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EDITORIAL

From concept to clinic: emerging paradigms and novel insights into liquid biopsy

Wenjie Guo[1,*], Yang Liu[2,*], Haiying Dong[3], Xiang Li[4], Xu Guo[1], Haitao Guo[1], Kaixiang Zhou[1], Jinliang Xing[1]

[1]State Key Laboratory of Holistic Integrative Management of Gastrointestinal Cancers and Department of Physiology and Pathophysiology, Fourth Military Medical University, Xi'an 710032, China; [2]State Key Laboratory of Holistic Integrative Management of Gastrointestinal Cancers and Department of Clinical Diagnosis, Tangdu Hospital, Fourth Military Medical University, Xi'an 710038, China; [3]Institute of Medical Research, Northwestern Polytechnical University, Xi'an 710129, China; [4]Department of Pharmacy, The Fourth Affiliated Hospital of China Medical University, Shenyang 110032, China

Liquid biopsy has emerged as a transformative, minimally invasive strategy for disease detection and longitudinal monitoring through the analysis of circulating molecular components, including cell-free DNA (cfDNA), cell-free RNA, extracellular vesicles, and circulating proteins in bodily fluids. Its central objective is to enable a continuum of precision clinical interventions, from early detection and diagnosis to therapeutic guidance and disease surveillance, thereby improving patient outcomes (**Figure 1**). Holistic integrative medicine is a patient-centered, systems-level framework that integrates prevention, screening, diagnosis, treatment, and rehabilitation into whole-process disease management. Advances in high-throughput sequencing and digital polymerase chain reaction (PCR) have markedly improved the detection of tumor-derived alterations in plasma, urine, and saliva. These technologies have enhanced both sensitivity and specificity in identifying genetic and epigenetic changes. In oncology, circulating tumor DNA (ctDNA) captures the spatial and temporal heterogeneity of tumors and provides a dynamic window into disease evolution, with resolution often surpassing that of single-site tissue biopsies[1]. Importantly, the scope of liquid biopsy is rapidly expanding beyond cancer to include prenatal testing, infectious diseases, neurodegenerative disorders, and immune-mediated conditions.

Despite these advances, key challenges persist. The low abundance of tumor-derived cfDNA, particularly in early-stage disease, as well as the variability introduced during sample collection, processing, and storage, continue to limit clinical robustness[2]. However, ongoing innovations in single-molecule sequencing, fragmentomics, and bioinformatics are accelerating the clinical translation of liquid biopsy technologies[3]. This Editorial highlights emerging paradigms in liquid biopsy research, spanning technological and economic considerations, expanding clinical applications, and integrative insights from immunogenomics and microbiome studies. Notably, we discuss pioneering work on cell-free mitochondrial DNA (cf-mtDNA) fragmentomics, illustrating how exploration beyond nuclear genomes may open new avenues for early cancer detection and precision medicine.

Foundation and clinical motivations

Liquid biopsy is based on the premise that circulating molecular biomarkers in disease states systematically diverge from those in healthy individuals, and therefore can reflect perturbations in genetic, epigenetic, and regulatory networks. These alterations are both disease-specific and stage-dependent, and they mirror the dynamic molecular evolution that accompanies disease initiation, progression, and therapeutic response. Seminal observations of fetal DNA in maternal circulation provided early evidence that pathological tissues, including tumors and virally infected or degenerating cells, release nucleic acids into the bloodstream, thereby enabling indirect molecular interrogation of otherwise inaccessible sites[4]. These circulating signals encompass diverse molecular phenotypes, including somatic mutations, chromosomal rearrangements, aberrant methylation patterns, and viral integration events.

The clinical utility of this paradigm is exemplified by non-invasive prenatal testing (NIPT), in which analysis of cell-free fetal DNA has transformed prenatal screening for chromosomal aneuploidies and substantially decreased the need for invasive diagnostic procedures. Similarly, in infectious diseases such as hepatitis B, hepatitis C, and AIDS, circulating viral nucleic acids are routinely used to guide antiviral therapy,

