

Assays for Qualification and Quality Stratification of Clinical Biospecimens Used in Research: A Technical Report from the ISBER Biospecimen Science Working Group

Fay Betsou,¹ Alexandre Bulla,² Sang Yun Cho,³ Judith Clements,⁴ Rodrigo Chuaqui,⁵ Domenico Coppola,⁶ Yvonne De Souza,⁷ Annemieke De Wilde,⁸ William Grizzle,⁹ Fiorella Guadagni,¹⁰ Elaine Gunter,¹¹ Stacey Heil,¹² Verity Hodgkinson,¹³ Joseph Kessler,¹⁴ Michael Kiehntopf,¹⁵ Hee Sung Kim,¹⁶ Iren Koppandi,¹⁷ Katheryn Shea,¹⁸ Rajeev Singh,¹⁹ Marc Sobel,²⁰ Stella Somiari,²¹ Demetri Spyropoulos,²² Mars Stone,²³ Gunnel Tybring,²⁴ Klara Valyi-Nagy,²⁵ Gert Van den Eynden,²⁶ and Lalita Wadhwa²⁷

This technical report presents quality control (QC) assays that can be performed in order to qualify clinical biospecimens that have been biobanked for use in research. Some QC assays are specific to a disease area. Some QC assays are specific to a particular downstream analytical platform. When such a qualification is not possible, QC assays are presented that can be performed to stratify clinical biospecimens according to their biomolecular quality.

Introduction

CLINICAL BIOSPECIMENS USED in research are subject to two types of laboratory analyses. The first of these is the analysis of established clinical biology/pathology parameters where reference ranges are usually known and

methods are validated (e.g., CLIA or ISO15189 accreditation). Results of these analyses are necessary to support any research on novel clinically relevant biomarkers (definition of true positive and negative cases, use as a reference method). The second type is analysis of research parameters where there are usually no established reference ranges, and

¹Integrated BioBank of Luxemburg (IBBL), Luxemburg.

²Biotheque-SML, Division of Genetics and Laboratory Medicine (DMGL), University Hospital of Geneva, Geneva, Switzerland.

³National Biobank of Korea, Cheongju, South Korea.

⁴Australian Prostate Cancer Bioresource/Queensland University of Technology, Brisbane, Australia.

⁵Cancer Diagnosis Program, Division of Cancer Treatment and Diagnosis (DCTD), National Cancer Institute, Rockville, Maryland.

⁶Moffitt Cancer Center, Department of Anatomic Pathology, University of South Florida, Tampa, Florida.

⁷University of California, San Francisco, AIDS Specimen Bank, San Francisco, California.

⁸Universitair Ziekenhuis Antwerpen, Edegem, Belgium.

⁹University of Alabama at Birmingham, Birmingham, Alabama.

¹⁰San Raffaele Rome University—IRCCS San Raffaele Pisana, Rome, Italy.

¹¹Specimen Solutions, LLC, Tucker, Georgia.

¹²Coriell Institute for Medical Research, Camden, New Jersey.

¹³Cancer Research Division, Cancer Council NSW, Woolloomooloo, Australia.

¹⁴Medpace Reference Laboratories, Cincinnati, Ohio.

¹⁵Universitätsklinikum Jena, Jena, Germany.

¹⁶Department of Pathology, Chung-Ang University College of Medicine, Dongjak-gu, South Korea.

¹⁷Cellular Technology Ltd, Shaker Heights, Ohio.

¹⁸Precision for Medicine, Inc. Frederick, Maryland.

¹⁹Houston Methodist Research Institute, Biorepository, Houston, Texas.

²⁰American Society for Investigative Pathology, Bethesda, Maryland.

²¹Biobank and Biospecimen Science Research, Windber Research Institute, Windber, Pennsylvania.

²²Department of Pathology and Laboratory Medicine, Children's Research Institute, Medical University of South Carolina, Charleston, South Carolina.

²³Blood Systems Research Institute, San Francisco, California.

²⁴Karolinska Institutet, Stockholm, Sweden.

²⁵University of Illinois Biorepository, Department of Pathology, College of Medicine, University of Illinois at Chicago, Chicago, Illinois.

²⁶Department of Pathology and Cytology, GZA Hospitals, Wilrijk, Belgium.

²⁷Baylor College of Medicine, Houston, Texas.

often methods are not validated by the laboratory as extensively as clinical biology/pathology methods.¹ Results of these analyses are used to discover novel clinical endpoint correlates (biomarkers).

In vivo and *in vitro* pre-analytical variations have a more or less significant impact on the output of analyses, depending on the biospecimen type, the pre-analytical variable, and the analyte of interest. According to the type of analysis above, the word “significant” has a different meaning. In the first type—the analysis of clinical biology/pathology parameters—“significant” means clinically consequential at the diagnostic level. In the second type—analysis of research parameters—“significant” means statistically significant. Examples illustrating this concept are shown in Table 1.

In some cases, the impact may be molecule- and even epitope-specific, for example tissue ischemia time may influence specific phospho-epitopes differently. A standard biospecimen research experimental protocol has been proposed for this type of research.²

Therefore, in all research comparing different groups of samples for biomarker discovery, it is critical that all samples are of comparable quality to avoid the introduction of uncontrolled variables and increase the power of analysis of biomarkers. There are two approaches to this end: either sample collections with careful pre-analytical annotations (SPREC),³ or retrospective collections with appropriate quality control (QC) and sample qualification or quality stratification. A combination of the two approaches to control compliance of procedures with specified SPRECs is also possible.

Biobanks underpin all three layers of biomarker discovery, validation, and use in clinical practice. In the biomarker discovery phase, biospecimens collected and processed with one Standard Operating Procedure (SOP), and corresponding to one quality category, should be used in order to avoid pre-analytical bias and increase the power of research. However, in the biomarker validation phase, biospecimens collected and processed with more than one known and documented SOPs and corresponding to more than one quality category should be used in order to validate the robustness of a biomarker to relevant pre-analytical variations. Finally, in the biomarker clinical implementation phase, biospecimens

collected and processed via validated SOPs should be used in order to ensure successful and accurate clinical diagnostic results. For these reasons, during recent years, biobank managers, auditors, and funding bodies have been asking what assays can be performed in order to assess the quality of biospecimens objectively. This technical review provides answers to this question. Although gaps exist, this review shows that many tools are already available and can be used for specimen qualification.

