ARCHER®

Immunoverse™

Immune Repertoire Sequencing Assays

Repertoire analysis on your own terms

Archer® Immunoverse™ kits are targeted NGS assays to characterize the human immune repertoire from RNA input. Powered by Anchored Multiplex PCR (AMP™), the lyophilized kits uniquely tag and amplify V(D)J rearrangements for sequencing on Illumina® platforms. Sequenced libraries are analyzed using the Immune Repertoire pipeline in Archer Analysis—a powerful and transparent tool for clonotype identification and frequency reporting.

- Unbiased amplification for true and reproducible measure of diversity
- Molecular barcode-based error correction
- High sensitivity for rare clone identification
- Simple library preparation with a wide range of input quantities
- Transparent and user-owned analysis

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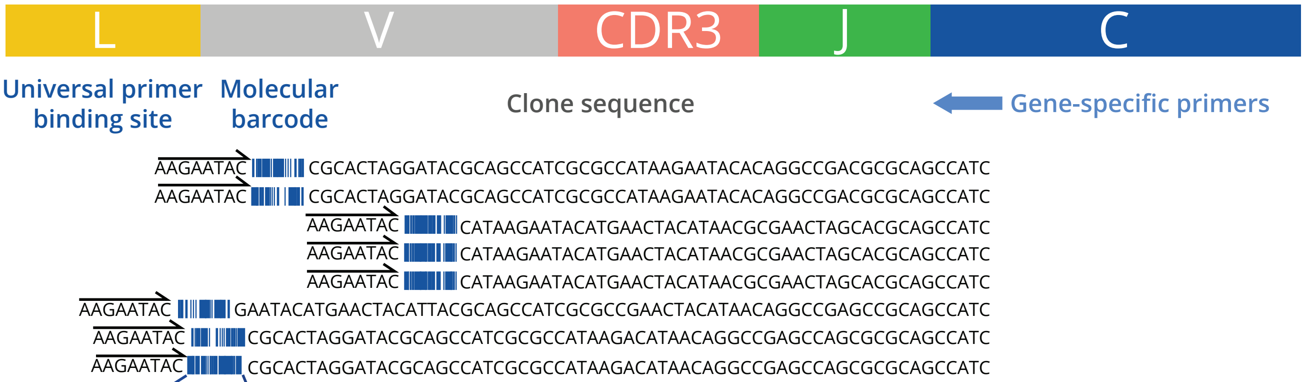
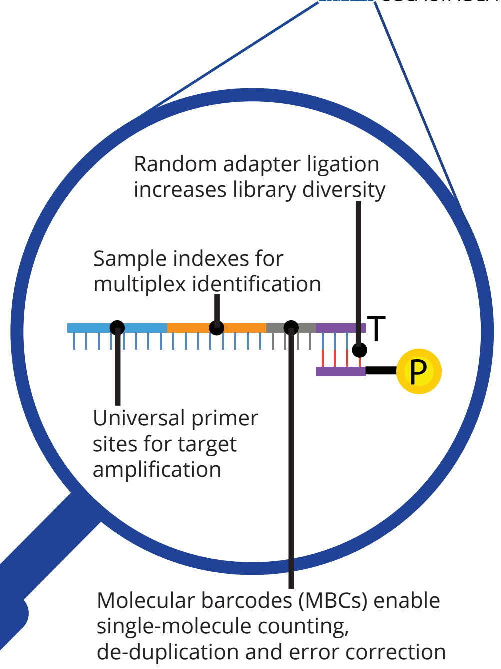
Learn more at
archerdx.com/immunoverse

