Covaris®
a PerkinElmer Company

Is Phlebotomy a Bottleneck for Genomics Studies? Rethinking and Redesigning Blood Collection Infrastructure for Large Scale Biology

Author: Deb Bhattacharyya, PhD | **Affiliation:** Covaris LLC, a PerkinElmer Company, Woburn, MA, USA 01801

Abstract

Advances in detection technologies have enabled better molecular insights across a wide array of Omics studies – from genomics to transcriptomics, and from proteomics to metabolomics. A combination of the data from all the omics studies are increasingly applied to large population cohorts, longitudinal clinical studies, and decentralized clinical trials. While the end-detection technologies experienced some significant developments in the last two to three decades, the sample collection and preparation approaches continue to be challenging, complex, time consuming, and lack standardization protocols. The infrastructure used to obtain biospecimens, especially, whole blood has evolved far more slowly than the analytical technologies used to study them. Most blood samples used in research and diagnostics are still obtained through venous phlebotomy performed in clinical environments. While historically adequate for diagnostic testing and small studies, this model presents growing limitations for large scale studies. Workforce shortages, geographic constraints, cold-chain logistics and variability in sample handling collectively limit the scalability of blood-based molecular profiling. Emerging remote blood collection technologies, including stabilized capillary blood sampling systems such as Covaris' truCOLLECT® Whole Blood Collection Solution offer a potential pathway toward decentralized biospecimen infrastructure compatible with modern analytical workflows. Here we examine how evolving blood collection technologies may reshape biological sampling for the laboratories focused on Genomics.

The Needed Revolution for Sample Collection Infrastructure

The past two decades have witnessed rapid advances in molecular measurement technologies.[1,2] High-throughput sequencing,[3] mass spectrometry[4] and single-cell analysis[5] have made it possible to profile biological systems across multiple molecular layers including DNA, RNA, proteins, and metabolites.

Large-scale initiatives such as population biobanks and precision medicine programs increasingly rely on genomics analysis of blood samples collected from large cohorts. Whole blood remains one of the most valuable biospecimens[6] because it enables analysis of multiple biomolecular classes simultaneously and allows longitudinal sampling over time. Modern biomedical research increasingly relies on Genomics approaches that integrate data across multiple molecular layers. Some key examples are listed in **Table 1**.

Table 1. List of typical Omics application areas and their molecular targets.

Omics Application	Molecular Targets
Genomics	DNA Sequence Variation
Transcriptomics	RNA Expression Profiles
Proteomics	Protein Abundance and Modification
Metabolomics	Small-molecule Metabolites
Epigenomics	Chromatin and DNA Methylation

When all the data obtained from each Omics layer detailed in **Table 1** are combined, the resulting datasets provide a systems-level view of biological state,[7] enabling researchers to study disease mechanisms,[8] therapeutic response,[9] and population health.[10]

Large scale initiatives such as precision medicine programs, population biobanks and biomarker discovery studies increasingly rely on genomics analysis of blood samples.[2, 11, 12] Whole blood is particularly valuable because it contains multiple molecular components simultaneously, allowing researchers to generate extensive datasets for DNA, RNA, Proteomes, and metabolomes. from a single specimen.[7, 12]

Despite several technological advances that the world of end-detection instruments witnessed in the last three decades, the infrastructure used to collect blood samples remains largely unchanged.[12-14] Most biospecimens are still obtained through venous phlebotomy, a procedure that requires a trained healthcare personnel and specialized clinical environments. As biological research shifts toward population scale datasets, the scalability of this traditional model is increasingly being questioned.[13, 15]

Whole Blood for Comprehensive Genomics

Whole blood is one of the most information rich biological samples available for human research.[16] It contains:

- Genomic DNA from circulating cells
- Messenger RNA from leukocytes
- Circulating proteins and cytokines
- Metabolites reflecting systemic metabolism
- Immune cell populations
- Extracellular nucleic acids

The wide variety of information offered by whole blood supports multiple analytical approaches such as Whole Genome Sequencing (WGS), proteomics studies, RNA sequencing, etc. Because blood can be collected repeatedly over time, it renders high value for disease monitoring and treatment response in addition to identification of diseases.