Methods

For the purposes of this technical report, the members of the International Society for Biological and Environmental Repositories (ISBER) Biospecimen Science Working Group held face-to-face meetings and teleconferences between 2013 and 2015. The chair of the Working Group performed a thorough literature review and compiled a list of relevant and effective QC attributes for different categories of biospecimens. This list was reviewed and complemented by members of the Working Group. When the information is based on published evidence, the corresponding reference is given. When no reference is given, the information corresponds to current practice or to the corresponding author’s opinion.

The following definitions were used:

- *Biospecimen*: any biological specimen, which may be a:
 - *Primary sample*: specimen directly collected from the donor (e.g., whole blood, urine, solid tissue);
 - *Simple derivative*: sample prepared through a simple laboratory manipulation (e.g., after centrifugation of collection tubes or mechanical disruption of tissues) without the addition of chemical substances, and without cell disruption or cell selection as part of a multi-step process; or
 - *Complex derivative*: derivative whose isolation requires usage of multiple steps and/or addition of chemical substances (e.g., nucleic acids, proteins, lipids, sorted cells, cultured cells, immortalized cells).
- *Qualification*: process of examination of a biospecimen or a collection of biospecimens, and verification, based on

TABLE 1. EXAMPLES ILLUSTRATING THE PROBABLE IMPACT OF PRE-ANALYTICAL CONDITIONS ON THE ANALYSIS OF CLINICAL OR RESEARCH PARAMETERS

<i>Pre-analytical condition</i>	<i>Biospecimen type</i>	<i>Analyzed parameter</i>	<i>Probable impact on the output of analyses</i>
Pre-centrifugation conditions	Serum	Clinical antibodies (e.g., anti-EBV IgG)	Non-significant (clinically)
Pre-centrifugation conditions	Serum	Research cytokines (e.g., IL-8)	Significant (statistically)
Pre-centrifugation conditions	Citrate plasma	Research cytokines (e.g., IL-8)	Non-significant (statistically)
Pre-centrifugation conditions	Citrate plasma	Coagulation parameters (e.g., factor V, factor VIII)	Significant (clinically)
Formalin fixation time	Lung tissue	IHC clinical antibodies (e.g., CK7)	Non-significant (clinically)
Formalin fixation time	Lung tissue	Mutation analysis by next-generation sequencing (e.g., allele frequency <10%)	Significant (not detectable mutation)
Alcohol fixation time	Lung tissue	Mutation analysis by next-generation sequencing (e.g., allele frequency <10%)	Non-significant (detectable mutation)

CK7, cytokeratin 7; EBV, Epstein–Barr virus; IgG, immunoglobulin G; IHC, immunohistochemistry; IL8, interleukin 8.

- objective analytical evidence, of their suitability for research use, either in a specific disease area or on a specific downstream analytical platform.
- *Quality stratification*: process of examination of a biospecimen or a collection of biospecimens, and their classification, based on objective analytical evidence, into distinct categories, each category corresponding to a specific *in vivo* biological characteristic (e.g., level of inflammation, % tumor, protein content) or to a specific *ex vivo* pre-analytical condition (e.g., pre-centrifugation conditions).
 - *Biomolecular integrity*: quality status of a biospecimen, reflecting whether biomolecules of interest have not un-

dergone either statistically or clinically significant changes relative to their *in vivo* state/levels.

- *Commutability*: equivalence of analytical methods, based on objective evidence.

The term “qualification” is used qualitatively. Therefore, a biospecimen is or is not qualified for use in research in a specific disease area or on a specific analytical platform.

The term “quality stratification” is used quantitatively. Therefore, one or more thresholds apply in order to stratify biospecimens in two or more quality categories. These quality categories correspond to defined *in vivo* or *in vitro* conditions.

TABLE 2. QC MEASURANDS FOR QUALIFICATION FOR USE IN SPECIFIC DISEASE AREAS

<i>Biospecimen type</i>	<i>Measurand</i>	<i>Scope of qualification (disease area)</i>	<i>Measurement method</i>
Serum	Brain natriuretic peptide (BNP), NT-proBNP ⁶	Cardiovascular	EIA
	Angiotensin-like 3 (ANFPTL3)		ECLIA/EIA
	Creatinine kinase MB isoenzyme (CK-MB)		EIA
Heparin plasma, serum	Endothelin 1 (ET-1)		
	Matrix metalloproteinase-3 (MMP-3), matrix metalloproteinase-9 (MMP-9)		EIA
All plasma, ^a serum	Troponin I & T		ECLIA/EIA
All plasma	Vasoactive intestinal peptide (VIP)		EIA
All plasma	Cholesterol ester transfer protein activity (CETP)	Lipid metabolism	Fluoroimmunoassay
Serum	Alanine aminotransferase (ALT) ⁷	Liver	Enzymatic assay
Serum, all plasma	Tumor necrosis factor alpha (TNF- α)	Autoimmune, inflammatory	Sensitive EIA
Serum	Insulin C peptide ⁸	Endocrinology and diabetes	Fluoroimmunoassay, EIA/RIA
	Insulin-like growth factor II precursor		EIA/RIA
All plasma	Glucagon-like peptide 1 (cleared by DPP4) ⁹		EIA/RIA
	Adenocorticotrophic hormone (ACTH)		ECLIA/RIA
All plasma, serum	Aldosterone		EIA
	Somatomedin C		
Citrate plasma	Anti-factor Xa	Coagulation	Clot detection
	Fibrinogen		
	Prothrombin fragments 1&2		EIA
	Plasminogen activator inhibitor type 1 activity or antigen		
	Thrombin generation assay		Fluoroimmunoassay
Urine	Tissue-type plasminogen activator antigen (TPA antigen)		EIA
	Beta 2 microglobulin	Nephrology	Nephelometry, EIA/RIA
All plasma, serum	Complement C3	Inflammation,	Nephelometry, EIA
All plasma, serum	Intercellular adhesion molecule 1 (ICAM-1)	immunology	EIA
Citrate/heparin plasma, serum	TNF- α		EIA
Serum	M65 EpiDeath	Oncology	EIA
Heparin plasma, serum	Vascular adhesion molecule I (VCAM-1)		EIA
Serum	Mid-osteocalcin, osteocalcin, calcitonin	Musculoskeletal	ECLIA, EIA
	Parathyroid hormone, intact (PTH)		ECLIA, EIA
All plasma, serum	Telopeptide C terminal, type 1 collagen		ECLIA, EIA
Serum	Vitamin B12	Nutritional	ECLIA
CSF, serum, all plasma	Amyloid Ab42	Neurodegenerative	EIA
Serum, CSF	Neuron-specific enolase ¹⁰		Kryptor immunoassay, EIA

^aAll plasma refers to all EDTA, citrate, and heparinized plasma.

