

GUARDANT

Exceptional technology. Extraordinary potential.

Introducing Guardant Infinity – the first and only commercial platform that combines epigenomic and genomic profiling via liquid biopsy to offer a truly multidimensional view of cancer.¹

Precision oncology has advanced our ability to match the right patient to the right treatment at the right time – but we are just getting started.

A NEW DIMENSION OF INSIGHTS: AN EPIGENOMIC EXAMPLE



Genomic profiling offers details into alterations of the genomic DNA...



...while **epigenomic profiling** can help detect alterations to the *expression* of the genome. Non and a star

The epigenome is a dynamic landscape providing breakthrough insights to offer a more complete view of cancer²⁻⁵

A growing body of evidence demonstrates that **epigenetic changes have a tremendous impact on cancer development and progression**.^{6,7}

Epigenomic insights, specifically methylation sequencing, can advance multiple precision oncology applications.



*compared to genomic-only detection

In a clinical setting, Guardant products powered by the Infinity platform can have:



Even faster turnaround times post- sample receipt¹³



Enhanced sensitivity, with 100x to 1000x more signals available to analyze¹



New insights across the continuum of care, from MRD to progression

Guardant Infinity will soon power our Treatment Selection & Monitoring portfolio of products.

The next era of precision oncology is here. See what's next, now, with Guardant Infinity.



References: 1 GuardantINFINTY[™], Specifications Sheet: Guardant Health, Inc. Redwood City, CA. January 4, 2023 2 Watts, GS., Futscher, BW., Holtan, N. et al. DNA methylation changes in ovarian cancer are cumulative with disease progression and identify tumor stage. BMC Med Genomics 1, 47 (2008). https://doi.org/10.1186/1755-8794-1-47 3 Muthamilaekan, Sangeetha, Abirami Raghavendran, and Ashok Palaniappan. "Stage-differentiated ensemble modeling of DNA methylation landscapes uncovers salient biomarkers and prognostic signatures in colorectal cancer progression." Plos one 17.2 (2022). e0249151 4 (Aligic J., Fleischer, T., Dejux, E. et al. Quantitative DNA methylation and secolation to clinico-pathological factors in breast tumors, BMC Cancer 13, 456 (2013). https://doi.org/10.1186/1471-2407-13-456 5 Oue, Naohide, et al. 'Accumulation of DNA methylation analyses reveal stage dependent DNA methylation and sacolation to clinico-pathological factors in breast tumors, BMC Cancer 13, 456 (2013). https://doi.org/10.1186/1471-2407-13-456 5 Oue, Naohide, et al. 'Accumulation of DNA methylation is associated with tumor stage in gastric cancer.' Cancer. Interdisciplinary International Journal of the American Cancer Society 106 6 (2006): 1250-1259. 6 Yoshimi A. Lin KT, Wiseman DH, et al. Coordinated alterations in RNA splicing and epigenetic regulation drive leukaemogenesis. *Nature*. 2019;774777/10101039/34t356-019-0168-0 7 Tekeria VH, Phpinkas CP, Pennycuick, & et al. Deciphering the genomic, exploration drive leukaemogenesis. *Nature*. 2019;774777/10101039/34t356-019-018-0 7 Tekeria VH, Phpinkas CP, Pennycuick, A, et al. Deciphering the genomic, exploration transcriptomic landscapes of pre-invasive lung cancer lesions. *Nat Med*. 2019;25(3):175-25, doi:10.1039/34t356-019-018-0 8 Greenwald WY. He Y. Chen S, et al. Accurate epigenomic as of circulating tumor fraction in large-scale clinical data. Poster presented at American Association for Cancer Research Annual Meeting. April 8-13, 2022. Philadelphia, PA Access

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