*These authors contributed equally to this work.
Correspondence to: Kaixiang Zhou and Jinliang Xing
E-mail: kaixiang_zhou@fmmu.edu.cn and xingjl@fmmu.edu.cn
ORCID ID: https://orcid.org/0009-0001-9612-3456 and https://orcid.org/0000-0002-7010-1822
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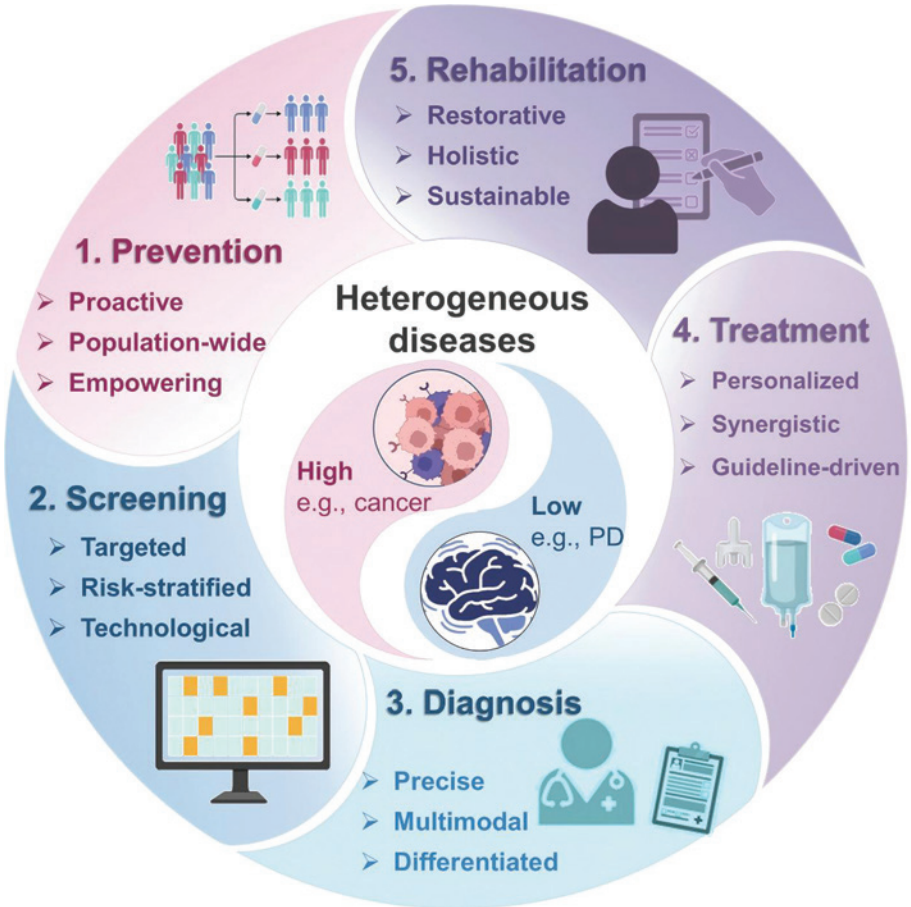


Figure 1 The whole-process management model for clinical diseases within the holistic integrative medicine framework. **Outer circle:** A five-stage continuum, including prevention, screening, diagnosis, treatment, and rehabilitation, addresses varying levels of disease heterogeneity. **Inner circle:** High-heterogeneity diseases (e.g., cancer) and relatively low-heterogeneity diseases (e.g., PD) demonstrate how this cyclical strategy can be tailored to diverse and complex clinical scenarios. Each stage integrates personalized strategies, evidence-based guidelines, and advanced technologies to facilitate comprehensive, patient-centered care. PD, Parkinson's disease.

assess treatment efficacy, and monitor adherence[5]. Together, these circulating biomarkers constitute a molecular "fingerprint" providing near-real-time insight into ongoing pathological processes, thus underscoring the central role of liquid biopsy in precision medicine.

In oncology, early detection is a primary clinical goal. The ability to detect trace amounts of ctDNA in asymptomatic or early-stage patients has promise for diagnosing malignancies in curable stages. Beyond diagnosis, longitudinal ctDNA profiling enables real-time monitoring of clonal dynamics, early identification of resistance mechanisms, and informed selection of subsequent therapeutic strategies[6]. Importantly, liquid biopsy enables repeated sampling with minimal patient burden, thereby overcoming the limitations of serial tissue biopsies, which are often invasive and impractical. Emerging fragmentomic approaches that exploit tumor-specific differences in cfDNA fragment size and genomic breakpoints further enhance analytical sensitivity and biological resolution[6].