Blood Collection: The Hidden Bottleneck in Genomics Research

In discussions about the limitations of large scale biological studies, attention often focuses on sequencing cost or computational analysis. Yet in many research programs the true bottleneck lies much earlier in the workflow, starting at the level of biospecimen acquisition.[13, 14] In a typical genomics workflow starting with whole blood,[17] the process comprises:

- Participant recruitment
- Biospecimen collection
- Sample stabilization and transport
- Analyte extraction
- Molecular profiling
- Computational analysis

Biospecimens such as whole blood collection remains a manual and labor intensive process, which in turn, exerts a negative impact on the rate at which biological data can be generated.

Workforce Constraints in Phlebotomy

Traditional venous blood collection depends on trained phlebotomists. Many healthcare systems are currently experiencing workforce shortages affecting laboratory and diagnostic services. In the United States alone, approximately 18,400 phlebotomist job openings occur annually,[18] largely due to workforce turnover and retirements. Phlebotomy services in hospitals also experience high turnover rates, in some cases approaching 25% annually, which complicates staffing and training.[19] These shortages are part of a broader crisis affecting clinical laboratories. Surveys indicate that nearly 40% of laboratories report significant understaffing, highlighting the growing pressure on diagnostic infrastructure.[20] For research studies, workforce limitations translate into:

- Limited appointment availability
- Delayed sampling schedules
- Higher operational costs
- Restricted sampling frequency

As study sizes increase, reliance on specialized personnel becomes a structural limitation.

Geographic and Accessibility Constraints

Traditional phlebotomy requires participants to visit hospitals, clinics or research centers. This requirement introduces geographic barriers that can affect study participation. These challenges are particularly pronounced for:

- Restricted access for geographically dispersed participants
- Limited appointment availability, especially for individuals with limited mobility
- Difficulty scheduling repeated sampling
- Increased cost/sample

Approximately 43 million rural Americans live in areas with shortages of healthcare professionals, highlighting the limitations of clinic-based sampling models.[21] These above-mentioned barriers can lead to sampling bias, where participants living near academic medical centers are disproportionately represented in research cohorts. For large population studies and global clinical trials, accessibility remains a major challenge.

Molecular Instability and Cold-Chain Dependence

Beyond logistical constraints, the biochemical properties of blood create additional challenges for genomics analysis. Whole blood contains multiple molecular components that are sensitive to degradation or alteration following collection. After collection, molecular components in blood begin to change rapidly. As an example:

- RNA degradation can occur within hours
- Proteins may undergo rapid proteolysis
- Metabolic pathways continue to alter metabolite levels
- Immune cells respond to environmental changes

Making necessary adjustments to prevent the above-mentioned conditions require rapid processing, refrigeration, or immediate freezing of samples. Cold chain transport and processing infrastructure introduce significant costs and can also create variability between study sites. Variability in processing conditions across sites can also introduce batch effects that affect genomics datasets.[22]

The Case of Non-Invasive Collection

The appeal of non-invasive biological sampling is intuitive. Saliva and buccal swabs offer a compelling alternative to venipuncture, particularly in settings where patient compliance, accessibility, or cost are primary concerns. Collection requires no trained phlebotomist, no needles, no specialized clinical infrastructure, and can in principle be collected by every individual at home. These attributes have made non-invasive oral sampling a cornerstone of consumer genetics (e.g., ancestry and direct-to-consumer genomic testing), epidemiological studies requiring large-scale enrollment, pediatric and geriatric populations where venipuncture is challenging, and point-of-care or remote diagnostics in low-resource settings.[23] From a molecular standpoint, saliva and buccal swabs are legitimate sources of human DNA, making them a reasonable source for genomics.[24] The human oral cavity harbors over 700 bacterial species, and DNA from these organisms is co-extracted alongside human nucleic acids in any saliva or buccal swab-based workflow.[25]

