The Benefits of Combined Molecular and Clinical Data For Patients

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ANALYSIS

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Integrated genomic profiling expands clinical options for patients with cancer

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"Extensive molecular profiling combined with clinical data identifies targeted therapies and clinical trials for a large proportion of cancer patients, and paired tumor/normal plus transcriptome sequencing outperforms tumor-only DNA panel testing."

STUDY DESIGN

- Study cohort consisted of 500 patients across the eight most common cancer types, rare malignancies, and tumors of unknown origin.
- Combined molecular genomic testing included tumor full-transcriptome RNA sequencing, tumor-matched normal DNA sequencing, and immunological biomarker analysis
- Structured clinical data abstraction was performed on all patients
- Integrated analytics were performed on both the molecular and clinical data

STUDY SUMMARY

This publication represents the first study to determine clinically relevant insights via comprehensive genomic analysis of a de-identified dataset derived from cancer patients nationwide

- Our results indicate paired tumor/normal DNA-seq and RNA profiling of cancer patients yields high rates of matching to targeted therapies and clinical trials
- Our results illustrate the potential value of integrated clinical and molecular data analysis to practicing physicians.

KEY FINDINGS

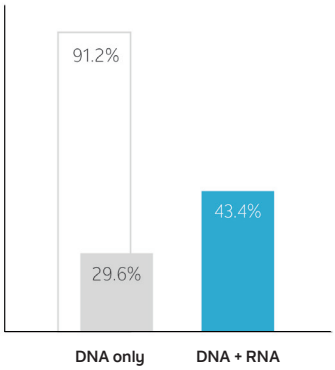
28% reduction in somatic false-positive calls compared to tumor-only analysis

↓28%

- Tempus xT tumor-matched normal DNA sequencing improved somatic versus germline variant detection.
- The use of matched normal reference increased the accuracy of somatic findings by 28%.

Increase in therapy matching for cancer patients

- Tumor DNA-only sequencing resulted in 91.2% of patients matching to therapies with some level of evidence (Level IA, IB, IIC, IID criteria).
- Of these, 29.6% of patients matched to targeted therapies supported by high levels of clinical evidence from consensus guidelines or well-powered studies.
- Combined DNA and RNA sequencing using Tempus xT increased the high level therapy matching rate to 43.4% of patients.

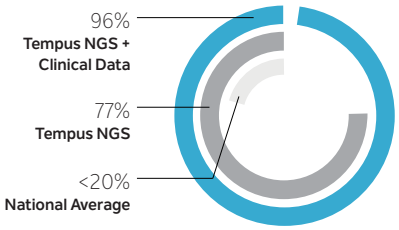


Increase in clinically relevant fusion detection via RNA sequencing

- Out of 32 total oncogenic gene fusions in the study, full transcriptome RNA sequencing discovered 2 that would have been missed using DNA sequencing only.
- Both of the RNA gene fusions could be matched to therapeutic options.

Increase in clinical trial matching

- Less than 20% of patients match to genomically-relevant clinical trials and less than 5% of the matched patients ultimately enroll [1,2].
- In this study, integrated analysis of clinical and molecular data resulted in 96.2% biomarker based clinical trial matching.



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