A central ongoing debate concerns biomarker strategy, i.e., whether to prioritize highly specific, disease-defined markers or broader, pan-disease signatures. Canonical examples such as EGFR mutations in non-small cell lung cancer or BCR-ABL fusions in chronic myeloid leukemia provide precise diagnostic and therapeutic value[7]. In contrast, pan-cancer approaches, such as assays targeting shared methylation or fragmentomic patterns, might be better suited for population-scale screening when the tissue of origin is unknown[8]. To successfully integrate these complementary strategies, careful optimization of sensitivity, specificity, and cost-effectiveness will be necessary, thus underscoring the need for rational assay design aligned with clinical intent.

Heterogeneity in disease applications

Metastatic malignancies, including advanced lung, pancreatic, and breast cancers, comprise diverse subclonal populations with distinct genetic and epigenetic landscapes[9]. Single-site tissue biopsies, which capture only a limited spatial snapshot, can therefore overlook clinically relevant subclones bearing resistance-associated alterations. In contrast, longitudinal profiling of ctDNA enables systemic and dynamic assessment of tumor evolution, and can reveal adaptive responses to therapeutic pressure in near real time. This comprehensive view supports more informed treatment stratification, facilitates early detection of emerging resistance, and provides a rationale for timely therapeutic switching or combination strategies aimed at delaying disease progression.

Importantly, the utility of liquid biopsy is not confined to conditions with extensive genomic heterogeneity. In disorders with more constrained genetic variability, circulating biomarkers can still yield clinically actionable insights. For example, pre-eclampsia arises from complex maternal-fetal interactions rather than extensive clonal diversification. Nevertheless, placental-derived cfDNA can exhibit early, disease-associated epigenetic signatures or fragmentomic patterns that signal elevated risk, thus enabling earlier clinical intervention[10]. Similarly, neurodegenerative diseases such as Alzheimer's disease and Parkinson's disease lack the overt clonal dynamics typical of cancer, thus complicating biomarker discovery. However, emerging evidence suggests that subtle yet reproducible cfDNA alterations may precede overt clinical manifestations, thereby offering a potential avenue for presymptomatic detection and disease monitoring. These findings exemplify how the adaptability of liquid biopsy supports its transformative potential in neurodegenerative research, by providing novel biomarkers that might reshape diagnostic pathways.

ctDNA *vs.* total cfDNA: complementary strategies

Liquid biopsy research in oncology has traditionally centered on ctDNA, with a goal of identifying tumor-specific genetic or epigenetic alterations. This targeted paradigm enables precise detection of clinically actionable mutations, such as EGFR variants in non-small cell lung cancer or ALK/ROS1 rearrangements, thereby directly informing personalized therapeutic decisions[11]. However, in early-stage disease, ctDNA often constitutes only a minute fraction of total circulating cfDNA and therefore poses substantial analytical challenges. To address this limitation, ultrasensitive platforms, including digital droplet PCR and error-corrected targeted next-generation sequencing, have been developed to enhance detection sensitivity and specificity.

In parallel, an emerging paradigm emphasizes analysis of total cfDNA rather than a focus on only tumor-derived fragments. This holistic approach interrogates global features such as fragmentation profiles, DNA methylation landscapes, and chromatin accessibility patterns across the entire cfDNA pool. By capturing system-wide molecular perturbations, total cfDNA analysis can reveal early disease-associated signals, infer tissue of origin, and reflect broader pathological states, including inflammation or multi-organ involvement. Although this strategy might sacrifice mutation-level specificity, it offers a more integrative view of disease biology. As analytical technologies continue to mature, the key challenge is no longer choosing between ctDNA-focused and global cfDNA approaches, but developing integrative frameworks that harness their complementary strengths to deliver more sensitive, informative, and clinically actionable liquid biopsy assays.

Immunogenomic insights and microbiome profiling

Beyond tumor- or tissue-derived biomarkers, the immunogenomic information provided by circulating cfDNA provides an additional dimension for understanding disease progression and therapeutic response. Profiling circulating T-cell receptor and B-cell receptor repertoires provides insights into adaptive immune dynamics in cancer, infection, and immune-mediated disorders[12]. Clonal expansion or contraction of specific lymphocyte populations detectable in plasma has been associated with responses to immunotherapies, including immune checkpoint blockade[13]. Beyond serving as descriptive immune snapshots, repertoire features can be mechanistically informative. Antigen-driven activation may lead to clonal expansion and diminished diversity, whereas effective therapy can alter these dynamics over time. In contrast, loss of dominant clones may indicate immune escape. In agreement with this possibility, recent data have suggested that circulating T-cell receptor signals can track tumor immune dynamics during checkpoint blockade and complement tumor-derived cfDNA in monitoring treatment response[14]. Integrating immune repertoire features with tumor-derived cfDNA may therefore enable more precise monitoring of immune activation, exhaustion, and treatment responsiveness, and consequently inform personalized immunotherapeutic strategies.

