INCOMPLETE KNOWLEDGE HAS CONSEQUENCES

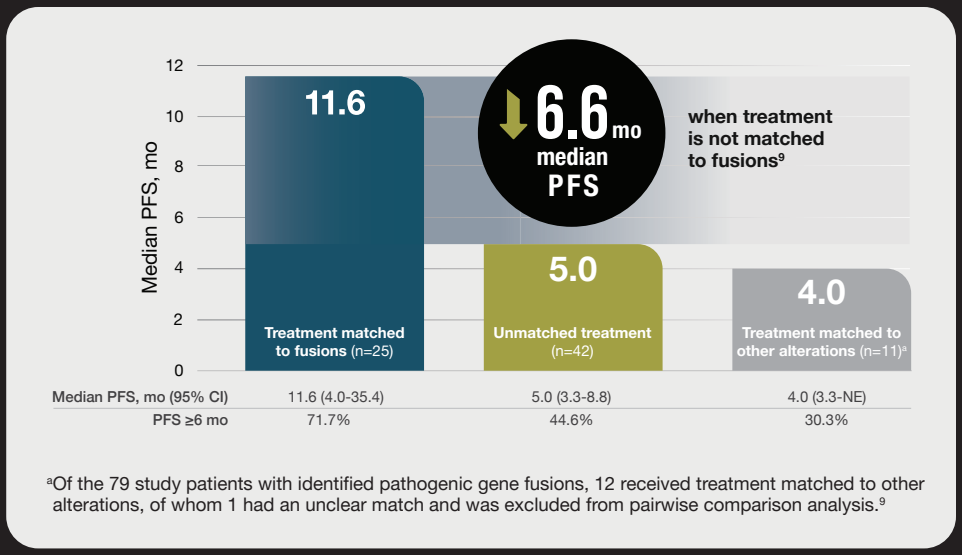
Detecting pathogenic gene fusions in cancer is critical for patients[1-5]

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[5,6]

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

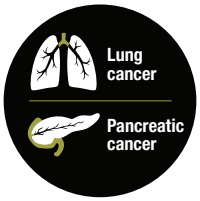
Pathogenic gene fusions are a contributing factor in 1 in 6 cancers and can impact how tumors respond to treatment[1-5,9]

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

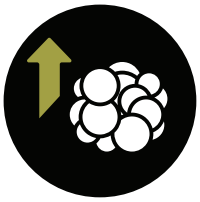


[a]Of the 79 study patients with identified pathogenic gene fusions, 12 received treatment matched to other alterations, of whom 1 had an unclear match and was excluded from pairwise comparison analysis.[9]

A pathogenic gene fusion receiving increasing attention is *NRG1*, due to poor clinical outcomes and resistance to standard therapies[11-16]



NRG1 fusions occur across many tumor types but are enriched in invasive mucinous lung adenocarcinoma (27%-31%) and *KRAS* wild-type pancreatic cancer (up to 6%).[11,12,15,17]

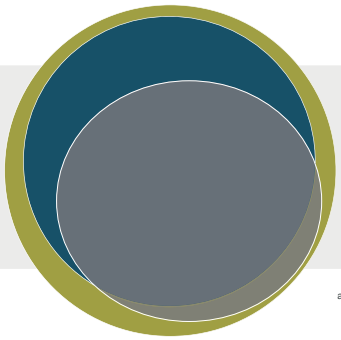


NRG1+ tumors have aggressive histological features associated with increased tumor growth, invasiveness, recurrence, resistance to therapy, metastasis, and worse prognosis in lung cancer.[10-15]

FISH, fluorescence in situ hybridization; IHC, immunohistochemistry; NE, not estimable; NGS, next-generation sequencing; *NRG1*, neuregulin 1; *NRG1*+, neuregulin 1 fusion positive; PFS, progression-free survival; RT-PCR, reverse transcription-polymerase chain reaction.

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[3,14,16]



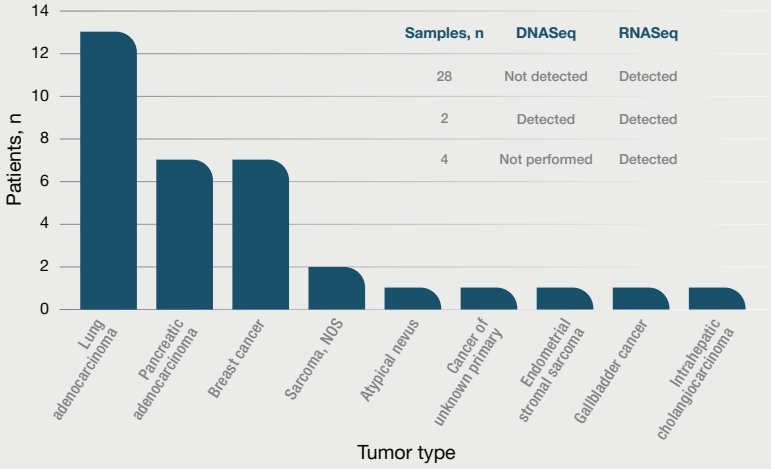
[a]Graphic for illustrative purposes only. Not drawn to scale or reflective of actual results captured by different methodologies.

DNA-based sequencing can lead to false-negative and false-positive results in a variety of cases, particularly in the detection of pathogenic gene fusions[2-4]

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

- Characteristics of *NRG1* can help it elude detection by conventional testing methods, including DNA-based NGS[11,13,16]
- Of 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[16]

Detection of *NRG1* Fusions Across Tumor Types[16]



Results from a retrospective study by the Memorial Sloan Kettering Cancer Center.[16]

Are you using RNA-based NGS to comprehensively screen your patients? Learn more at **FindTheFusions.com**

NOS, not otherwise specified.

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