ARCHER™ Now part of Integrated DNA Technologies

Comprehensive identification and tracking of immune repertoire clonotypes

Immunoverse™ research panels are targeted next-generation sequencing (NGS) assays to characterize the immune repertoire from RNA input.

Immunoverse™
Immune repertoire analysis

Powered by Anchored Multiplex PCR (AMP™), the customizable panels enable unbiased amplification for a true and reproducible measure of diversity of the immune repertoire in as little as **3 days**. Sequenced libraries are analyzed with a powerful and transparent analysis platform featuring dynamic visualizations for confident clonotype identification and frequency reporting.

Immunoverse™
A world of applications

- **Immune repertoire sequencing**
- **Profile tumor infiltrating lymphocytes**
- **Track disease progression**
- **Track clonotype dynamics over time**

Repertoire analysis simplified

	Amplicon-based DNA-seq methods	Immunoverse
	Requires more biological input due to lower fraction of target sequences (1 µg – 24 µg)	Since TCR and BCRs are highly expressed, required biological input is lower (as little as 25 ng)
	T and B cells can easily be drowned out by non-immune cell genetic input due to the low frequency of immune cells in the tissue	TCR or BCR sequences are selectively enriched at the cDNA synthesis step, prior to amplification, ensuring the non-immune cell genetic input doesn't interfere with the assay
	Send out tests can take up to 8 weeks for results	Sequencing ready libraries in a single day workflow, with 2.5 hours hands-on time at your lab of choice. Results in as little as 3 days

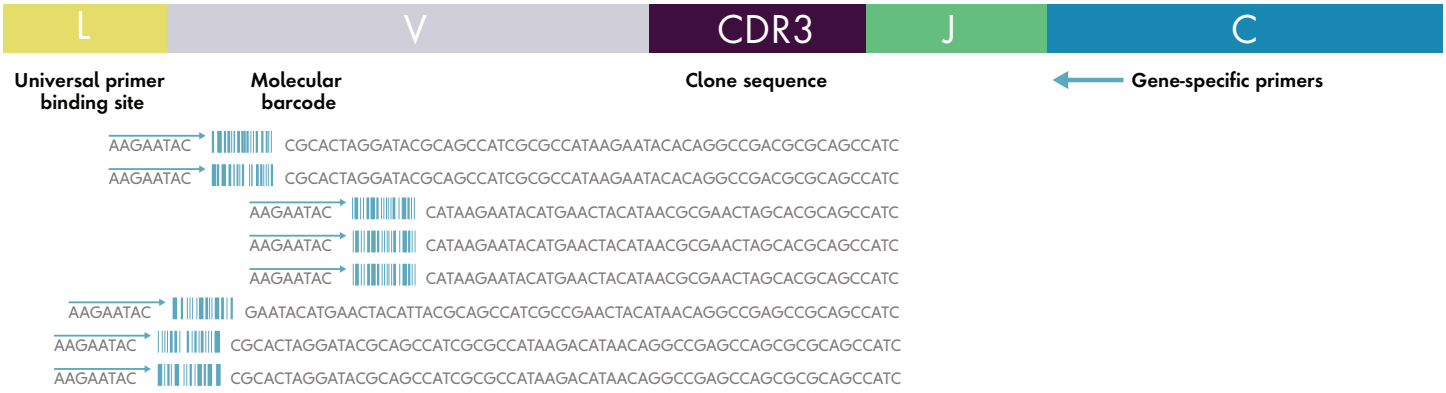
For Research Use Only. *Not for use in diagnostic procedures.*

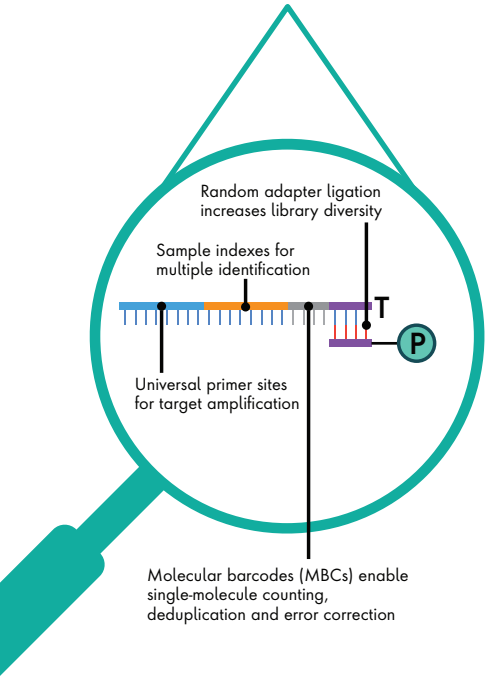
RNA-based workflow

Ensures that only transcribed sequences are detected. Open-ended amplification and sequencing of V(D)J region, means increased coverage of the CDR3.