CSF, cerebrospinal fluid; DPP4, dipeptidylpeptidase 4; ECLIA, electrochemiluminescent immunoassay; EIA, enzyme immunoassay; QC, quality control; RIA, radioimmunoassay.

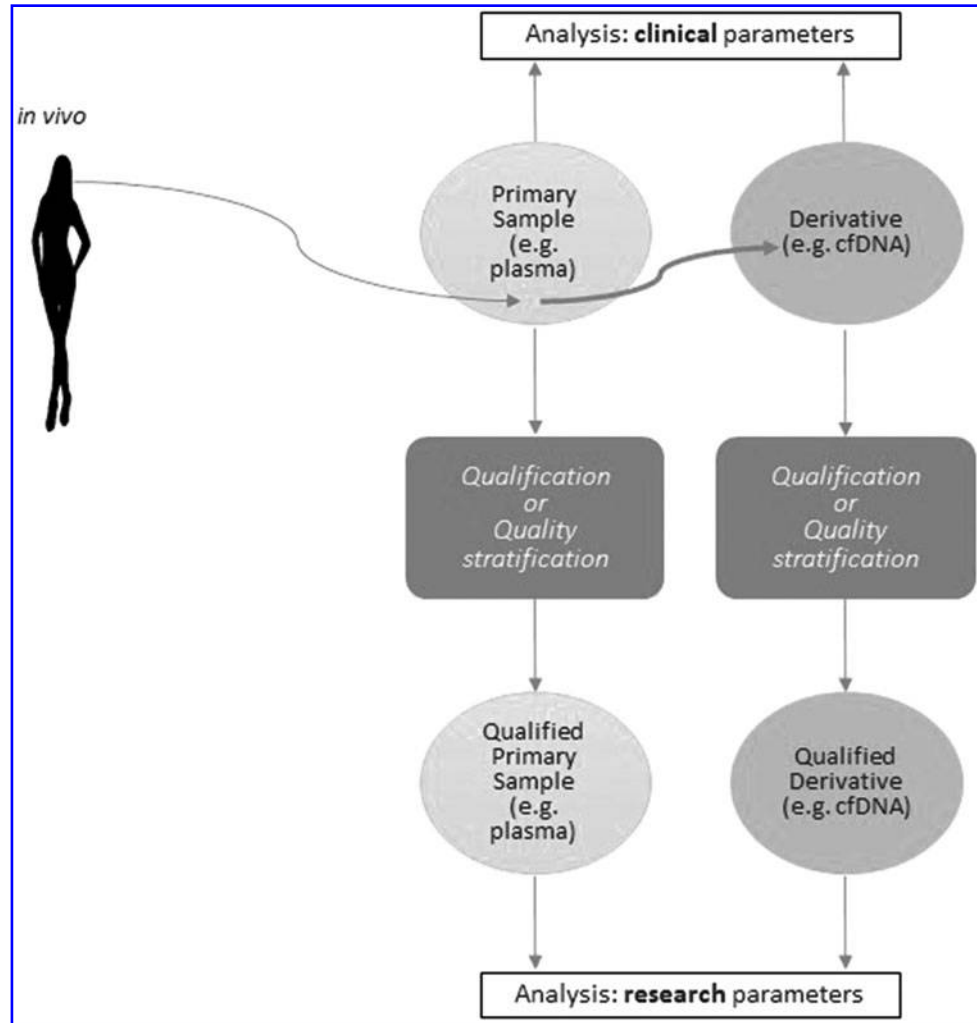


FIG. 1. Flow diagram illustrating sample preparation and qualification for use in research.

When qualification is not possible because of lack of relevant assays, then quality stratification can be made. In some cases, qualification can be achieved for biomarker research in a specific disease area (Table 2) or on a specific downstream analytical platform. For primary

samples, qualification depends on their biomolecular integrity. For simple or complex derivatives, qualification depends both on the biomolecular integrity of the primary sample from which the derivative has been extracted and on the efficiency/performance of the extraction, culture,

TABLE 3. QC MEASURANDS FOR QUALIFICATION OF FLUID BIOSPECIMENS AND THEIR DERIVATIVES

<i>Biospecimen type</i>	<i>Qualification parameter</i>	<i>Measurand</i>	<i>Scope of qualification</i>	<i>Measurement method</i>
Cf DNA	Contamination by blood cell DNA	DNA fragment size 100–300 bp ¹¹	Cf DNA genotyping	Microfluidic electrophoresis
Cf miRNA	Extraction efficiency	Spike in miRNA control (www.qiagen.com/lu/resources/resourcedetail?id=710c0168-e408-408b-95af-91df5b5b1dd6&lang=en)	Cf miRNA analysis	qRT PCR
		miRNA 16 or other ubiquitous miRNA target	Cf miRNA analysis	qRT PCR
Stool DNA	Inhibitors	SPUD ¹²	PCR applications	qPCR
	Extraction efficiency	Bacterial DNA content Human DNA content	Bacterial DNA analysis Human DNA analysis	qPCR qPCR
Whole-blood cell DNA	Inhibitors	SPUD ¹²	PCR applications	qPCR

Cf, cell free; qRT PCR, quantitative reverse transcription polymerase chain reaction.

