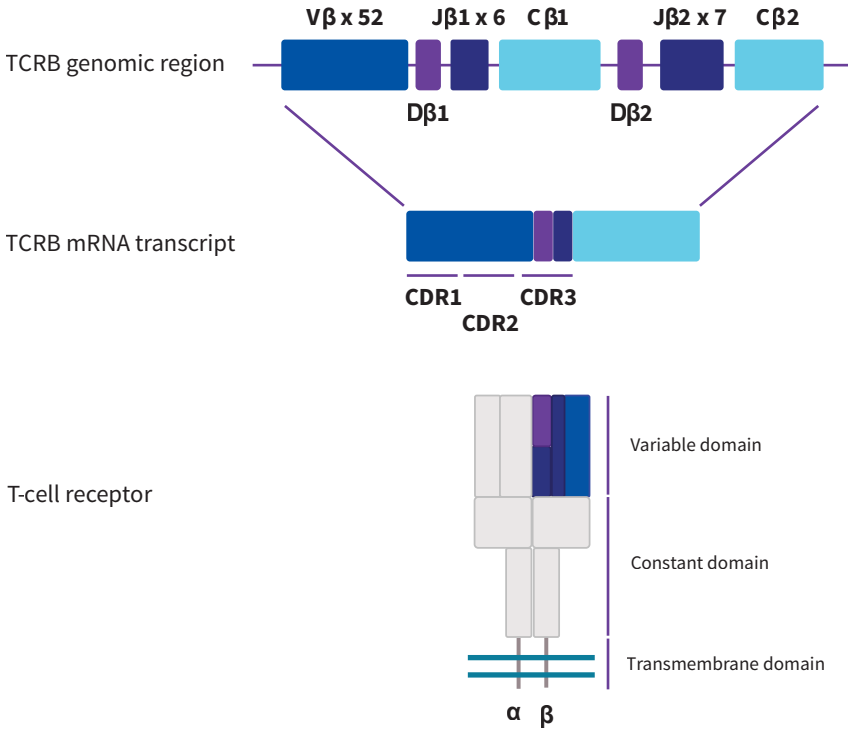
The OmniSeq® TCRβ repertoire assay

Probe the diversity of the T-cell receptor immune repertoire

The OmniSeq TCRβ repertoire assay uses short-read (SR) using RNA or DNA sequencing to analyze the diversity of 46 T-cell receptor beta variable (TRBV) genes, 13 T-cell receptor beta joining (TRBJ) genes and two T-cell receptor beta constant (TRBC) genes from fresh-frozen (FF), formalin-fixed, paraffin-embedded (FFPE) or whole blood samples.

By analyzing the T-cell receptor β (TCRβ) repertoire, oncology researchers can capture the diversity of TCRβ clonotypes in a patient's tumor sample or peripheral blood mononuclear cells. The high-resolution OmniSeq TCRβ repertoire assay enables detection of polymorphisms within the highly variable complementarity-determining region 3 (CDR3), which largely determines the antigen specificity of each T-cell receptor (TCR).

The OmniSeq TCRβ assay provides an SR solution using either Illumina® or Ion Torrent® platforms to facilitate translational research studies for understanding the complexity of cellular immunology as a predictive biomarker of response to immunotherapies. These solutions enable you to detect TCRβ clonotypes to determine CDR3 nucleotide and amino acid sequences, clonotype counts and frequency.



Overview of the TCRB genomic region, structure of TCRB mRNA after V(D)J recombination and the T-cell receptor. The OmniSeq TCRβ-SR DNA and RNA assays sequence 46 TRBV genes, 13 TRBJ genes and 2 TRBC genes.

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OmniSeq TCR β-SR assay

This assay interrogates 46 functional TRBV genes, 13 TRBJ genes and two TRBC genes of CDR3 region of β chain (available for mouse and human).

Characterize T-cell response

Identify low-frequency clones

Sequence the beta chain of the T-cell receptor with genomic DNA or RNA

Quality analysis

OmniSeq reports detailed TCRβ sequencing quality control (QC) metrics along with variable, diversity and joining (VDJ) rearrangements and secondary analysis of repertoire features. Only high-quality and on-target reads are included in the analysis. Clonotype assignment and repertoire features are determined by using The International ImMunoGeneTics Information System® (IMGT) database as reference for variable, diversity and joining genes. Additionally, OmniSeq data analysis provides publication-ready, sample-specific figures detailing repertoire metrics and down-sampling analysis required to estimate repertoire completeness, as well as custom tertiary (multidimensional) analysis of repertoire changes.

OmniSeq TCR β-SR assay	
Starting Materials	FFPE and FF tissue, peripheral blood mononuclear cells (PBMC)/whole blood, sorted T cells, genomic DNA
Input Requirements	DNA = 200 ng RNA = 25 – 200 ng
Assay	Oncomine™ TCR Beta-SR Assay (Thermo Fisher Scientific)
Regions Interrogated	46 Functional TRBV genes, 13 TRBJ genes and 2 TRBC genes of the CDR3 region
Applications	Clonality assessment, identify low frequency and antigen-specific T cells