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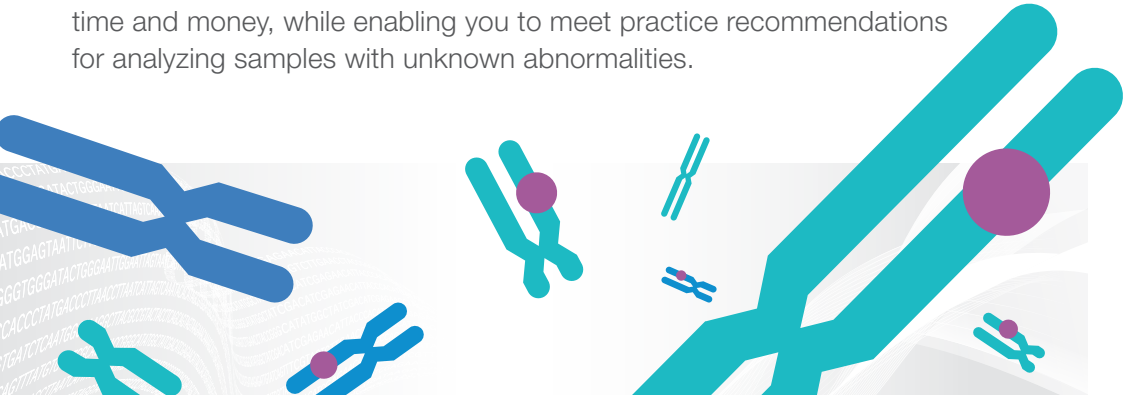
# Discover why cytogeneticists are using NGS in tandem with FISH

Lab directors are inundated with cases, so gaining efficiency is critical. Next-generation sequencing (NGS) can complement FISH, saving you time and money, while enabling you to meet practice recommendations for analyzing samples with unknown abnormalities.



# Efficient. Fast. Extensive.


50% of people with myeloid disorders are not identified by FISH or karyotype.[1]

NGS panels are invaluable for subclassifications and risk stratification.


However, 70% of the patient population could still harbor at least one mutation.[1]

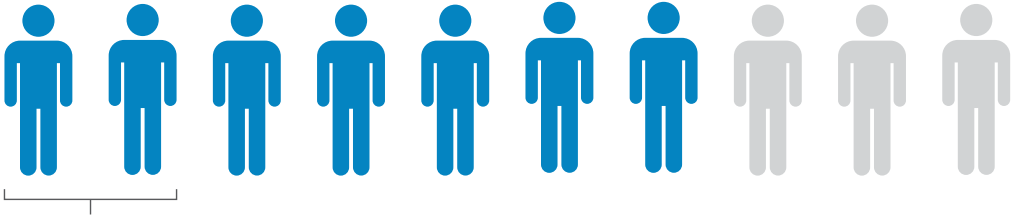

Reduce the risk of and time spent on inconclusive results.

There is a median of 3 mutations per patient.[2]

Detect many mutations simultaneously.

# Applying NGS and FISH to: MDS

**70%** of MDS patients have a detectable mutation...

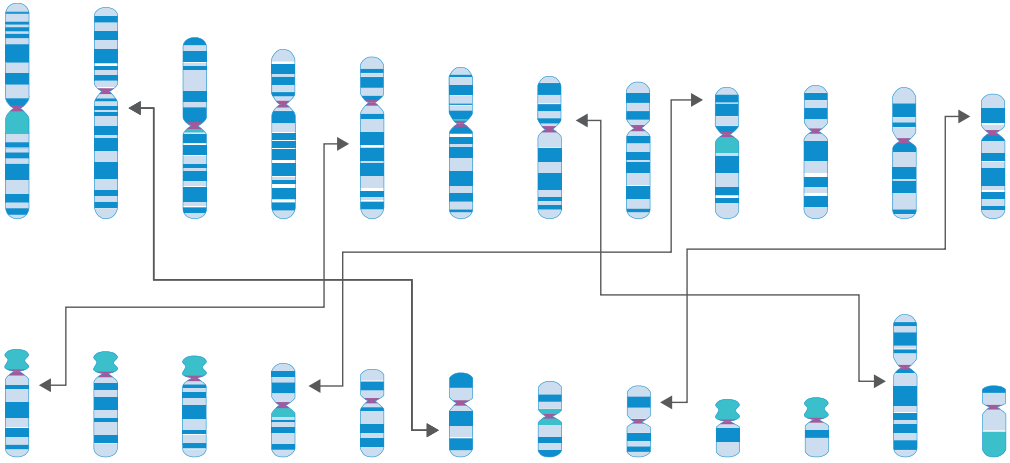


but no 1 specific mutation has been identified in more than 20% of cases.[1]

- Some cases have characteristics that implicate specific disease classifications, or specific cytogenetic abnormalities that can be quickly assessed with FISH.
- In these cases, NGS and FISH allow for a more comprehensive view.

# Applying NGS and FISH to: sarcomas

Close to 100 gene fusions have been found in soft tissue tumors.[3]

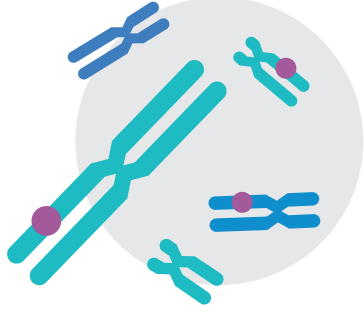


- Using only FISH, you need many distinct probes to cover all fusions.
- With NGS and FISH, one assay provides a broader perspective.

# Advance your breakthroughs using NGS and FISH

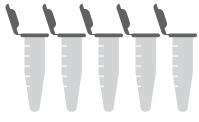
- Rapid identification of fusions with NGS can be followed up with FISH for confirmation or analysis of variations over time.

- Use FISH to test for high-probability targets in tandem with NGS to cover the possibility of negative FISH results.
- Use reflexive testing for more comprehensive analysis.



# Benefits of NGS

Supplementing FISH with NGS can help advance breakthroughs with a more comprehensive solution.



**Cover dozens or hundreds of genes in a single assay.**

Reduce the need for sequential testing.


**Detect many aberrations at the same time.**

Including small variants, gene fusions, and changes in expression.

**Access user-friendly on-instrument and cloud-based data analysis.**

Without the need for bioinformatics expert.

**Low price point for any lab.**

Cover multiple genes in single, low-cost assays.


**Streamline your workflow.**

Experience ease of use from start to finish.

**Transition with ease.**

Save time and frustration. Ramp up quickly.

# What people are saying

"It is not cost effective and [is] also labor intensive to maintain a wide range of individual CLIA-approved diagnostic tests for the many mutations and translocations that occur in the various sarcoma subtypes. Application of next generation sequencing technology to this field opens possibilities for a more efficient and, ultimately, more cost-effective way to detect these genetic abnormalities."[4]

– *Histopathology,* 2014

To find out more about why cytogeneticists are using NGS in tandem with FISH, visit **www.illumina.com/cytogenetics.**

## References


1. Nybakken GE, Bagg A. The genetic basis and expanding role of molecular analysis in the diagnosis, prognosis, and therapeutic design for myelodysplastic syndromes. *J Mol Diagn*. 2014;16(2):145-158.
2. Haferlach T, Nagata Y, Grossmann V, et al. Landscape of genetic lesions in 944 patients with myelodysplastic syndromes. *Leukemia*. 2014;28(2):241-247.
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Pub. No. 1170-2016-018 Current as of 28 July 2016


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