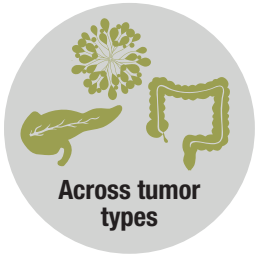
Pathogenic gene fusions are a contributing factor in 1 in 6 cancers[1]

Among 9624 patients who had their tumors genetically tested with RNA-based sequencing, pathogenic gene fusions were found in 16.5% of samples[1]

Why should I be concerned about pathogenic gene fusions?

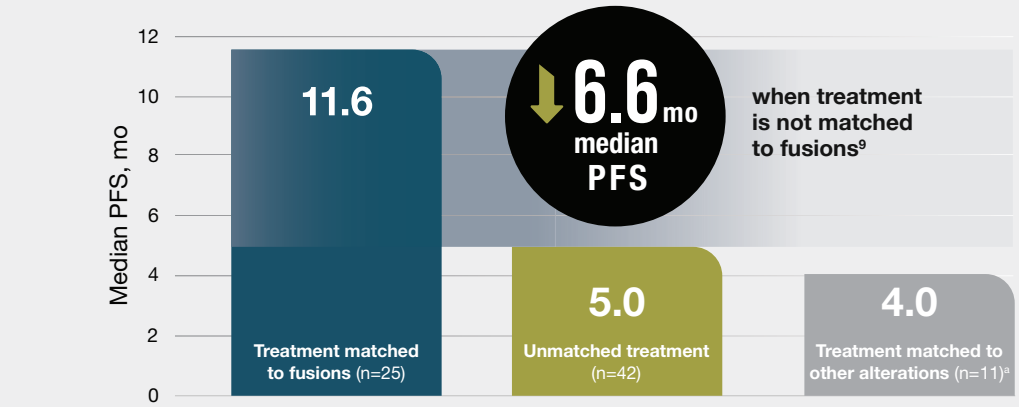
Gene fusions are independent prognostic factors for poor outcomes in lung cancer, regardless of age, sex, tumor tissue type, smoking status, and cancer stage (I-IV)[1-7]



They can occur across tumor types and play a critical role in oncogenesis[1-9]

How can targeting pathogenic gene fusions improve outcomes?

Pathogenic gene fusions may impact clinical management and outcomes, especially if targeted treatment is available.[1-7,9]



	Treatment matched to fusions (n=25)	Unmatched treatment (n=42)	Treatment matched to other alterations (n=11)[a]
Median PFS, mo (95% CI)	11.6 (4.0-35.4)	5.0 (3.3-8.8)	4.0 (3.3-NE)
PFS ≥6 mo	71.7%	44.6%	30.3%

In an analysis of 79 patients with identified gene fusions, poorer outcomes were observed in patients with pathogenic gene fusions who were not matched to an FDA-approved fusion-targeted therapy.[9]

[a]Of the 12 patients who received treatment matched to other alterations, 1 had an unclear match and was excluded from pairwise comparison analysis.[9]

NE, not estimable; PFS, progression-free survival.

NRG1: A dangerous pathogenic gene fusion receiving increased attention

NRG1 fusions have been identified across many tumor types and generally occur in the absence of other driver mutations[2-8]

NRG1+ tumors are reported to be aggressive[2-7]

- 10x more likely to have concurrent intra- and extrathoracic metastases (50% *NRG1+* vs 5% *KRAS+*)[4]
- >2x more likely to have metastases at diagnosis (67% *NRG1+* vs 32% *KRAS+*)[4]
- *NRG1+* tumors are associated with lower OS, DFS, and PFS[4-7]

Studies observed histological features associated with increased tumor growth, invasiveness, recurrence, resistance to therapy, and metastasis in lung cancer.[2-7]

As with other genomic alterations, *NRG1* fusions are frequently associated with:

In a retrospective global registry study of 110 patients, *NRG1+* NSCLC was associated with limited response to available therapies[3]

Activity of systemic therapy in *NRG1+* NSCLC[3,a]	ORR, %	Median PFS, mo (95% CI)
Platinum-doublet chemotherapy (n=15)	**13**	**5.8** (2.2-9.8)
Taxane-based chemotherapy (n=7)	**14**	**4.0** (0.8-5.3)
Combination chemotherapy and immunotherapy (n=9)	**0**	**3.3** (1.4-6.3)
Single-agent immunotherapy (n=5)	**20**	**3.6** (0.9-undefined)
Targeted therapy with kinase inhibitor (n=20)	**25**	**2.8** (1.9-4.3)

[a]Patients either diagnosed with or who developed metastatic disease during the course of their disease.

How can you identify pathogenic gene fusions such as ***NRG1***?
Learn more at **FindTheFusions.com**

DFS, disease-free survival; *NRG1*, neuregulin 1; *NRG1+*, neuregulin 1 fusion positive; NSCLC, non–small cell lung cancer; ORR, overall response rate; OS, overall survival.

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Merus closing in on cancer