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

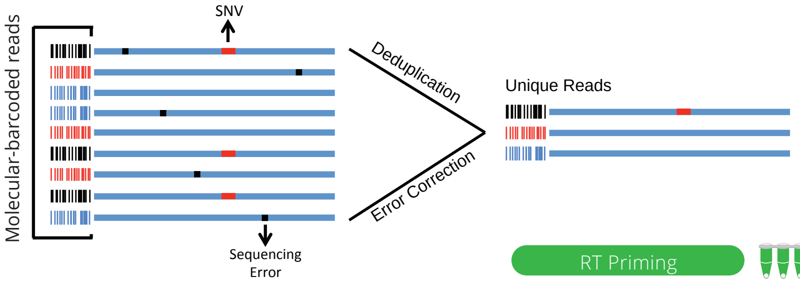
Immunoverse assays utilize AMP chemistry for open-ended amplification from molecular barcoded (MBC) adapters, eliminating the need for complicated opposing primer-based amplification schemes and uniformity assumptions. This unbiased approach towards V(D)J recombination can yield more than 100,000 clonotypes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

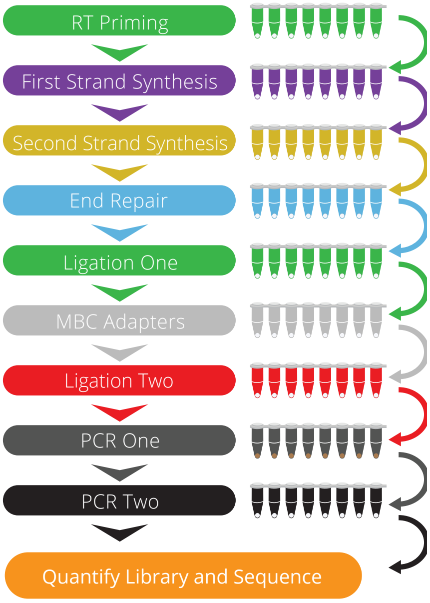




Molecular barcode-based deduplication and error correction enable true quantification

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.



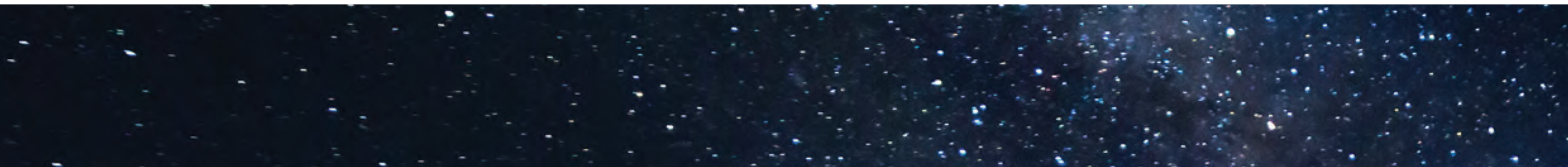


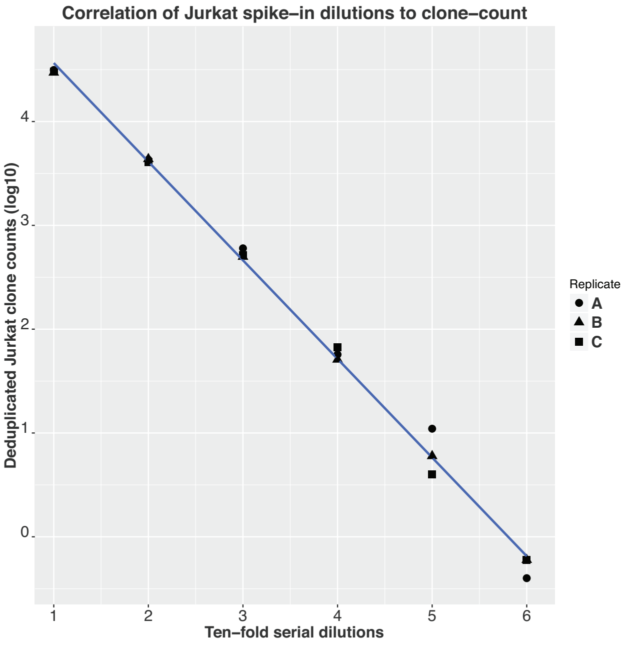
Single-use lyophilized library prep reagents

