# Precision medicine: Peer-reviewed journal articles featuring Fortrea oncologists

The revolution in the biology of cancer combined with remarkable developments in diagnostics creates a unique platform for establishing precision medicine. At Fortrea, we believe that the future hope of oncology lies in precision oncology. Our scientific and operational experts are at the forefront of this transformation—bridging the gap between molecular insights and clinical execution.

Fortrea supports our sponsors with a team of 50+ oncologists who employ a collaborative approach, resulting in contributions to peer-reviewed journal articles.

We are proud to contribute to the field of precision oncology through impactful research. Our recent publications highlight the value of comprehensive genomic profiling over single-gene testing, reveal age- and sex-based molecular differences in NSCLC, and identify rare but actionable gene fusions—advancing personalized cancer care.

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| 2024 | |
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| **Number** | **Authors, Title, Journal** |
| 2024.1 | Nesline MK, Subbiah V, Previs RA, Strickland KC, Ko H, DePietro P, Biorn MD, Cooper M, Wu N, Conroy JM, Pabla S, Zhang S, Wallen ZD, Sathyan P, Saini KS, Eisenberg M, Caveney B, Severson EA, Ramkissoon SH. **The Impact of Prior Single-Gene Testing on Comprehensive Genomic Profiling Results for Patients with Non-Small Cell Lung Cancer.** *Oncology & Therapy*. March 2024.<br>https://link.springer.com/article/10.1007/s40487-024-00270-x<br><br>**Summary:** Minimally invasive techniques for obtaining biopsy samples are much preferred by patients. However, the quantity of samples thus obtained is limited. Therefore, it is incredibly important to implement a testing strategy that optimizes the use of the valuable biosamples. This study evaluates how prior single-gene testing (SGT) affects the outcomes of subsequent comprehensive genomic profiling (CGP) in non-small cell lung cancer (NSCLC) patients. The research found that patients who underwent SGT first had higher rates of CGP test cancellations, longer turnaround times, and incomplete molecular profiling due to tissue insufficiency. Despite these challenges, 46% of patients with negative SGT results had positive CGP results for recommended biomarkers, highlighting the importance of CGP for thorough molecular profiling. |
| 2024.2 | Wallen ZD, Ko H, Nesline MK, Hastings S, Strickland KC, Previs RA, Zhang S, Pabla S, Conroy JM, Jackson J, Saini KS, Jensen T, Eisenberg M, Caveney B, Sathyan P, Severson EA, Ramkissoon SH. **Real-world comprehensive genomic and immune profiling reveals distinct age- and sex-based genomic and immune landscapes in tumors of patients with non-small cell lung cancer.** *Frontiers in Immunology*. June 2024.<br>https://www.frontiersin.org/journals/immunology/articles/10.3389/fimmu.2024.1413956/full<br><br>**Summary:** This study analyzes the genomic and immune profiles of NSCLC tumors in a large cohort of patients, revealing significant differences based on age and sex. Younger patients (<50 years) exhibited distinct genomic alterations and reduced immune system activation compared to older patients. The study also found that male patients had more pronounced differences in immune activation, emphasizing the need for personalized treatment strategies based on age and sex. |
| 2024.3 | Strickland KC, Nesline MK, Previs RA, Ko H, Wallen ZD, Pabla S, Conroy JM, Sausen M, Saini KS, Cantini L, Jensen T, Caveney B, Eisenberg M, Severson EA, Ramkissoon SH. **Single Gene Testing and Comprehensive Genomic Profiling in Non-Small Cell Lung Cancer: A Case Series of Divergent Results from a Large Reference Laboratory.** *Frontiers in Oncology*. October 2024.<br>https://www.frontiersin.org/journals/oncology/articles/10.3389/fonc.2024.1445668/full<br><br>**Summary:** This case series highlights the limitations of single-gene testing (SGT) compared to comprehensive genomic profiling (CGP) in identifying actionable genetic alterations in NSCLC. The study presents four cases where CGP identified clinically relevant alterations that SGT missed, demonstrating the superiority of CGP in providing a complete genetic profile for informed treatment decisions. |

## Full list of published journals continued:

| 2023 | |
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| **Number** | **Authors, Title, Journal** |
| 2023.1 | Severson EA, Achyut BR, Nesline MK, Pabla S, Previs RA, Kannan G, Chenn A, Zhang S, Klein R, Conroy JM, Sausen M, Sathyan P, Saini KS, Ghosh A, Jensen T, Reddy P, Ramkissoon SH. **RNA sequencing identifies novel NRG1-fusions in solid tumors that lack co-occurring oncogenic drivers.** *The Journal of Molecular Diagnostics*. May 2023. https://doi.org/10.1016/j.jmoldx.2023.03.011<br><br>**Summary:** This research identifies novel NRG1 gene fusions in various solid tumors using RNA sequencing. The study found that these fusions are rare but therapeutically relevant, occurring in multiple tumor types without other co-occurring oncogenic drivers. The findings underscore the importance of RNA sequencing in detecting these fusions, which are crucial for targeted therapies. |

See a full list of Fortrea oncology publications starting in 2020.

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