Anchored Multiplex PCR (AMP™)-powered V(D)J amplification

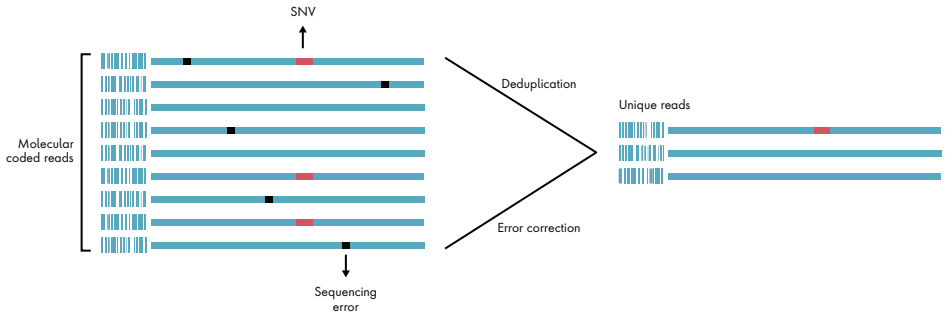
Immunoverse panels utilize AMP chemistry for open-ended amplification from molecular barcoded (MBC) adapters, eliminating the need for opposing primer-based amplification schemes and uniformity assumptions. This unbiased approach towards V(D)J recombination can yield more than 100,000 clonotypes in a single reaction, without fear of PCR bias. The figure below shows a simplified schematic of AMP-enabled V(D)J enrichment.





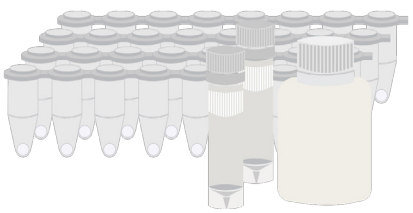
Molecular barcode-based deduplication and error correction enable true quantification

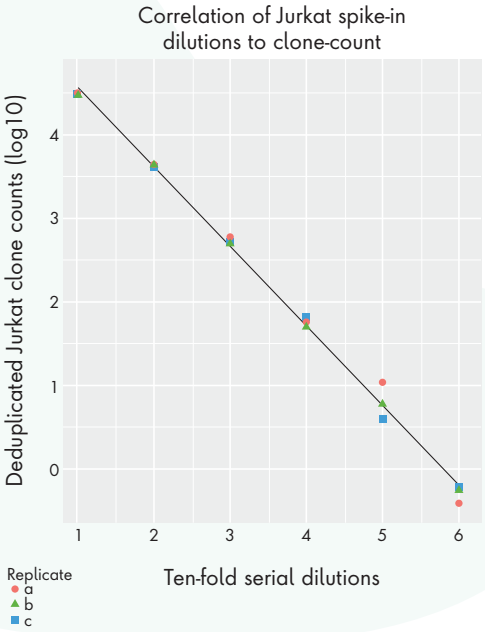
Archer® Analysis utilizes the AMP-specific molecular barcode adapters for deduplication and PCR sequencing error correction to provide a true measure of sample complexity. Additionally, unique molecule identification enables highly quantitative analysis of clonotype frequencies.



Designed for your needs

Customizable NGS panels with a simple workflow. Compatible with FFPE, PMBC, fresh frozen, and whole blood tissue types with input ranging from 25 ng – 6 µg of RNA or TNA. Lyophilized reagents in 8-tube strips, 2.5 hours hands-on time and no cell sorting required.





High sensitivity clonotype identification

Rare clonotype tracking across 6 orders of magnitude for a dilution series of RNA.

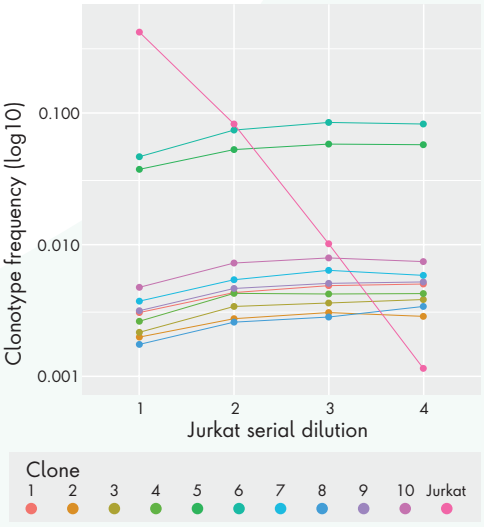
Jurkat cell line dilution in PBL background down to 1 in 10^6 from 400ng input shows strong linearity and detection of Jurkat sequences at expected frequencies across replicates.

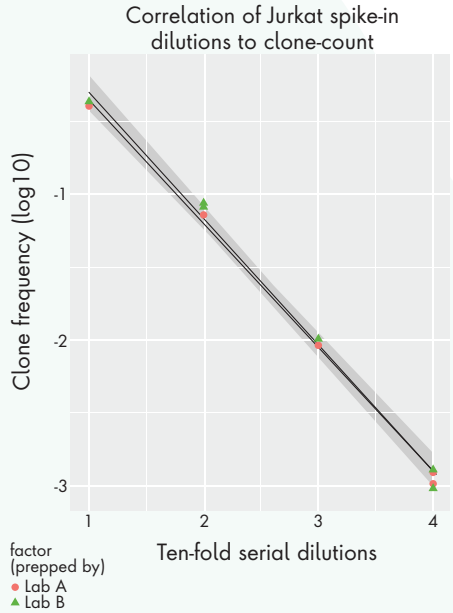
Libraries prepared using the Immunoverse TCR ß/ɣ kit and sequenced on an Illumina® NextSeq® instrument using a 300-cycle kit. Libraries were normalized to 0.5M reads and 2.5M reads (dilution 6) and analyzed with Archer Analysis.

