*ion*torrent



Ion AmpliSeq Immune Repertoire Assay Plus, TCR β

Studies aimed at leveraging an individual's own immune system as a potential strategy toward the advancement of precision oncology has been a shared goal of scientists for many years. However, the complexities of tumor–immune interactions warrant a multidimensional approach to facilitate well-designed translational research studies and interpretation of results. Genomic analysis solutions based on next-generation sequencing (NGS) can be powerful tools to help gain significant insights in translational and clinical research.

Harness the power of the immune repertoire with an Ion Torrent longread NGS assay

Analyzing the immune repertoire to capture the diversity of T cell receptor (TCR) rearrangements can help you make significant progress in immuno-oncology research. The Ion AmpliSeq[™] Immune Repertoire Assay Plus, TCR β, provides researchers with a rapid, long-read NGS tool for studying the complexity of cellular immunology. This comprehensive solution enables you to:



Discover immune response biomarkers—accurately measure T cell repertoire diversity and clonal expansion, and identify antigen-specific T cells to accelerate translational research



Optimize the function and manufacture of potentially therapeutic T cells—characterize TCR β chain sequences and optimize the manufacture of genetically engineered T cells



Investigate markers for immune-mediated adverse events (IMAEs)—analyze all three complementarity-determining regions (CDR1, 2, and 3) for allele-specific polymorphisms that may be linked to autoimmune diseases and IMAEs





*ion*torrent



From complex to comprehensible-in just two days

Based on robust, highly referenced Ion AmpliSeq[™] technology, our NGS solution has been carefully designed to significantly improve your turnaround time—go from sample to analysis in as little as 48 hours (Figure 1). The Ion AmpliSeq Immune Repertoire Assay Plus, TCR β, is comprehensive with up to 400 bp read-length amplicons for complete characterization of CDR1, CDR2, and CDR3 (Figure 2). It is highly accurate with mRNA-based sequencing and exerts extremely low PCR-driven primer bias.



Figure 2. Stacked barplot indicating the representation of variable genes among clones identified in a sample. Color segments within each bar indicate the frequency of particular variable gene alleles. IMGT[™] annotation of identified alleles is indicated on the x-axis.



Data security—you have full control of your data (with no service model or additional fees) and full transparency in analysis, and your TCR sequences stay with you



Accuracy—with RNA as a starting point, you can interrogate productive rearrangement of TCR β chain genes and benefit from low substitution error rates achieved on the lon S5 System



Low input requirement—create your Ion AmpliSeq library from a range of input amounts (10 ng–1 µg), depending on your sample constraints and application preferences

Figure 1. Workflow overview. Manual library construction is followed by automated template preparation using the Ion Chef[™] System. Sequencing is performed on the Ion S5 System with data analysis using Ion Reporter Software.

Find out more about our immunosequencing solution at thermofisher.com/immune-repertoire



For Research Use Only. Not for use in diagnostic procedures. © 2017 Thermo Fisher Scientific Inc. All rights reserved. All trademarks are the property of Thermo Fisher Scientific and its subsidiaries unless otherwise specified. IMGT is a trademark of CNRS. COL14495 0817