TABLE 4. QC MEASURANDS FOR QUALITY STRATIFICATION OF FLUID BIOSPECIMENS AND THEIR DERIVATIVES

Biospecimen type	Quality stratification parameter	Quality stratification parameter category	Measurand	Quality stratification threshold	Measurement method and reference
Serum	Pre-centrifugation conditions	>8 h 4°C	Transferrin receptor	>300 IU/mL	ELISA ¹³
	Post-centrifugation conditions	>24 h RT	sCD40L	<4 ng/mL	ELISA ¹⁴
	Coagulation conditions	Not effectively coagulated	Fibrinogen	>100 mg/mL	ELISA
	Hemolysis	Hb contaminated	Hb	>50 mg/L	ELISA, spectrophotometry (www.ifcc.org/ifccfiles/docs/130401002end.pdf)
	Inflammation	Inflamed	C-reactive protein (CRP)	>10 mg/L	Nephelometry, ELISA ⁵
	Pre-centrifugation conditions	>48 h 4°C	Progastrin-releasing peptide (proGRP)	<30 pg/mL	Architect instrument ⁵
	Pre-centrifugation conditions	<3 h RT	Lacase	<5	Enzymatic assays ¹⁶
	Pre-centrifugation conditions	<2 h, 2–6 h, >6 h RT	Metanomics	MxP score ≥90, 89–70, <70	GC MS ^{1,7}
	Post-centrifugation conditions	>24 h RT	sCD40L	<0.3 ng/mL	ELISA (Betsou, unpublished)
	Post-centrifugation conditions	>4 h RT	Complement component 3 peptide (C3f), complement component 4 (C4)	C4, 1896.1 m/z C3f, 2021.1 m/z	MALDI-TOF-MS LC-ESI-MS/ ^{18,19}
Citrate plasma	Platelet contamination	Platelet poor	Platelets	<10 ⁴ /mL	Cell count (https://en.wikipedia.org/wiki/Platelet-poor_plasma)
	Platelet activation	Activated platelets	β-thromboglobulin (βTG)	>200 ng/mL	ELISA ²⁰
	Hemolysis	Hb contaminated	Hb	>20 mg/L	ELISA, spectrophotometry ²¹
	Inflammation	Inflamed	CRP	>10 mg/L	(www.ifcc.org/ejifcc/vol13no4/13041002.htm)
	Pre-centrifugation conditions	>26 h 4°C	F VIII:C activity	<50 IU/dL	Nephelometry, ELISA
	Post-centrifugation conditions	>9 years –80°C	Protein S activity	<50%	Coagulation activity assay ²²
	Freezing	>6 months –20°C	Alkaline phosphatase activity	<0.1 IU/mmol creatinine	Coagulation activity assay ²³
	Protein content	Low, intermediate, high, very high protein content	Creatinine Cystatin C	10, 50, 100 mg/dL 10, 50, 100 ng/mL	Enzymatic assay ²⁴
	acidity	Alcaline	pH	>8	ELISA ²⁵ pH paper

(continued)

TABLE 4. (CONTINUED)

Biospecimen type	Quality stratification parameter	Quality stratification parameter category	Measurand	Quality stratification threshold	Measurement method and reference
CSF	Post-centrifugation conditions	>32 h 4°C >3 months -20°C	Transferrin (TTR) isoforms Cystatin C (CycC) truncation	Unmodified TTR-Cys10 peak <60% Intact CycC>truncated CysC peak	ESI-MS ²⁶ MALDI-TOF-MS, SELDI MS ^{27,28}
	Hemolysis Inflammation Double-strandedness	Hb contaminated Inflamed Highly double stranded	Hb Calprotectin Spectrofluorimetry	>15 ng/mL >50 mg/kg >70%	ELISA ²⁸ ELISA ²⁹ Spectrophotometry, spectrofluorimetry
Stool	Integrity	No degraded With no strand breaks	MW Long-range amplifiability	≥30 kb 15 kb	Gel electrophoresis PCR
	Purity	Not protein contaminated TBD	A260/A280 ratio	≥1.5	Spectrophotometry
Whole blood	Damage (oxidation, deamination, alkylation)	TBD	Apurinic/apyrimidinic sites	TBD	Colorimetric detection (aldehyde reactive probe-based)
	Post-bisulfitation quality	Of high DNA integrity	PCR amplicon size	≥600 bp	Multiplex PCR ³⁰
Whole blood	rRNA integrity	Of high integrity	RIN	>7	Microfluidic electrophoresis
	mRNA integrity	Not 5' degraded Not protein contaminated	mRNA index A260/A280 ratio	ΔCt <1 >1.6	qRT PCR ³¹ Spectrophotometry
cell DNA	Pre-centrifugation conditions	>24 h RT	Gene targets ^b	TBD	qRT PCR ^{32,33}
cell RNA	WBC subpopulation composition	Normal composition	Lymphocytes, granulocyte, monocyte numbers	Neutrophils: $2.5-7.5 \times 10^9/L$ Lymphocytes: $1.5-3.5 \times 10^9/L$ Monocytes: $0.2-0.8 \times 10^9/L$	Blood count ³⁴ (http://emedicine.medscape.com/article/2085133-overview)

^aAll plasma refers to all EDTA, citrate, and heparinized plasma.

^bUnder investigation by the International Society for Biological and Environmental Repositories (ISBER) Biospecimen Science Working Group. ELISA, enzyme-linked immunosorbent assay; Hb, hemoglobin; LC-ESI-MS, liquid chromatography electrospray ionization mass spectrometry; MALDI-TOF-MS, matrix-assisted laser desorption/ionization time of flight mass spectrometry; RT, room temperature; SELDI MS, surface-enhanced laser desorption/ionization mass spectrometry; TBD, to be defined; WBC, white blood cell.

TABLE 5. QC MEASURANDS FOR QUALIFICATION OF TISSUE BIOSPECIMENS AND THEIR DERIVATIVES

<i>Biospecimen type</i>	<i>Qualification parameter</i>	<i>Measurand</i>	<i>Scope of qualification</i>	<i>Measurement method</i>
Frozen tissue	Freeze–thaw	Cell lysis	IHC, RNA-based analyses	H&E staining
Viable frozen tissue	Sterility Cryopreservation conditions	Absence of contaminants Post-thaw viability	Tissue culture	Growth on agar; mycoplasma testing Growth in flasks

H&E, hematoxylin and eosin.

cryopreservation, or other laboratory manipulation (e.g., cfDNA from plasma; Fig. 1).

Results

The results are presented in the form of Tables for fluid (Tables 3 and 4), tissue (Tables 5 and 6), and cytological biospecimens and their derivatives.