In NGS library preparation from oral samples, microbial DNA is indiscriminately amplified and sequenced alongside human DNA. Clinical WGS studies report a median of approximately 13% non-human mapped reads from buccal swab and saliva samples, with over 80% of samples exceeding 5% and a significant proportion exceeding 20%.[26] These non-human reads carry no diagnostic value yet represent a direct and unavoidable sequencing cost. In a fixed output sequencing run, every microbial read is a human read lost — wasted flow cell capacity that cannot be recovered computationally. Hence, to achieve whole blood human sequencing depth from an oral sample, laboratories must sequence appreciably more, driving up reagent costs, run times, and bioinformatic overhead. Whole blood (and plasma extracted from it) delivers a substantially higher proportion of on-target human reads for every sequencing dollar spent, making it not just the analytically superior matrix, but the more economical one at scale.[27] In some study types such as, germline variant detection,[28] pharmacogenetic profiling[29] or biobank/population genomics,[30] saliva or buccal swab samples have been found to have reduced or inconsistent performance compared with blood-based testing.

Oral Matrices Fall Short

The limitations of oral matrices become significant and clinically important when the diagnostic goal extends beyond simple molecular analyses. Several instances where oral matrices (saliva, buccal swabs, etc.) fail to reach the quality obtained from whole blood samples are shown in **Table 2** and can be described as follows:

- Biological complexity and contamination. Saliva is a mixture of glandular secretions, epithelial cells, food debris, and a high, variable microbial load. Buccal swabs yield inconsistent cell numbers depending on technique and collector. Both introduce variability that is difficult to normalize and incompatible with the reproducibility standards required for clinical diagnostics.
- Rapid analyte degradation. Saliva's high protease and amylase content aggressively degrades proteins and nucleic acids post-collection. Without immediate stabilization, proteomic and transcriptomic signals deteriorate within minutes, thereby making oral matrices particularly poorly suited to protein biomarker detection.
- Low and inconsistent biomarker concentrations. Most clinically relevant markers (e.g. troponin, PSA, CA-125, HbA1c, cytokines, circulating tumor DNA) are either undetectable or unreliably quantifiable in saliva. They are present in blood at concentrations orders of magnitude higher, with validated reference ranges and established clinical thresholds.
- Lack of systemic representation. Most critically, saliva reflects local oral biology, which may not comprehensively mimic a systemic disease. Blood integrates molecular signals from every organ, carrying shed proteins, metabolites, immune mediators, and nucleic acids from diseased tissues throughout the body. A pancreatic tumor, a neuroinflammatory process, or early cardiac injury leaves a detectable footprint in circulation long before it appears in the oral cavity (if at all).

Table 2. Matrix Comparison: Saliva, Buccal Swab, and Blood.

Parameter	Saliva	Buccal Swab	Blood (Plasma/Serum)
Collection	Non-invasive, self-administered	Non-invasive, self-administered	Requires trained phlebotomist
Patient Compliance	High	High	Moderate
Sample Consistency	Poor — high biological variability	Moderate — technique-dependent	High — standardized protocols
Analyte Stability	Poor — rapid protease degradation	Poor to moderate	High — well-characterized
Protein Biomarkers	Very limited / unreliable	Very limited/unreliable	Excellent
Circulating DNA/cfDNA	Not suitable	Not suitable	Gold standard
Genomic DNA	Adequate	Adequate	Suitable
Systemic Disease Representation	Poor — reflects local oral biology	Poor — reflects local oral biology	Excellent — whole-body integration
Clinical Validation	Limited	Limited	Extensive
Omics Suitability	Genomics only	Genomics only	Genomics, proteomics, metabolomics, transcriptomics

