**Gene Silencing: Another Mechanism of Resistance?**


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**ABSTRACT**

Abstract

METHODS

- Next-generation sequencing (NGS) is an important tool in clinical oncology as it enables personalized cancer treatment.
- Not all patients respond to therapies selected based on sequence information, and NGS alone has not revealed the mechanism(s) underlying such resistance.
- RNAseq identifies which genes are expressed and can stratify the expression of these genes.
- Combining NGS with RNAseq allows for a more comprehensive approach to gene mutation-expression pattern recognition.

**RESULTS**

- Demographics overview for cohort (N=1879)
- Number of non-somatic variants
- Percentage of non-somatic variants across hotspot genes

**CONCLUSIONS**

- ~52% (985/1879) of patients have at least 1 rare SNP in the 50-gene panel that could be falsely reported as somatic.
- 66% (931/1417) of paired DNA/RNAseq patients have at least 1 true somatic SNV in the panel.
- 85% (1856/2190) were expressed in RNAseq.
- ~15% of mutations found in NGS are not expressed in the RNA level.
- Combining NGS with RNAseq offers insights into why certain patients may not respond to NGS-driven targeted treatments.