Table 2 includes information on QC measurands for qualification for use of samples in specific disease areas.^{4,5} The measurands in this table are molecules that are recognized biomarkers in the respective disease areas and are also known to be labile. Detection of the measurand above the method's level of detection is necessary (though not always sufficient) for qualification of a sample. As an example for reading Table 2, if Aβ42 is undetectable in CSF samples, then these samples cannot be qualified for research in the area of neurodegenerative diseases.

Tables 3, 5, and 7 include information that can be used for the qualification of fluid, tissue, or cytological specimens, respectively, in the scope of different types of downstream analyses. In these tables, “qualification parameter” is the quality aspect of the biospecimen that is being evaluated; “measurand” is the molecule, or the morphological or functional characteristic that is being measured and whose positive or negative result is necessary for the qualification; “scope of qualification” is the type of downstream analysis for which the biospecimen is being qualified as fit-for-purpose; and “measurement method” is the type of method that is used to measure the measurand.

Tables 4, 6, and 8 include information that can be used for the quality stratification of a fluid, tissue, or cytological biospecimen, respectively. In these tables, “qualification parameter” is the quality aspect of the biospecimen for which the biospecimen is being stratified; “measurand” is the molecule, or the morphological or functional characteristic that is being measured and whose level is used to stratify the biospecimens in categories; “quality stratification thresholds” are the levels of the measurand, which are critical for the quality stratification; and “measurement method” is the type of method that is used to measure the measurand. The quality stratification thresholds listed in Tables 4, 6, and 8 classify the biospecimens into the categories of the qualification parameter given. The “time xxx/temperature yyy” categories correspond to available experimental data, but they should be understood as “time xxx/temperature yyy or equivalent conditions.” The quality stratification thresholds listed in Tables 4, 6, and 8 are those corresponding to the measurement methods described in the

references. Application of a threshold with a measurement method that is different from the method that has been used for the establishment of the threshold requires previous demonstration of the commutability of the methods.

Tissue type specificities

Assays for tissue qualification or quality stratification may be tissue type-specific. Some examples are given below. Fixation conditions have a significant impact on P-Akt and P-Erk1/2 in breast cancer tissue.³⁵ Ischemia has a significant impact on estrogen and progesterone receptors in breast tissue.^{36,37} A Tissue Quality Index has been proposed for formalin-fixed, paraffin-embedded breast tissue in order to assess its cold ischemia time by immunohistochemistry.³⁸ Stathmin^{2–20} has been proposed as indicator of degradation in brain tissue by matrix-assisted laser desorption/ionization time of flight mass spectrometry.³⁹ AKT-P has been proposed as indicator of postmortem conditions in brain tissue by western blot.⁴⁰ Superoxide dismutase in the liver and peptidyl-prolyl-cis-trans isomerase and insulin C-peptides in the pancreas have been associated with postmortem delay and assessed by two-dimensional difference in gel electrophoresis.⁴¹

Discussion

This article proposes a biospecimen QC strategy, based on current state of knowledge, in the form of summary tables (Fig. 2).

The qualification and quality stratification assays presented in this technical report do not aim for an absolute assessment of the quality of samples, since a sample can be of high enough quality (fit-for-purpose) for one type of analysis (e.g., antibody analysis), but not for other types of analyses (e.g., metabolite analysis). Therefore, scientists should devote time and effort to understand and define what sample quality is needed to obtain consistent results with a given downstream analytical platform. As can be seen from Tables 3, 5, and 7, there are several gaps in the area of biospecimen qualification for use on specific analytical platforms. These include, for example, urine, saliva, or frozen tissue qualification for use in proteomic analyses, serum, plasma, or other body fluid qualification for use in miRNome analyses, or DNA qualification for use in methylation analyses. In the absence of such knowledge, this technical report offers a strategy for sample quality stratification so that bias due to samples of inconsistent quality levels can be minimized.

TABLE 6. QC MEASURANDS FOR QUALITY STRATIFICATION OF TISSUE BIOSPECIMENS AND THEIR DERIVATIVES

<i>Biospecimen type</i>	<i>Quality stratification parameter</i>	<i>Quality stratification parameter category</i>	<i>Measurand</i>	<i>Quality stratification threshold</i>	<i>Measurement method and reference</i>
Tumor	% tumor	Tumor-rich	Tumor	>70%	H&E staining, digital pathology
FFPE	Fixation time	>72 h	None to date ^a	TBD	qRT PCR
	Fixation conditions	NBF (no acidic formalin)	Size range RT PCR	~250 bp	RT PCR
	Cold ischemia	>12 h	None to date ^a	TBD	qRT PCR
	Cold ischemia	>12 h	None to date ^a	TBD	qRT PCR
Frozen tissue	Fixation conditions	Highly deaminated	qPCR ΔCt	ΔCt ≥1.55	Illumina FFPE QC kit
	(cross-linking); extraction efficiency				Agilent NGS FFPE QC kit or equivalent ⁴²
FFPE DNA	DNA integrity	CGH compatible	PCR amplicon size	≥200bp,	Multiplex PCR ^{43,44}
		WGA compatible	WGA score	≥300 bp	
		Of good integrity		≥3 μg yield	WGA (www.enziflifsciences.com/ENZ-42440/bioscore-screening-and-amplification-kit-20-reactions)
FFPE RNA	mRNA integrity	Of good integrity	DIN	>7	Microfluidic electrophoresis
		Extremely 5' degraded	mRNA index	ΔCt >8	
		Of good mRNA integrity	Size range RT PCR	~250 bp	
		>72 h	Gene targets ^a	TBD	
		>12 h	Gene targets ^a	TBD	
FFPE proteins	Ischemia time	TBD	Phospho-Tyrosine (P Tyr 100)	TBD	IHC ⁴⁵
	Ischemia time	TBD	Long range PCR	15 kb	
Frozen tissue DNA	Processing/storage conditions; extraction efficiency	With no strand breaks			
	Processing/storage conditions; extraction efficiency	Of high integrity	RIN RIS DV200 or equivalent	>6	Microfluidic electrophoresis (www.agilent.com/cs/library/applications/5989-1165EN.pdf), (www.qiagen.com/gb/shop/automated-solutions/dna-analysis/qiaxcel-advanced-system/), (www.aati-us.com/product/fragment-analyzer/download_dv200_metric)
Frozen tissue RNA	mRNA integrity	Not 5' degraded	mRNA index	ΔCt <1	qRT PCR ³¹
	Purity	Not protein contaminated	A260/A280 ratio	>1.6	
Frozen tissue proteins	Postmortem interval/ ischemia	>48 h cold ischemia	αII spectrin cleavage (no 285 kDa, only 150 kDa)	285 kDa >150 kDa	Spectrophotometry Western blot ⁴⁶

^aUnder investigation by the ISBER Biospecimen Science Working Group. FFPE, formalin-fixed, paraffin-embedded; NBF, normal buffered formalin.