Why Blood Remains the Gold Standard

Plasma and serum provide systemic biomarker coverage, well-characterized pre-analytical workflows, and validated assay performance across thousands of clinical applications. Deep plasma proteomics has demonstrated the ability to reveal disease-associated signatures across oncology, neurodegeneration, cardiovascular disease, and metabolic disorders. Liquid biopsy approaches detecting circulating tumor DNA in plasma have reached clinical deployment with sensitivity and specificity that no saliva-based equivalent currently approaches. Compared to blood, while non-invasive oral sampling finds some specific uses, those preferences are usually governed by ease of accessibility where analytical precision is not warranted. However, for most critical applications, from protein biomarkers to circulating nucleic acids, from metabolomic profiling to detection of systemic disease, saliva and buccal swabs are a compromise with measurable diagnostic cost.[31] As the world of precision medicine aims for confident, earlier detection and multi-omics integration, matrix selection must be driven by what the biology demands, which is whole blood.

Implications for Decentralized Clinical Trials

Clinical research is increasingly moving toward decentralized and hybrid trial models, where participants can enroll and contribute data remotely. Digital health technologies, wearable sensors and telemedicine platforms are enabling new approaches to clinical research. However, biospecimen collection remains one of the most difficult elements to decentralize. Participants need to visit clinical sites solely for phlebotomy, creating friction in otherwise remote study designs. This discrepancy between digital trial infrastructure and physical sample collection highlights the need for new blood collection technologies.

Remote blood sampling approaches have therefore become a key area of innovation. These technologies allow participants to collect small volumes of blood at home and stabilize analytes for downstream analysis. Such approaches can enable geographically distributed sampling while reducing dependence on clinical facilities.

Emerging Technologies for Remote Blood Collection

Several emerging platforms aim to enable self-administered blood collection outside clinical environments. These systems typically involve:

- Finger-stick capillary blood sampling
- Fixed-volume microsampling
- Integrated analyte stabilization
- Ambient temperature shipping

Studies have demonstrated the feasibility of remote blood collection for transcriptomic analysis, with participants successfully collecting and stabilizing capillary blood samples at home.[32] Similarly, remote blood sampling devices have been developed for telehealth applications and population monitoring programs.[33]

Covaris truCOLLECT Solution

Covaris' truCOLLECT Solution is designed specifically to support remote collection of blood for molecular analysis workflows. The device enables:

- Fixed-volume (50 µL) capillary whole blood collection
- Active immobilization and desiccation to stabilize biomolecules at ambient temperature
- Transport without cold-chain logistics
- Ready-to-deploy laboratory extraction reagents and workflow powered by Covaris' Adaptive Focused Acoustics® (AFA®) Technology

These unique and differentiated features of truCOLLECT can offer stabilized whole blood samples to be processed for multiple molecular analytes, ensuring high quality and integrity for each analyte, ultimately enabling genomics analysis from remotely collected samples. By standardizing sample volume and stabilization conditions, truCOLLECT aims to reduce variability and enable distributed biological sampling at scale across every laboratory focused on working with one form of Omics to genomics studies.

Toward Scalable Biospecimen Infrastructure

As biological research moves toward population scale datasets, the infrastructure used to collect biospecimens must evolve accordingly. An ideal system for blood collection should:

- Enable decentralized sampling
- Maintain stability of multiple molecular analytes
- Minimize dependence on specialized personnel
- Integrate with automated extraction and analysis workflows

In the constantly evolving landscape of genomics studies, whole blood collection can be viewed as a form of biological data infrastructure. Advances in sequencing technologies have already transformed molecular measurement, while the last decade and half witnessed some remarkable growth in Proteomics; similar innovation in sample collection may be necessary to fully realize the potential of genomics research. The truCOLLECT Solution ensures high quality analytes across genomics is delivered from home to the analytical laboratories seamlessly, and with unprecedented ease.

