Detecting Somatic Variants In RNA

We have designed a highly accurate expression-based somatic variant detection pipeline utilizing extensive discovery and filtering methods to overcome the challenges inherent in RNA somatic variant calling. We validated our pipeline using a combination of well-characterized cell lines, commercially available reference standards, and real-world FFPE patient samples.

Validating Somatic Variant Detection In RNA

Analytical Sensitivity

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We are currently developing a neoantigen detection pipeline, which builds upon our existing comprehensive ACE platform and highly accurate DNA and RNA cancer analysis pipelines. Small variants will be classified as neoantigens through analysis of many important features, including MHC presentation prediction, similarity to known antigens, similarity to self, gene expression levels, variant expression level, and variant allele frequency.

Conclusion

We have developed a highly accurate RNA-based somatic variant detection pipeline, which we have validated using previously characterized variants from paired tumor-normal cell lines. We are further using our RNA somatic detection pipeline as a major component in a neoantigen pipeline.