In parallel, circulating microbial cfDNA has emerged as a complementary and increasingly informative analyte. Disruptions in microbial homeostasis across the gut, oral cavity, or other niches can allow bacterial or viral DNA fragments to enter the bloodstream, thereby reflecting systemic dysbiosis or occult infection. Accumulating evidence suggests that specific microbial signatures influence tumor biology and modulate responses to immunotherapy by shaping the tumor microenvironment and host immune tone[15]. Consequently,

longitudinal profiling of microbial cfDNA may aid in predicting therapeutic efficacy, detecting treatment-related complications, and contextualizing inflammatory states.

Novel frontiers: cf-mtDNA fragmentomics in early tumor screening

Because of the high copy number of mitochondrial genomes per cell, cf-mtDNA is often detectable at higher baseline levels than nuclear cfDNA, even in early-stage malignancies. Beyond copy number changes, recent studies have demonstrated that cf-mtDNA fragmentomic features, including fragment length distributions, 5′ end motifs, and sequence preferences, can robustly distinguish tumor-associated signals from healthy backgrounds[16].

Multicenter studies have shown that cf-mtDNA fragmentomics enables sensitive detection of early-stage colorectal cancer and advanced adenomas, and frequently outperforms conventional DNA methylation-based assays[17]. Early neoplastic lesions are consistently characterized by features such as relatively short fragment sizes, altered 5′ end base composition, and diminished motif diversity. Importantly, integrating cf-mtDNA fragmentomics with established nuclear cfDNA assays further enhances diagnostic performance, thereby underscoring their complementarity. Similar aberrant cf-mtDNA fragmentation patterns have been observed across multiple solid tumors, including liver, breast, and lung cancers[16]. Large-scale multi-cancer analyses have indicated that cf-mtDNA fragmentomic signatures not only can discriminate states of cancer *vs.* health but also can inform tissue-of-origin prediction. In hepatocellular carcinoma, whose early diagnosis remains challenging, cf-mtDNA fragment-level alterations appear early in tumorigenesis and show promise for early detection and disease monitoring[18].

Despite its promising performance in early neoplasia detection, cf-mtDNA fragmentomics faces challenges in specificity. Circulating mtDNA can increase in non-malignant conditions such as tissue injury and sterile inflammation, in which it serves as a damage-associated molecular pattern and correlates with inflammatory mediators. Future studies should benchmark cf-mtDNA signatures against common inflammatory and autoimmune conditions, and prioritize large-scale prospective cohorts to assess false-positive risk and refine decision thresholds.

Collectively, these findings position cf-mtDNA fragmentomics as a robust and scalable strategy for pan-cancer early screening. Capture-based sequencing approaches targeting mtDNA offer high coverage at relatively low cost, and support simultaneous assessment of copy number, mutations, and fragmentation patterns. Although mechanistic understanding and large prospective validation remain ongoing challenges, cf-mtDNA fragmentomics is a compelling frontier poised to reshape noninvasive cancer detection paradigms.

From theory and mechanism to translation

Liquid biopsy research exemplifies the iterative progression from conceptual discovery to mechanistic understanding and ultimately clinical translation. The initial detection of cfDNA in maternal plasma established the foundational concept that pathological tissues can release nucleic acids into circulation[4]. Subsequent mechanistic studies elucidated active and passive DNA release pathways, including exosomal secretion, apoptosis, and necrosis, thus revealing that fragmentation patterns and molecular endpoints contain biologically meaningful information[19]. Investigations on virus-associated malignancies, such as Epstein-Barr virus–driven nasopharyngeal carcinoma and hepatitis B virus–associated hepatocellular carcinoma, have further clarified how infectious agents and host immunity shape circulating DNA profiles. More recently, immunogenomic analyses of circulating T- and B-cell receptor repertoires have expanded this framework, by capturing adaptive immune dynamics in response to disease and therapy[20]. Parallel advances in multi-cancer early detection assays based on ctDNA methylation underscore the feasibility of translating mechanistic insights into scalable clinical applications[8].