Conclusion

Phlebotomy has served as the foundation of blood collection in medicine and research for more than a century. However, the expanding scale of genomics research and decentralized clinical trials is revealing limitations in this traditional model. Workforce shortages, geographic barriers, and logistical complexity collectively restrict the scalability of venous blood collection. truCOLLECT remote blood collection solution lies in the forefront of the emerging remote blood collection technologies and can offer new solutions by enabling decentralized sampling compatible with modern molecular analyses.

References

1. D'Adamo, G. L.; James T Widdop; Giles, E. M. The future is now? Clinical and translational aspects of "Omics" technologies. Immunology and cell Biology 2021, 99 (2), 168–176. Kim, Y. J.; Takahashi, K. Emerging technologies of single-cell multi-omics. Haematologica 2025, 110 (6), 1269–1277.
2. Ikwelle, T. A.; Ihim, A. C.; Ozuruoke, D. F. N.; Obi, P. C.; Obi, C. U.; Onuora, I. J.; Chimezie, A. J.; Romanus, O. O. Multi-Omics Integration in Personalized Medicine: Advancing Laboratory Diagnostics and Precision Therapeutics in the Era of Individualized Healthcare Journal of Drug Delivery & Therapeutics 2025, 15 (5), 132-134.
3. Dongare, D. B.; Nishad, S. S.; Mastoli, S. Y.; Saraf, S. A.; Srivastava, N.; Dey, A. High-throughput sequencing: a breakthrough in molecular diagnosis for precision medicine. Functional and Integrative Genomics 2025 Jan 22;25(1):22. doi: 10.1007/s10142-025-01529-w.
4. Challen, B.; Cramer, R. Advances in ionisation techniques for mass spectrometry-based omics research.Proteomics: Proteomics and Systemics Biology 2022, 22 (15-16). Muehlbauer, L. K.; Jen, A.; Zhu, Y.; He, Y.; Shishkova, E.; Overmyer, K. A.; Coon, J. J. Rapid Multi-Omics Sample Preparation for Mass Spectrometry. Analytical Chemistry 2023, 95 (2), 659–667.
5. Flynn, E.; Almonte-Loya, A.; Fragiadakis, G. K. Single-Cell Multiomics. Annual Review of Biomedical Data Science 2023, 6, 313–337.
6. Jo, H.-Y.; Kim, S. C.; Ahn, D.-h.; Lee, S.; Chang, S.-H.; Jung, S.-Y.; Kim, Y.-J.; Kim, E.; Kim, J.-E.; Kim, Y.-S.; et al. Establishment of the large-scale longitudinal multi-omics dataset in COVID-19 patients: data profile and biospecimen. BMB Reports 2022, 55 (9), 465–471. Marshall, J. L.; Peshkin, B. N.; Yoshino, T.; Vowinckel, J.; Danielsen, H. E.; Melino, G.; Tsamardinos, I.; Haudenschild, C.; Kerr, D. J.; Sampaio, C.; et al. The Essentials of Multiomics. The Oncologist 2022, 27 (4), 272–284.
7. Ponzi, E.; Thoresen, M.; Nøst, T. H.; Møllersen, K. Integrative, multi-omics, analysis of blood samples improves model predictions: applications to cancer. BMC Bioinformatics 2021, 22, 395.
8. Hasin, Y.; Seldin, M.; Lusis, A. Multi-omics approaches to disease. Genome Biology 2017, 18, 83. Doran, S.; Arif, M.; Lam, S.; Bayraktar, A.; Turkez, H.; Uhlen, M.; Boren, J.; Mardinoglu, A. Multi-omics approaches for revealing the complexity of cardiovascular disease. Briefings in Bioinformatics 2021, 22 (5), 1–19.
