Product Profile

QIAseq™ Immune Repertoire RNA Library Kits

For preparation of RNAseq libraries for targeted sequencing of alpha, beta, gamma and delta chains

The QIAseq Immune Repertoire RNA Library Kit integrates unique molecular index (UMI) technology into a gene-specific, single primer extension (SPE)-based target enrichment process for the combined detection of all four chains of the expressed human or mouse T-cell receptor (TCR) repertoire (alpha, beta, gamma and delta) including the CDR1, CDR2 and CDR3 regions from cells, tissues or biofluids.

QIAseq Immune Repertoire Kits provide:

- UMIs for accurate quantification and sequencing results
- Comprehensive coverage of alpha, beta, gamma and delta chains from a single library
- Coverage for human or mouse samples
- Online data analysis with GeneGlobe Data Analysis Center
- Multiplexing of up to 384 samples with QIAseq Sample Indices (ordered separately)

Innovative, optimized workflow

By using UMIs, the QIAseq Immune Repertoire RNA Library Kit Panel eliminates PCR duplicates and minimizes artifacts that may arise during the library preparation process or during the sequencing run. This ensures sensitive, accurate and unbiased quantification of the number of TCR transcripts captured and sequenced.

The QIAseq Immune Repertoire RNA Library Kit relies on a highly efficient, TCR-specific cDNA synthesis reaction, ligation of sample index adapters containing UMIs and TCR gene-specific primer enrichment for sensitive TCR clonotype and diversity assessment.

Each kit contains species-specific TCR reverse transcriptase and enrichment panel primers, together with QIAseq reaction cleanup beads and library reagents. The QIAseq Immune Repertoire RNA Library Kit is designed to enrich TCR α, β, γ and σ subunits using 10–1000 ng RNA from human or mouse samples. ▷

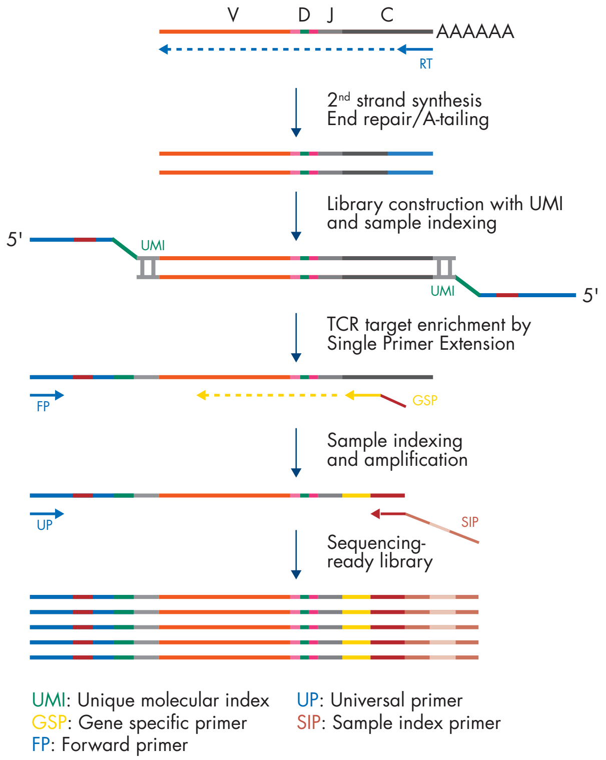

Figure 1. QIAseq Immune Repertoire RNA Library workflow.

Comprehensive view of the T-cell immune repertoire

The heatmaps allow for easy identification of enriched clonotypes across the sample. Figure 2 shows the major clonotype of the Jurkat cell, as well as the diversity of the PBMC background.

The data analysis included with the purchase of the QIAseq Immune Repertoire T-cell receptor panels includes an online portal that seamlessly integrates with Illumina® BaseSpace® and provides primary read mapping, UMI demultiplexing and reports on sequencing performance, TCR chain usage, CDR3 peptide sequence and length distributions, together with rarefaction and V/D/J usage heat maps.

