discuss data format needs, please contact BWHCAMDResearchCore@bwh.harvard.edu. Results are returned only to the user that submitted the samples or associated study team members.

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Data File Transfer (BAM or standard Excel files)

The **Data File Transfer** service is available for investigators to request sequencing data files (e.g., BAM files) or aggregated signed out data (e.g., OncoPanel or RHP variants) for samples processed through the CAMD TBC. For examples of standard Excel data files, please contact BWHCAMDResearchCore@bwh.harvard.edu. Results are returned only to the user that submitted the samples or associated study team members.

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