9. Wang, X.; Li, Z.; Chang, Y.; Li, S.; Wu, W.; Chang, F.; Chang, Y.; Zhu, D.; Gong, D.; Zhang, M.; et al. Early assessment of therapeutic efficacy in lymphoma patients via a blood-based multi-omics response monitoring test. BMC Cancer 2025, 25, 1078.
10. Yang, G.; Mishra, M.; Perera, M. A. Multi-Omics Studies in Historically Excluded Populations: The Road to Equity. Clinical Pharmacology and Therapeutics 2023, 113 (3), 541–556. Gillette, M. A.; Jimenez, C. R.; Carr, S. A. Clinical Proteomics: A Promise Becoming Reality. Molecular & Cellular Proteomics 2024, 23 (2), 100688 February 2024.
11. Lin, B.; Ma, Y.; Wu, S. Multi-Omics and Artificial Intelligence-Guided Data Integration in Chronic Liver Disease: Prospects and Challenges for Precision Medicine. OMICS: A Journal of Integrative Biology 2022, 26 (8), 7. Guarnaccia, M.; Cognata, V. L.; Gentile, G.; Morello, G.; Cavallaro, S. Multi-Omics Integration for Advancing Glioma Precision Medicine. Annals of Clinical and Translational Neurology 2026, 13 (1), 4-13. Xiao, Y.; Bi, M.; Guo, H.; Li, M. Multi-omics approaches for biomarker discovery in early ovarian cancer diagnosis. eBioMedicine 2022, 79.
12. Michalska-Falkowska, A.; Niklinski, J.; Juhl, H.; Sulewska, A.; Kisluk, J.; Charkiewicz, R.; Ciborowski, M.; Ramlau, R.; Gryczka, R.; Piwkowski, C.; et al. Applied Molecular-Based Quality Control of Biobanked Samples for Multi-Omics Approach. Cancers 2023 Jul 24;15(14):3742. doi: 10.3390/cancers15143742.
13. Zhuang, Y.-J.; Mangwiro, Y.; Wake, M.; Saffery, R.; Greaves, R. F. Multi-omics analysis from archival neonatal dried blood spots: limitations and opportunities. Clin Chem Lab Med 2022, 60 (9), 1318–1341.
14. Lee, J.-E.; Kim, Y.-Y. Impact of Preanalytical Variations in Blood-Derived Biospecimens on Omics Studies: Toward Precision Biobanking? OMICS: A Journal of Integrative Biology 2017, 21 (9), 499–508.
15. Vogeser, M.; Bendt, A. K. From research cohorts to the patient – a role for "omics" in diagnostics and laboratory medicine? Clin Chem Lab Med 2023, 61 (6), 7. Anwar, M. A.; Keshteli, A. H.; Yang, H.; Wang, W.; Li, X.; Messier, H. M.; Cullis, P. R.; Borchers, C. H.; Fraser, R.; Wishart, D. S. Blood-Based Multiomics-Guided Detection of a Precancerous Pancreatic Tumor. OMICS: A Journal of Integrative Biology 2024, 28 (4), 11.
16. Yurkovich, J. T.; Hood, L. Blood is a window into health and disease. Clinical Chemistry 2019, 65 (10), 3. Müller, S.; Kröger, C.; Schultze, J. L.; Aschenbrenner, A. C. Whole blood stimulation as a tool for studying the human immune system. European Journal of Immunology 2024 Feb;54(2):e2350519. doi: 10.1002/eji.202350519.
17. Kohl, M.; Megger, D. A.; Trippler, M.; Meckel, H.; Ahrens, M.; Bracht, T.; Weber, F.; Hoffmann, A.-C.; Baba, H. A.; Sitek, B.; et al. A practical data processing workflow for multi-OMICS projects. Biochimica et Biophysica Acta (BBA) - Proteins and Proteomics 2014, 1844 (1), 11.
18. Phlebotomists: Occupational Outlook Handbook. Statistics, U. S. B. o. L., Ed.; 2024.