TABLE 7. QC MEASURANDS FOR QUALIFICATION OF CYTOLOGICAL BIOSPECIMENS

<i>Biospecimen type</i>	<i>Qualification parameter</i>	<i>Measurand</i>	<i>Scope of qualification</i>	<i>Measurement method</i>
All cell suspensions	Sterility	Absence of contaminants	Culture	Growth on agar; mycoplasma testing
	Identity	Protein markers	Any type of downstream analysis	ICC, ELISA, FC
	Purity	Genetic identity Absence of protein markers Absence of cellular impurities	Any type of downstream analysis	PCR, STR genotyping, FISH, karyology ICC, ELISA, FC
Cell line	Genomic stability	Chromosomal stability Phenotypic stability	Any type of downstream analysis	FC G-banding, ICC, FC, microscopy
	Identity	STR, karyotype, SNP fingerprint ⁴⁷	Any type of downstream analysis	PCR, karyology/FISH, sequencing/arrays
	Sterility	Absence of contaminants	Culture, functional assays	Growth on agar; mycoplasma testing, HIV, HBV, HCV, EBV, CMV, syphilis, fungus, bacteria, endotoxin
Stem cells	Normal karyotype	Karyotype	Any type of downstream analysis	G-banding
	Identity matching	Match parent cells	Any type of downstream analysis	STR
	Non oncogenicity	C-Myc, P53, p21, p16 absence of expression	Any type of downstream analysis	Immunostaining, gene expression
Lymphoblastoid cell lines (LCL)	Normal karyotype	Karyotype	Any type of downstream analysis	G-banding
	EBV transformation	EBV gene expression	Any type of downstream analysis	RT PCR ⁴⁸
	Cancer phenotype	EpCam+, CK8+, 18+, 19+, CD45-	Any type of downstream analysis	Immunostaining ⁴⁹

CMV, cytomegalovirus; FC, flow cytometry; FISH, fluorescent in situ hybridization; HBV, hepatitis B virus; HCV, hepatitis C virus; HIV, human immunodeficiency virus; ICC, immunocytochemistry; SNP, single nucleotide polymorphism; STR, short tandem repeats.

TABLE 8. QC MEASURANDS FOR QUALITY STRATIFICATION OF CYTOLOGICAL BIOSPECIMENS

<i>Biospecimen type</i>	<i>Quality stratification parameter</i>	<i>Quality stratification parameter category</i>	<i>Measurand</i>	<i>Quality stratification threshold</i>	<i>Measurement method and reference</i>
Peripheral blood mononuclear cells (PBMCs)	Cryopreservation Specificity (granulocyte contamination)	Of high viability <12–14 h RT post venipuncture; With no T-cell function inhibition	Post thaw viability CD15+ granulocytes	>80% <20%	FC; trypan blue FC ³⁰
All cell suspensions	Biological activity	Cell type specific	Receptors Secreted proteins mRNA expression Migration	Cell type-specific	ICC, FC, microscopy, FRET microscopy, ELISA, qRT PCR, microarray Dunn, Boyden or Impedance Chamber, Scratch assay, Matrigel invasion assay
	Concentration, viability	Of high viability	Cell number Viability	>80%	FC, impedance, microscopy
Sperm	DNA integrity	Of compromised DNA integrity	Acridine Orange staining and acid-induced denaturation	COMP _a ^a >30%	Viability assays Sperm chromatin structure assay ⁵¹
Viable RBC	Storage lesion	>4 days 4°C	2,3-diphosphoglycerate (2,3-DPG)	<2 mmol/L	Spectrophotometry (340 nm) ⁵²
Viable platelets	Activation	With highly activated platelets	Surface P selectin (CD62)	>70%	Flow cytometry ⁵³
Stem cells	Cryopreservation conditions Surface antigen expression of stem cell markers Pluripotency	Efficiently cryopreserved Stem cell positive Pluripotent	Colony formation and diameter doubling expression SSEA-4, expression SSEA-1 Upregulation of genes associated with each of the three germ layers Number of cells % of cells with expected immunophenotype, e.g., T cells (CD3), NK cells (CD16/56), B cells (CD19/20), monocytes (CD14), functional memory B cells (CD19, CD27, CD45, CD38, CD138)	<5 days >80%, <20% 2-fold compared to control (at least one gene per germ layer) <i>Downstream application-specific</i> >90%	Colony doubling Immunostaining qRT PCR
Liquid biopsy-based cytology specimens Sorted cells	Cell concentration Purity	<i>Downstream application-specific</i> Pure			Cell count Flow cytometry

^aCOMP, cells outside the main population.
FRET, fluorescence resonance energy transfer; RBC, red blood cell; SSEA, stage-specific embryonic antigen.

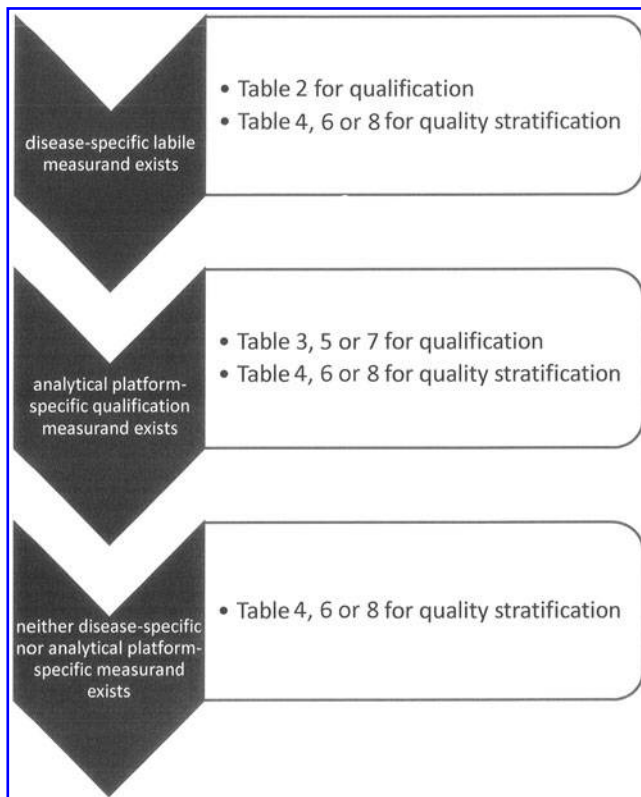


FIG. 2. Decision tree for any given specimen type.

