

# INCOMPLETE KNOWLEDGE HAS CONSEQUENCES

Detecting pathogenic gene fusions in cancer is critical for patients<sup>1-5</sup>

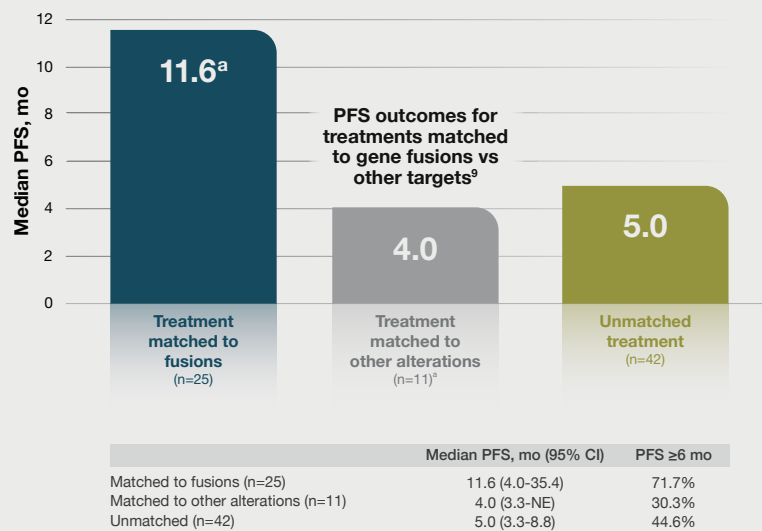
Cancer care is evolving from thinking about cancer according to site of origin to thinking about cancer according to tumor genomics, for a more tailored approach to care<sup>5,6</sup>

- Genomic alterations are becoming increasingly actionable and can include point mutations and pathogenic gene fusions<sup>6-11</sup>
- Targeting the genomic alterations of a patient's cancer may potentially lead to improved outcomes<sup>5-8,12</sup>



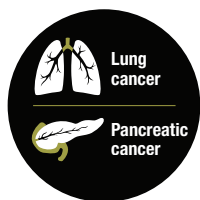
Pathogenic gene fusions are a contributing factor in 1 in 6 cancers and can impact how tumors respond to treatment<sup>1-5,9</sup>

- Fusions occur across many tumor types and are an independent prognostic factor for poor outcomes in lung cancer<sup>1,10-13</sup>
- In patients with pathogenic gene fusions, FDA-approved fusion-targeted treatments demonstrated improved PFS<sup>9</sup>

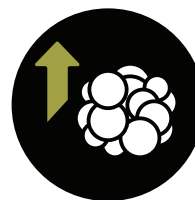


<sup>a</sup>Of the 79 study patients with identified pathogenic gene fusions, 12 received treatment matched to other alterations, of whom 1 had an unclear match and was excluded from pairwise comparison analysis.<sup>9</sup>

A pathogenic gene fusion receiving increasing attention is *NRG1*, due to poor clinical outcomes and resistance to standard therapies<sup>11-16</sup>



*NRG1* fusions occur across many tumor types but are enriched in invasive mucinous lung adenocarcinoma (up to 31%) and *KRAS* wild-type pancreatic cancer (up to 3%).<sup>11,12,15,17-19</sup>



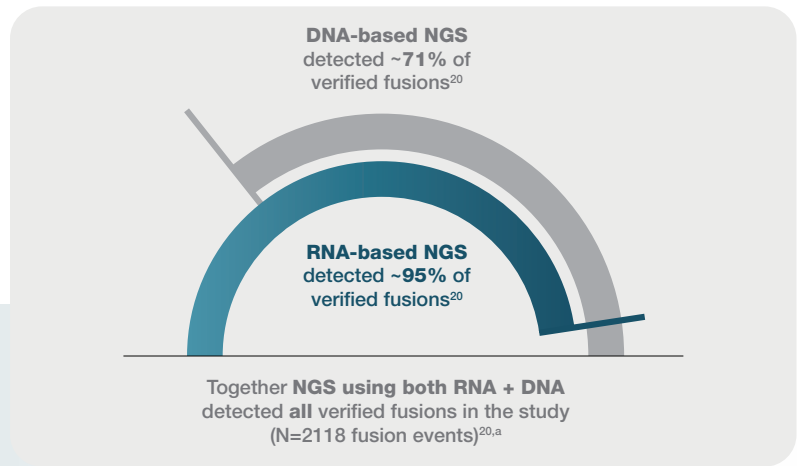
*NRG1*+ tumors have aggressive histological features associated with increased tumor growth, invasiveness, recurrence, resistance to therapy, metastasis, and worse prognosis in lung cancer.<sup>10-15</sup>



# Are you optimizing the detection of pathogenic gene fusions such as *NRG1*?

Comprehensive testing with RNA-based NGS, which includes DNA and RNA sequencing, is recommended to capture what DNA-based NGS alone can miss<sup>3,14,16</sup>

DNA-based sequencing can lead to false-negative and false-positive results in a variety of cases, particularly in the detection of gene fusions<sup>2-4</sup>

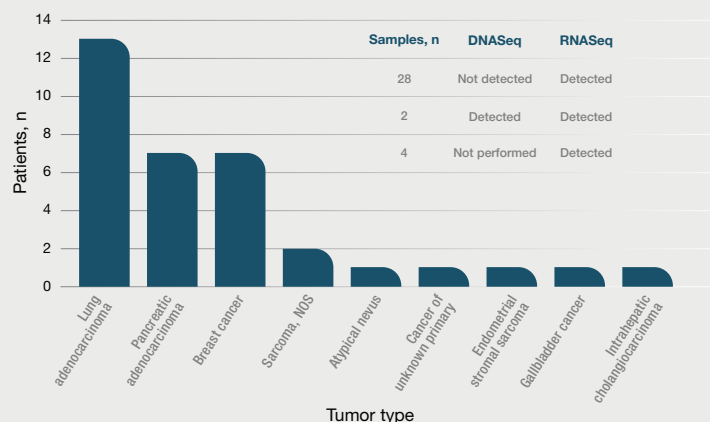


<sup>a</sup>Based on NGS testing of tissue samples.<sup>20</sup>

RNA-based NGS testing is a comprehensive way to detect genomic alterations, including pathogenic gene fusions such as *NRG1*<sup>2-4</sup>

- Characteristics of *NRG1* can help it elude detection by conventional testing methods, including DNA-based NGS<sup>11,13,16</sup>
- Of 34 samples from 30 patients with *NRG1*+ tumors who had both DNA- and RNA-based NGS, 28 were identified by RNA-based NGS but were undetected by DNA-based NGS<sup>16</sup>

## Detection of *NRG1* Fusions Across Tumor Types (MSKCC Experience)



Results from a retrospective study by the Memorial Sloan Kettering Cancer Center.<sup>16</sup>



Are you using RNA-based NGS to comprehensively screen your patients? Learn more at [FindTheFusions.com](https://www.findthefusions.com)

MSKCC, Memorial Sloan Kettering Cancer Center; NOS, not otherwise specified.

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