The current central challenge is integrating these diverse insights, spanning ctDNA, global cfDNA features, microbial cfDNA, and cf-mtDNA, into a unified, patient-centric diagnostic paradigm (**Figure 2**). Achieving this goal will require standardized pre-analytical workflows, analytically validated assays, comprehensive reference datasets, and computational frameworks capable of synthesizing multi-omic signals into clinically actionable outputs. As illustrated by recent advances in cf-mtDNA fragmentomics, bridging molecular innovation with clinical utility is particularly critical for early cancer detection. Successful translation will depend on rigorous prospective validation, regulatory alignment, and cost-effective implementation, with implications extending beyond oncology to immunological, autoimmune, and transplant-related diseases.

Future perspectives

As liquid biopsy advances toward broader clinical implementation, the extreme scarcity of tumor-derived DNA within the total cfDNA pool, particularly in early-stage disease, remains a central challenge. This “needle-in-a-haystack” problem is compounded by background cfDNA originating from normal tissue turnover and leukocyte lysis, which can obscure low-frequency tumor signals. Continued progress will therefore require improvements in analytical sensitivity and

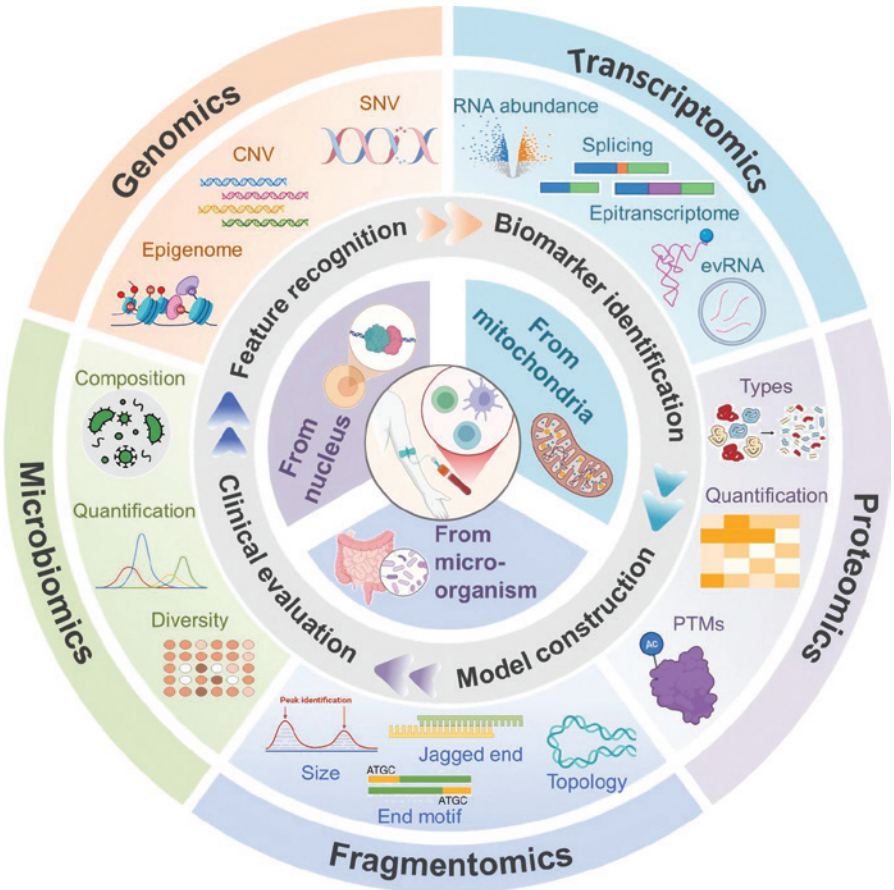


Figure 2 A comprehensive multi-omics liquid biopsy pipeline integrating nuclear, mitochondrial, and microbial sources. This schematic presents a cyclical, four-stage workflow **(middle circle)**, including feature recognition, biomarker discovery, model construction, and clinical evaluation, on the basis of liquid biopsy specimens derived from nuclear, mitochondrial, and microbial origins **(inner circle)**. The outer circle highlights 5 major omics layers (genomics, transcriptomics, proteomics, fragmentomics, and microbiomics) that provide a systems-level understanding of disease processes. Each layer highlights distinct molecular features, such as SNVs, RNA abundance, protein quantification, fragment size, and microbial composition. These integrated molecular profiles collectively support the identification of biomarkers and the development of predictive models for subsequent clinical application. SNVs, single nucleotide variants; CNV, copy number variation; evRNA, extracellular vesicle RNA; PTMs, post-translational modifications.