The information provided in this report is important because its application will enable and support bioprocessing method validation by providing relevant readouts (measurands); assessment of the quality of biospecimens of unknown history; biomarker discovery by ensuring use of qualified biospecimens or biospecimens belonging to a specific quality category; validation of biomarker robustness by using quality-stratified biospecimens belonging to different, defined quality categories; implementation of novel biomarkers in clinical practice; and characterization and production of clinical reference materials.

For the above purposes, QC measurands of clinical biospecimens can be assessed either by the biobanks themselves, or by subcontractors/collaborators who are accredited or successfully participate in relevant Proficiency Testing schemes. The results of the QC can be used by biobanks for qualification of legacy collections (the definition of cutoff values for acceptance of legacy collections or specific samples can be made and disclosed by the biobank), by end users for stratification of samples of different origins, or by funding agencies for assessment of the fitness for purpose of collections to be used in the context of grant allocation.

Author Disclosure Statement

F.B. is listed as co-inventor in patent no. 0704237 and in the filed patent 15195301.5-1408 (on sCD40L and LacaScore, respectively).

References

- Cummings J, Raynaud F, Jones L, et al. Fit-for-purpose biomarker method validation for application in clinical trials of anticancer drugs. *Br J Cancer* 2010;103:1313–1317.
- Betsou F, Barnes R, Burke T, et al. Human biospecimen research: experimental protocol and quality control tools. *Cancer Epidemiol Biomarkers Prev* 2009;18:1017–1025.
- Lehmann S, Guadagni F, Moore H, et al. Standard pre-analytical coding for biospecimens: review and implementation of the Sample PREanalytical Code (SPREC). *Biopreserv Biobank* 2012;10:366–374.
- Siest G, Henny J, Schiele F. *Références en Biologie Clinique*. Paris: Elsevier;1990.
- Ghnassia J-C. *Échantillons Biologiques Phase Pré-analytique et Prélèvements en Biologie Médicale*. Paris: Elsevier;1998.
- Belenky A, Smith A, Zhang B, et al. The effect of class-specific protease inhibitors on the stabilization of B-type natriuretic peptide in human plasma. *Clin Chim Acta* 2004;340:163–172.
- Williams KM, Williams AE, Kline LM, et al. Stability of serum alanine aminotransferase activity. *Transfusion* 1987;27:431–433.
- Gislefoss RE, Grimsrud TK, Morkrid L. Stability of selected serum proteins after long-term storage in the Janus Serum Bank. *Clin Chem Lab Med* 2009;47:596–603.
- Kim W, Egan JM. The role of incretins in glucose homeostasis and diabetes treatment. *Pharmacol Rev* 2008;60:470–512.
- Ramont L, Thoannes H, Volondat A, et al. Effects of hemolysis and storage condition on neuron-specific enolase (NSE) in cerebrospinal fluid and serum: implications in clinical practice. *Clin Chem Lab Med* 2005;43:1215–1217.
- Breitbach S, Tug S, Helmig S, et al. Direct quantification of cell-free, circulating DNA from unpurified plasma. *PLoS One* 2014;9.
- Nolan T, Hands RE, Ogunkolade W, et al. SPUD: a quantitative PCR assay for the detection of inhibitors in nucleic acid preparations. *Anal Biochem* 2006;351:308–310.
- De Jongh R, Vranken J, Vundelinckx G, et al. The effects of anticoagulation and processing on assays of IL-6, sIL-6R, sIL-2R and soluble transferrin receptor. *Cytokine* 1997;9:696–701.
- Lengelle J, Panopoulos E, Betsou F. Soluble CD40 ligand as a biomarker for storage-related preanalytical variations of human serum. *Cytokine* 2008;44:275–282.
- Korse CM, Holdenrieder S, Zhi XY, et al. Multicenter evaluation of a new progastrin-releasing peptide (ProGRP) immunoassay across Europe and China. *Clin Chim Acta* 2015;438:388–395.
- Trezzi J-P, Bulla A, Bellora C, et al. LacaScore: a novel plasma sample quality control tool based on ascorbic acid and lactic acid levels. *Metabolomics* 2016; in press.
- Kamlage B, Maldonado SG, Bethan B, et al. Quality markers addressing preanalytical variations of blood and plasma processing identified by broad and targeted metabolite profiling. *Clin Chem* 2014;60:399–412.
- Yi J, Kim C, Gelfand CA. Inhibition of intrinsic proteolytic activities moderates preanalytical variability and instability of human plasma. *J Proteome Res* 2007;6:1768–1781.
- Marshall J, Kupchak P, Zhu W, et al. Processing of serum proteins underlies the mass spectral fingerprinting of myocardial infarction. *J Proteome Res* 2003;2:361–372.
- Chong BH, Murray B, Berndt MC, et al. Plasma P-selectin is increased in thrombotic consumptive platelet disorders. *Blood* 1994;83:1535–1541.
- Thomas L. Haemolysis as influence and interference factor. Available at www.ifcc.org/ifccfiles/docs/130401002end.pdf (accessed March 30, 2016).