- Break-away reaction tubes enable run size flexibility
- Lyophilized reagents minimize user error and contamination
- Simple workflow requires less than 3.5 hours hands-on time and 8.5 hours total time

Flexible input requirements

- From 25ng to 2µg RNA
- Compatible with PMBC, FFPE or fresh frozen tissue





Sensitive clonotype identification

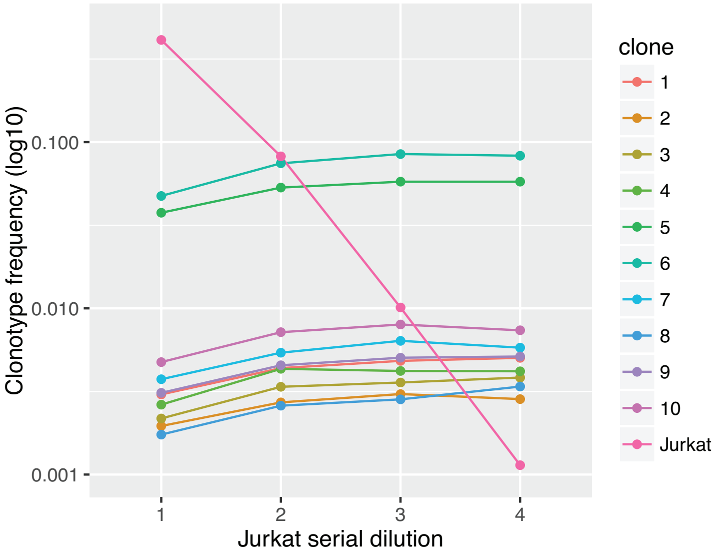
Jurkat cell line dilution in PBL background down to 10^{-6} from 400ng input shows strong linearity and detection of Jurkat sequences at expected frequencies across replicates.

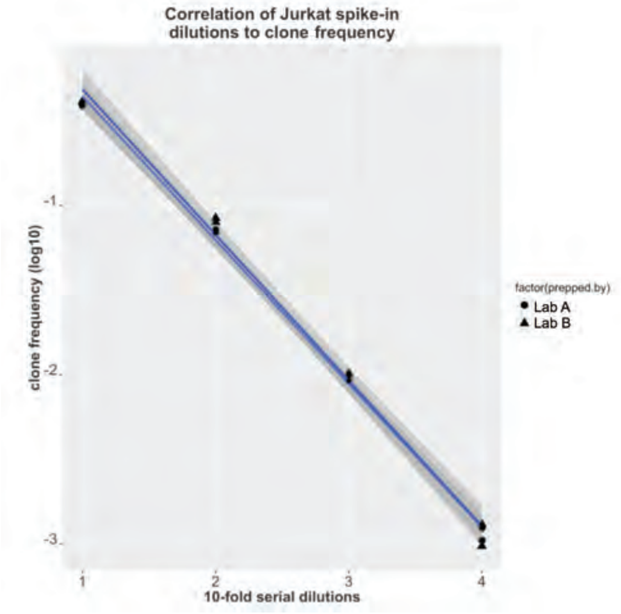
Libraries were prepared using the Immunoverse TCR beta/gamma kit and sequenced on an Illumina® NextSeq® instrument using a 300-cycle kit. Libraries were normalized to 0.5M reads and 2.5M reads (dilution 6) and analyzed with Archer Analysis.

Precise quantitation across a broad dynamic range

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

Libraries were prepared from 400ng input using the Immunoverse TCR beta/gamma 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.