Sensitive to at least 0.01%

RNA from Jurkat cells was spiked into RNA extracted from peripheral blood mononuclear cells (PBMCs; Precision Medicine) at 10%, 1%, 0.1% and 0.01% and used to make an RNAseq library. Table 1 shows the number of raw reads and the demultiplexed unique captures (UMIs) per Jurkat TCR-alpha and TCR-beta clonotype. Even when present at only 0.01%, the Jurkat RNA is readily quantifiably identified. For data analysis, UMIs and Raw Reads are used to ensure high precision around each clonotype sequence identified. ▷

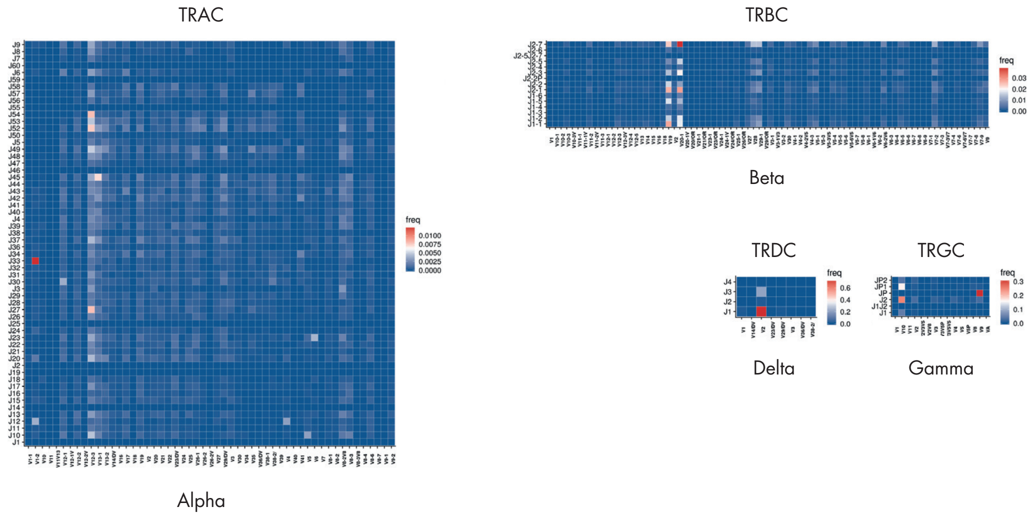

Figure 2. Typical HTML report. V-J Usage Heatmaps for a single sample. Jurkat RNA was spiked into normal human PBMC RNA at a dilution of 1:10,000 (800 Jurkat cells in 8,000,000 PBMCs).