22. Carlebjork G, Blomback M, Akerblom O. Improvement of plasma quality as raw material for factor VIII:C concentrates. Storage of whole blood and plasma and interindividual plasma levels of fibrinopeptide A. *Vox Sang* 1983;45:233–242.
23. Betsou F, Roussel B, Guillaume N, et al. Long-term stability of coagulation variables: protein S as a biomarker for preanalytical storage-related variations in human plasma. *Thromb Haemost* 2009;101:1172–1175.
24. Berg KJ, Kristoffersen DT, Djoseland O, et al. Reference range of some enzymes and proteins in untimed overnight urine and their stability after freezing. *Clin Chim Acta* 1998;272:225–230.
25. Uchida K, Gotoh A. Measurement of cystatin-C and creatinine in urine. *Clin Chim Acta* 2002;323:121–128.
26. Poulsen K, Bahl JM, Tanassi JT, et al. Characterization and stability of transthyretin isoforms in cerebrospinal fluid examined by immunoprecipitation and high-resolution mass spectrometry of intact protein. *Methods* 2012;56:284–292.
27. Hansson SF, Simonsen AH, Zetterberg H, et al. Cystatin C in cerebrospinal fluid and multiple sclerosis. *Ann Neurol* 2007;62:193–196; discussion 205.
28. Greco V, Pieragostino D, Piras C, et al. Direct analytical sample quality assessment for biomarker investigation: qualifying cerebrospinal fluid samples. *Proteomics* 2014;14:1954–1962.
29. Tibble JA, Bjarnason I. Fecal calprotectin as an index of intestinal inflammation. *Drugs Today (Barc)* 2001;37:85–96.
30. Ehrlich M, Zoll S, Sur S, et al. A new method for accurate assessment of DNA quality after bisulfite treatment. *Nucleic Acids Res* 2007;35:e29.
31. Vermeulen J, De Preter K, Lefever S, et al. Measurable impact of RNA quality on gene expression results from quantitative PCR. *Nucleic Acids Res* 2011;39:e63.
32. Debey S, Schoenbeck U, Hellmich M, et al. Comparison of different isolation techniques prior gene expression profiling of blood derived cells: impact on physiological responses, on overall expression and the role of different cell types. *Pharmacogenomics J* 2004;4:193–207.
33. Benita Y, Kikuchi H, Smith AD, et al. An integrative genomics approach identifies Hypoxia Inducible Factor-1 (HIF-1)-target genes that form the core response to hypoxia. *Nucleic Acids Res* 2009;37:4587–4602.
34. Curry CV. Differential Blood Count Medscape. Available at: <http://emedicine.medscape.com/article/2085133-overview> (accessed March 30, 2016).
35. Pinhel IF, Macneill FA, Hills MJ, et al. Extreme loss of immunoreactive p-Akt and p-Erk1/2 during routine fixation of primary breast cancer. *Breast Cancer Res* 2010;12:R76.
36. Masood S, von Wasielewski R, Mengel M, et al. Influence of fixation, antibody clones, and signal amplification on steroid receptor analysis. *Breast J* 1998;4:33–40.
37. Yildiz-Aktas IZ, Dabbs DJ, Bhargava R. The effect of cold ischemic time on the immunohistochemical evaluation of estrogen receptor, progesterone receptor, and HER2 expression in invasive breast carcinoma. *Mod Pathol* 2012;25:1098–1105.
38. Neumeister VM, Parisi F, England AM, et al. A tissue quality index: an intrinsic control for measurement of effects of preanalytical variables on FFPE tissue. *Lab Invest* 2014;94:467–474.
39. Skold K, Svensson M, Norrman M, et al. The significance of biochemical and molecular sample integrity in brain proteomics and peptidomics: stathmin 2–20 and peptides as sample quality indicators. *Proteomics* 2007;7:4445–4456.
40. Ferrer I, Santpere G, Arzberger T, et al. Brain protein preservation largely depends on the postmortem storage temperature: implications for study of proteins in human neurologic diseases and management of brain banks: a BrainNet Europe Study. *J Neuropathol Exp Neurol* 2007;66:35–46.
41. Scholz B, Skold K, Kultima K, et al. Impact of temperature dependent sampling procedures in proteomics and peptidomics—a characterization of the liver and pancreas post mortem degradome. *Mol Cell Proteomics* 2011;10.
42. Serizawa M, Yokota T, Hosokawa A, et al. The efficacy of uracil DNA glycosylase pretreatment in amplicon-based massively parallel sequencing with DNA extracted from archived formalin-fixed paraffin-embedded esophageal cancer tissues. *Cancer Genet* 2015;208:415–427.
43. van Beers EH, Joosse SA, Ligtenberg MJ, et al. A multiplex PCR predictor for aCGH success of FFPE samples. *Br J Cancer* 2006;94:333–337.
44. Wang F, Wang L, Briggs C, et al. DNA degradation test predicts success in whole-genome amplification from diverse clinical samples. *J Mol Diagn* 2007;9:441–451.
45. Gajadhar AS, Johnson H, Slebos RJ, et al. Phosphotyrosine signaling analysis in human tumors is confounded by systemic ischemia-driven artifacts and intra-specimen heterogeneity. *Cancer Res* 2015;75:1495–1503.
46. Li J, Kil C, Considine K, et al. Intrinsic indicators for specimen degradation. *Lab Invest* 2013;93:242–253.
47. Dirks WG, Drexler HG. Authentication of scientific human cell lines: easy-to-use DNA fingerprinting. *Methods Mol Biol* 2005;290:35–50.
48. Jeon JP, Nam HY, Shim SM, et al. Sustained viral activity of Epstein-Barr virus contributes to cellular immortalization of lymphoblastoid cell lines. *Mol Cells* 2009;27:143–148.
49. Lowes LE, Hedley BD, Keeney M, et al. User-defined protein marker assay development for characterization of circulating tumor cells using the CellSearch® system. *Cytometry A* 2012;81:983–995.
50. McKenna KC, Beatty KM, Vicetti Miguel R, et al. Delayed processing of blood increases the frequency of activated CD11b+ CD15+ granulocytes which inhibit T cell function. *J Immunol Methods* 2009;341:68–75.
51. Evenson D, Jost L. Sperm chromatin structure assay is useful for fertility assessment. *Methods Cell Sci* 2000;22:169–189.
52. Bennett-Guerrero E, Veldman TH, Doctor A, et al. Evolution of adverse changes in stored RBCs. *Proc Natl Acad Sci U S A* 2007;104:17063–17068.
53. Holme S, Sweeney JD, Sawyer S, et al. The expression of p-selectin during collection, processing, and storage of platelet concentrates: relationship to loss of *in vivo* viability. *Transfusion* 1997;37:12–17.

Address correspondence to:

Fay Betsou, PhD

Integrated BioBank of Luxembourg

6 rue Nicolas Ernest Barblé

L-1210

Luxembourg

E-mail: fay.betsou@ibbl.lu