signal-to-noise discrimination. Technologies such as droplet digital PCR and single-molecule sequencing have substantially advanced rare-variant detection by minimizing amplification bias and background interference. Nevertheless, technical gains alone are insufficient. Pre-analytical variability, including blood collection, processing time, storage conditions, and centrifugation protocols, remains a major source of inconsistency. Therefore, standardized workflows and rigorously enforced quality controls are needed. For example, the choice of blood collection tube (e.g., standard EDTA *vs.* cfDNA-stabilizing tubes) and delays in plasma processing can increase leukocyte lysis-derived background DNA, thereby altering fragment-size distributions and hindering tumor signal detection[21]. Similarly, differences in centrifugation protocols (e.g., single-spin *vs.* double-spin) affect residual debris and genomic DNA contamination, thus highlighting the need for standardized workflows. Community efforts are increasingly promoting harmonized practices and quality assurance guidelines for ctDNA testing[22].

Beyond technical considerations, economic feasibility is a critical determinant of large-scale use, particularly for population-level screening in asymptomatic individuals. Although sequencing costs continue to decline, comprehensive multi-analyte assays remain resource-intensive. Future solutions will require a balance between analytical depth and cost efficiency, supported by automation, optimized sequencing strategies with reduced read depth requirements, and artificial intelligence–driven bioinformatics pipelines for rapid interpretation and data integration. For multi-cancer early detection tests, population implementation introduces

additional considerations beyond analytical performance. Key issues include the effects of false positives, diagnostic burden, cost-effectiveness, resource use, and integration into clinical pathways. Evidence frameworks emphasize the need for well-designed prospective studies that capture detection metrics, clinical harms, diagnostic trajectories, and health outcomes, to enable informed integration into screening programs.

In the future, the field is expected to combine multiple liquid biopsy dimensions, including ctDNA mutations, global cfDNA fragmentomics, immunogenomic signals, microbial cfDNA, and cf-mtDNA, into unified, clinically actionable frameworks. Such integration promises a more holistic and dynamic view of disease biology from a single blood draw. As validation in large prospective cohorts progresses, and regulatory and economic barriers are addressed, liquid biopsy is likely to become a cornerstone of precision medicine, by enabling earlier detection, real-time monitoring, and increasingly proactive disease management in oncology and beyond.

Conflict of interest statement

No potential conflicts of interest are disclosed.

Author contributions

Conceived and designed the paper: Jinliang Xing and Kaixiang Zhou.
Collected and synthesized the literature: Wenjie Guo and Yang Liu.
Contributed data or analysis tools: Haiying Dong and Xiang Li.
Wrote the paper: Wenjie Guo and Yang Liu.
Performed the analysis: Xu Guo and Haitao Guo.
Reviewed and revised the paper: Jinliang Xing and Kaixiang Zhou.