Precise quantitation across a dynamic range

Highly reproducible clonotype frequency reporting of top 10 clones between replicates in Jurkat dilution into PBL background.

Libraries prepared from 400ng input using the Immunoverse TCR ß/ɣ kit and sequenced on an Illumina® MiSeq® instrument using a 600-cycle kit. Libraries were normalized to 0.6M reads and analyzed with Archer Analysis.





Consistent performance between labs

Strong linearity and reproducibility is shown in dilution series across two different laboratories.

Ten-fold serial dilutions of Jurkat cell line mRNA into PBL background were performed in duplicates in two labs. Libraries were sequenced on Illumina® NextSeq® instruments using a 300-cycle kit and normalized to 0.5M reads and analyzed using Archer Analysis. Pearson correlation between labs: 0.996, p-value ≤ 0.001. Grey shaded area = 95% confidence interval.

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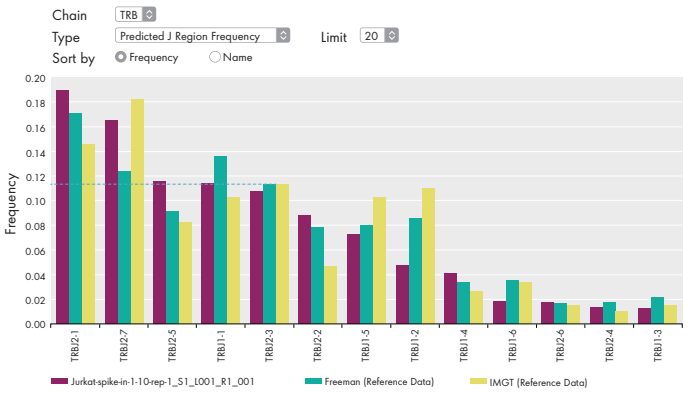
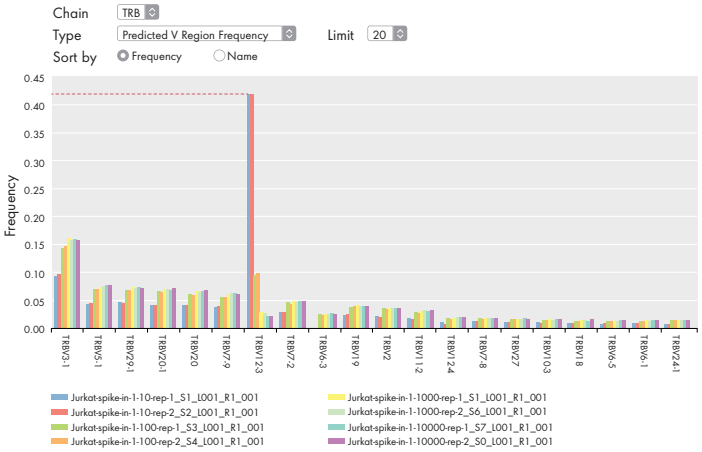
Purpose-built repertoire analyses

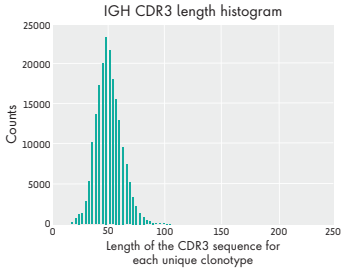
Segment usage comparison to known databases



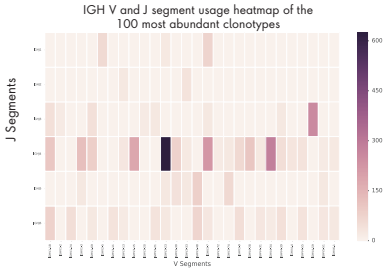
Segment usage between samples



CDR3 length histogram



Segment usage heatmap



Number of clonotypes	Number of clones	Shannon index
197,865	227,544	12.0788

ARCHER® Analysis

Archer Analysis is a powerful and transparent tool for immune repertoire analysis. Clone and clonotype information, including clone tracking, is provided in custom-filtered tables, dynamic visualizations and full data exports to answer complex research questions. Archer Analysis is available for private cloud and local installation behind your firewall, allowing ownership of your data.

Get started with Immunoverse NGS panels

- TCRB/G: T-cell receptor beta/gamma
- TCRA/D: T-cell receptor alpha/delta
- IGH: IG heavy chain
- IGK/L: IG kappa/lambda
- Custom: Mix and match chains

Learn more at archerdx.com or email us at sales@archerdx.com

AssayDesigner
Design your own panel or add to an existing product. It's your panel, your way.

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