19. Novis DA, Nelson S, Blond BJ, Guidi AJ, Talbert ML, Mix P, Perrotta PL. Laboratory Staff Turnover: A College of American Pathologists Q-Probes Study of 23 Clinical Laboratories. Arch Pathol Lab Med. 2020 Mar;144(3):350-355. doi: 10.5858/arpa.2019-0140-CP. Epub 2019 Jul 17. PMID: 31313958.
20. New Survey Reveals Burnout in Clinical Labs Impacts Patient Care, Staff Safety; Optimism that Automation, AI Will Help Tackle Challenges. https://www.siemens-healthineers.com/en-us/press-room/press-releases/harris-poll-clinical-labs, 2024.
21. Horstman, C.; Shah, A. The state of rural primary care in the United States. 2025. The Commonwealth Fund. Issue Briefs November 17, 2025
22. Yu, Y.; Mai, Y.; Zheng, Y.; Shi, L. Assessing and mitigating batch effects in large-scale omics studies. Genome Biology 2024, 25 (254).
23. Vandenbergh, D. J.; Anthony, K.; Whitfield, K. E. Optimizing DNA yield from buccal swabs in the elderly: Attempts to promote buccal cell growth in culture. American Journal of Human Biology 2003, 15 (5). Milne, E.;van Bockxmeer, F. M. v.; Robertson, L.; Brisbane, J. M.; Ashton, L. J.; Scott, R. J.; Armstrong, B. K. Buccal DNA Collection: Comparison of Buccal Swabs with FTA Cards. Cancer Epidemiology, Biomarkers, & Prevention 2006, 15 (4).
24. Hansen, T. v. O.; Simonsen, M. K.; Nielsen, F. C.; Hundrup, Y. A. Collection of Blood, Saliva, and Buccal Cell Samples in a Pilot Study on the Danish Nurse Cohort: Comparison of the Response Rate and Quality of Genomic DNA. Cancer Epidemiology, Biomarkers, & Prevention 2007, 16 (10).
25. Belstrøm, D.; Sembler-Møller, M. L.; Grande, M. A.; Kirkby, N.; Cotton, S. L.; Paster, B. J.; Holmstrup, P. Microbial profile comparisons of saliva, pooled andsite-specific subgingival samples in periodontitis patients. PLOS One 2017, 12 (8). DOI: https://doi. org/10.1371/journal.pone.0182992.
26. Kumar A, Skrahina V, Atta J, et al. Microbial contamination and composition of oral samples subjected to clinical whole genome sequencing. Front Genet. 2023;14:1081424. doi:10.3389/fgene.2023.1081424; Weyrich L.S., Farrer A.G., Eisenhofer R., et al. Laboratory contamination over time during low-biomass sample analysis. Molecular Ecology Resources 2019;19:15. doi:10.1111/1755-0998.13011; Eisenhofer R., Minich J.J., Marotz C., et al. Contamination in Low Microbial Biomass Microbiome Studies: Issues and Recommendations. Trends in Microbiology 2019;27(2):13.
27. Vlaminck, I. D.; Valantine, H. A.; Snyder, T. M.; Strehl, C.; Cohen, G.; Luikart, H.; Neff, N. F.; Okamoto, J.; Bernstein, D.; Weisshaar, D.; et al. Circulating cell-free DNA enables noninvasive diagnosis of heart transplant rejection. Science Translational Medicine 2014, 6 (241). Salter, S. J.; Cox, M. J.; Turek, E. M.; Calus, S. T.; Cookson, W. O.; Moffatt, M. F.; Turner, P.; Parkhill, J.; Loman, N. J.; Walker, A. W. Reagent and laboratory contamination can critically impact sequence-based microbiome analyses. BMC Biology 2014, 12 (87), 12.
28. Trost B, Walker S, Haider SA, et al. Impact of DNA source on genetic variant detection from human whole-genome sequencing data. J Med Genet. 2019;56(12):809-817. doi:10.1136/jmedgenet-2019-106281.