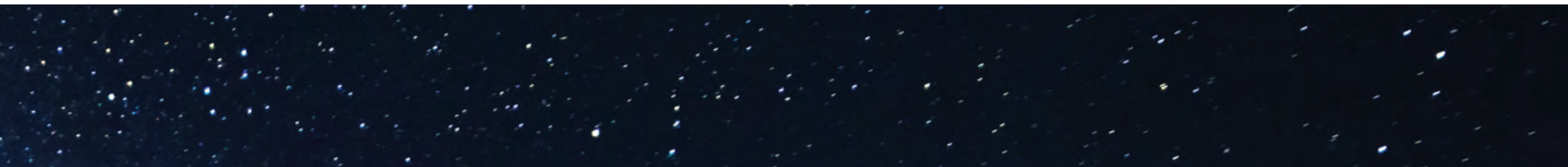




Consistent performance between labs

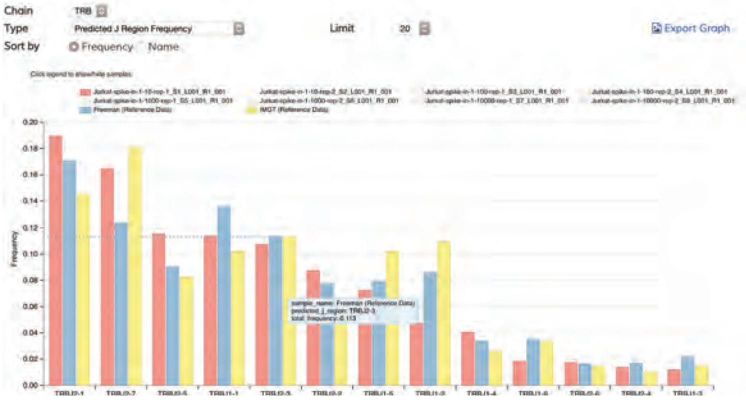
Strong linearity and reproducibility is shown in dilution series across two different laboratories.

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.



Repertoire analysis on your own terms

Segment usage comparison to known databases



Chain TRB
Type Predicted J Region Frequency
Limit 20
Sort by ● Frequency ○ Name

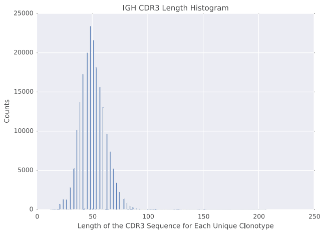
sample_name: Freeman (Reference Data)
predicted_j_region: TRBJ2-3
total_frequency: 0.113

Segment usage between samples

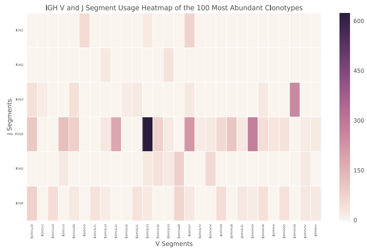
Chain TRB
Type Predicted V Region Frequency
Limit 20
Sort by ● Frequency ○ Name

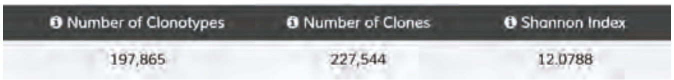
sample_name: Jurkat-spike-in-1-10-rep-2_S2_L001_R1_001
predicted_v_region: TRBV12-3
total_frequency: 0.419

CDR3 Length Histogram



Segment Usage Heatmap





❶ Number of Clonotypes	❶ Number of Clones	❶ Shannon Index
197,865	227,544	12.0788

ARCHER® Analysis Unlimited

ARCHER® Analysis Vault

Archer Analysis is a powerful and transparent tool for immune repertoire analysis, providing extensive clone and clonotype information in custom-filtered tables, dynamic visualizations and full data exports to answer advanced research questions. Archer Analysis is available for private cloud and local installation behind your firewall.

Get started with Immunoverse Assays

TCRB/G	TCRA/D	IGH	IGK/L	Custom
T-cell receptor beta/gamma	T-cell receptor alpha/delta	IG heavy chain	IG kappa/lambda	Choose your own chain

Demo data and training available on request.

ARCHER®

Learn more at
archerdx.com/immunoverse

RUO **For research use only.** Not for use in diagnostic procedures.