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References

1. Welsh JA, Goberdhan DCI, O'Driscoll L, Buzas EI, Blenkiron C, Bussolati B, et al. Minimal information for studies of extracellular vesicles (MISEV2023): from basic to advanced approaches. J Extracell Vesicles. 2024; 13: e12404.
2. Fusco N, Jantus-Lewintre E, Serrano MJ, Gandara D, Malapelle U, Rolfo C. Role of the International Society of Liquid Biopsy (ISLB) in establishing quality control frameworks for clinical integration. Crit Rev Oncol Hematol. 2025; 209: 104619.
3. Tang WHW, Yimer H, Tummala M, Shao S, Chung G, Clement J, et al. Performance of a targeted methylation-based multi-cancer early detection test by race and ethnicity. Prev Med. 2022; 167: 107384.
4. Lo YM, Corbetta N, Chamberlain PF, Rai V, Sargent IL, Redman CW, et al. Presence of fetal DNA in maternal plasma and serum. Lancet. 1997; 350: 485-7.
5. Huang Z, LaCourse SM, Kay AW, Stern J, Escudero JN, Youngquist BM, et al. CRISPR detection of circulating cell-free mycobacterium tuberculosis DNA in adults and children, including children with HIV: a molecular diagnostics study. Lancet Microbe. 2022; 3: e482-92.
6. Magbanua MJM, Brown Swigart L, Ahmed Z, Sayaman RW, Renner D, Kalashnikova E, et al. Clinical significance and biology of circulating tumor DNA in high-risk early-stage HER2-negative breast cancer receiving neoadjuvant chemotherapy. Cancer Cell. 2023; 41: 1091-102.e4.
7. Diehl F, Li M, Dressman D, He Y, Shen D, Szabo S, et al. Detection and quantification of mutations in the plasma of patients with colorectal tumors. Proc Natl Acad Sci U S A. 2005; 102: 16368-73.
8. Jamshidi A, Liu MC, Klein EA, Venn O, Hubbell E, Beausang JF, et al. Evaluation of cell-free DNA approaches for multi-cancer early detection. Cancer Cell. 2022; 40: 1537-49.e12.
9. Liang Y, Zhang H, Song X, Yang Q. Metastatic heterogeneity of breast cancer: molecular mechanism and potential therapeutic targets. Semin Cancer Biol. 2019; 60: 14-27.
10. Wu Y, Shen L, Zhao L, Lin X, Xu M, Tu Z, et al. Noninvasive early prediction of preeclampsia in pregnancy using retinal vascular features. NPJ Digit Med. 2025; 8: 188.
11. Bobin C, Iddir Y, Butterworth C, Masliah-Planchon J, Saint-Charles A, Bellini A, et al. Sequential analysis of cfDNA reveals clonal evolution in patients with neuroblastoma receiving ALK-targeted therapy. Clin Cancer Res. 2024; 30: 3316-28.
12. Zhang Q, Luo J, Wu S, Si H, Gao C, Xu W, et al. Prognostic and predictive impact of circulating tumor DNA in patients with advanced cancers treated with immune checkpoint blockade. Cancer Discov. 2020; 10: 1842-53.
13. Sivapalan L, Murray JC, Canzoniero JV, Landon B, Jackson J, Scott S, et al. Liquid biopsy approaches to capture tumor evolution and clinical outcomes during cancer immunotherapy. J Immunother Cancer. 2023; 11: e005924.
14. Soleimani S, Li X, Wang BX, Pedersen S, Bruce JP, Eagles J, et al. T cell receptor repertoire in cell-free DNA as a proxy for tumor infiltrates in patients treated with pembrolizumab. Cell Rep. 2025; 44: 116190.
15. Newsome RC, Yang Y, Jobin C. The microbiome, gastrointestinal cancer, and immunotherapy. J Gastroenterol Hepatol. 2021; 37: 263-72.
16. Liu Y, Peng F, Wang S, Jiao H, Dang M, Zhou K, et al. Aberrant fragmentomic features of circulating cell-free mitochondrial DNA as novel biomarkers for multi-cancer detection. EMBO Mol Med. 2024; 16: 3169-83.

17. Wang S, Peng F, Dang M, Jiao H, Zhang H, Zhou K, et al. Early detection of colorectal cancer using aberrant circulating cell-free mitochondrial DNA fragmentomics. Gut. 2025; 74: 961-70.
18. Liu Y, Peng F, Wang S, Jiao H, Zhou K, Guo W, et al. Aberrant fragmentomic features of circulating cell-free mitochondrial DNA enable early detection and prognosis prediction of hepatocellular carcinoma. Clin Mol Hepatol. 2024; 31: 196-212.
19. Loy C, Ahmann L, De Vlaminck I, Gu W. Liquid biopsy based on cell-free DNA and RNA. Annu Rev Biomed Eng. 2024; 26: 169-95.
20. Ren Y, Li R, Feng H, Xie J, Gao L, Chu S, et al. Single-cell sequencing reveals effects of chemotherapy on the immune landscape and TCR/BCR clonal expansion in a relapsed ovarian cancer patient. Front Immunol. 2022; 13: 985187.
21. Sorber L, Zwaenepoel K, Jacobs J, De Winne K, Van Casteren K, Augustus E, et al. Specialized blood collection tubes for liquid biopsy: improving the pre-analytical conditions. Mol Diagn Ther. 2020; 24: 113-24.
22. Fusco N, Venetis K, Pepe F, Shetty O, Farinas SC, Heeke S, et al. International society of liquid biopsy (ISLB) perspective on minimal requirements for ctDNA testing in solid tumors. J Liq Biopsy. 2025; 8: 100301.

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