29. Xu H, Jiang H, Dolan ME. Genotyping Performance between Saliva and Blood-Derived Genomic DNAs on the DMET Array: A Comparison. PLoS One. 2012;7(3):e33968. doi:10.1371/journal.pone.0033968. PMID: 22479465.
30. Yao RA, Akinrinade O, Chaix M, Mital S. Quality of whole genome sequencing from blood versus saliva derived DNA in cardiac patients. BMC Med Genomics. 2020;13(1):11. doi:10.1186/s12920-020-0664-7. PMID: 31996225.
31. Hou, Y.-C. C.; Yu, H.-C.; Martin, R.; Caskey, C. T. Precision medicine integrating whole-genome sequencing, comprehensive metabolomics, and advanced imaging. Proceedings of teh National Academy of Sciences 2020, 117 (6), 10. DOI: https://doi. org/10.1073/pnas.1909378117. Seymour, C. W.; Gomez, H.; Chang, C.-C. H.; Clermont, G.; Kellum, J. A.; Kennedy, J.; Yende, S.; Angus, D. C. Precision medicine for all? Challenges and opportunities for a precision medicine approach to critical illness. Critical Care 2017, 21. DOI: https://doi.org/10.1186/s13054-017-1836-5.
32. Brown, L. G.; Wei, X.; Milton, L. A.; Alizai, M. Y.; MacDonald, J. W.; Bammler, T. K.; Zeng, Y.; Robertson, I.; Adams, K. N.; Toh, Y.-C.; et al. From Home to Transcriptome: Comparing the Transcriptomic Profile of Induced Immune Response via Lipopolysaccharide Stimulation in homeRNA and Venous Blood. Analytical Chemistry 2026, 98 (4), 12. Husseini, A. A.; Derakhshandeh, M.; Tatlisu, N. B. Comprehensive review of Transcriptomics (RNAs) Workflows from Blood Specimens. Separation & Purification Reviews 2022, 51 (1), 21. Chen, Q.; Guo, X.; Wang, H.; Sun, S.; Jiang, H.; Zhang, P.; Shang, E.; Zhang, R.; Cao, Z.; Niu, Q.; et al. Plasma-Free Blood as a Potential Alternative to Whole Blood for Transcriptomic Analysis. Phenomics 2024, 4, 16.
33. Koulman, A.; Rennie, K. L.; Parkington, D.; Tyrrell, C. S.; Catt, M.; Gkrania-Klotsas, E.; Wareham, N. J. The development, validation and application of remote blood sample collection in telelhealth programmes. Journal of Telemedicine and Telecare 2024, 30 (4), 8. Hegde, S.; Eid, N. S. Telehealth and Remote Patient Monitoring After the COVID Pandemic. PEDIATRIC ALLERGY, IMMUNOLOGY, AND PULMONOLOGY 2021, 34 (4), 2. Ding, X.; Clifton, D.; Ji, N.; Lovell, N. H.; Bonato, P.; Chen, W.; Yu, X.; Xue, Z.; Xiang, T.; Long, X.; et al. Wearable Sensing and Telehealth Technology with Potential Applications in the Coronavirus Pandemic. IEEE REVIEWS IN BIOMEDICAL ENGINEERING 2021, 14, 23.
34. Daviso, E.; Abarzua, L.; Giese, H.; Vasantgadkar, S.; Endress, G.; Thomann, U.; Fox, S.; Sabarre, L.; Schlosser, H.; Geier, T. truCOLLECT Solution: High-Fidelity Genomic DNA Extraction from Decentralized, Dry-stabilized Whole Blood for Biomarker Identification. In Covaris Application Note, Covaris: http://www.covaris.com, 2026.

Covaris® a PerkinElmer Company

Tel: +1 781-932-3959 info@covaris.com

Learn more about our truCOLLECT Solution

US: +1 781.932.3959
customerservice@covaris.com

EU: +44 (0)845 872 0100
emeacustomerservice@covaris.com

Applications
applicationsupport@covaris.com

Service and Support
techsupport@covaris.com