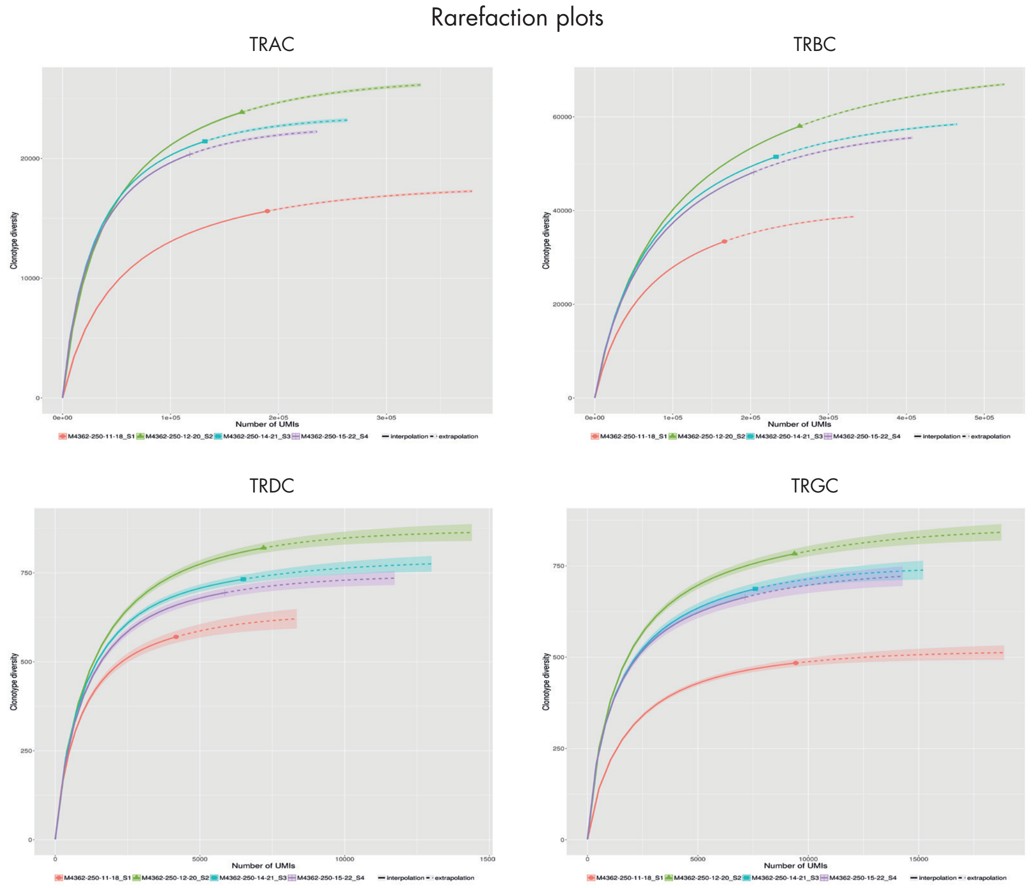

Figure 3. HTML report. Rarefaction plots across all samples sets. Rarefaction plots across all samples sets reveals the TCR richness of each receptor per sample.

Table 1. Quantifiable Jurkat RNA, even at low levels

Chain	% Jurkat cells	Rank	Reads	UMIs
TCR-alpha	10	1	751,749	107,150
	1	1	146,959	20,692
	0.1	1	10,708	1,742
	0.01	10	1,306	217
TCR-beta	10	1	383,594	40,943
	1	1	65,920	7,541
	0.1	2	5,401	620
	0.01	61	457	60

GeneGlobe data analysis

Online analysis through the GeneGlobe Data Analysis Center (**www.qiagen.com/GeneGlobe**) using our UMI-aware pipeline provides key sequencing QC metrics, alignment of V, D and J regions against IMGT reference sequences, and reporting of frequency and identity of each unique clonotype. Downstream analyses including V and J segment usage, CDR3 length distribution and diversity metrics are also provided in a comprehensive report.

Ordering Information

Product	Contents	Cat. no.
QIAseq Immune Repertoire RNA Library Kit Human TCR Panel, 12 or 96 samples	For sequencing the V(D)J region of the alpha, beta, delta and gamma genes, including the CDR3 regions for 12 or 96 human samples	333705 IMHS-001Z-12 IMHS-001Z-96
QIAseq™ Immune Repertoire RNA Library Kit Mouse TCR Panel, 12 or 96 samples	For sequencing the V(D)J region of the alpha, beta, delta and gamma genes, including the CDR3 regions for 12 or 96 mouse samples	333705 IMMM-001Z-12 IMMM-001Z-96
QIAseq 12-Index I (48)	Box containing oligos, enough for a total of 48 samples, for indexing up to 12 samples	333714
QIAseq 96-Index I Set A, B, C or D (384)	Box containing oligos, enough for a total of 384 samples, for indexing up to 96 samples for targeted panel sequencing on Illumina platforms; one of four sets required for multiplexing 384 samples	333727 333737 333747 333757

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at www.qiagen.com or can be requested from QIAGEN Technical Services or your local distributor.

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