LymphoTrack® IGH Assay - PGM,
Product Flyer

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LymphoTrack® IGH Assay

Assay Uses
This research use only (RUO) assay identifies clonal IGH V-J rearrangements, the associated V-J region DNA sequences, and provides the frequency distribution of V region and J region segment utilization using the Life Technologies Ion PGM™ platform.

Background
The immunoglobulin heavy chain (IGH) gene locus on chromosome 14 (14q32.3) includes 46-52 functional and 30 non-functional variable (VH) gene segments, 27 functional diversity (DH) gene segments, and 6 functional joining (JH) gene segments spread over 1250 kilobases.

Lymphoid cells are different from the other somatic cells in the body. During development, the antigen receptor genes in lymphoid cells undergo somatic gene rearrangement (Tonegawa S. et al., 1983). For example, during B-cell development, genes encoding the IGH molecules are assembled from multiple polymorphic gene segments that undergo rearrangements and selection. These gene rearrangements of the VH, DH, and JH generate VH-DH-JH combinations of unique length and sequence for each cell. Since leukemias and lymphomas originate from the malignant transformation of individual lymphoid cells, all leukemias and lymphomas generally share one or more cell-specific or “clonal” antigen receptor gene rearrangements. Therefore, tests that detect IGH clonal rearrangements can be useful in the study of B cell malignancies.

Specimen Requirement
50 ng of genomic DNA.

References

Method
The LymphoTrack IGH assay represents a significant improvement over existing clonality assays using fragment analysis as it efficiently detects the majority of IGH gene rearrangements using a single multiplex master mix. At the same time, the assay identifies the DNA sequence specific to each clonal gene rearrangement.

Therefore, this product has two important and complementary uses: it aids both in the detection of initial clonal populations, and identifies sequence information required to track those clones in subsequent samples. Our single multiplex master mix targets the conserved framework region 1 (FR1) and the joining (J) region. Primers included in the master mix are designed with 12 indices and adapters for the Ion PGM instrument. This allows for a one-step PCR reaction and pooling of amplicons from several different samples for loading onto the Ion PGM chip.

The LymphoTrack PGM Software enables simplified analysis and visualization of data generated from this assay.

Positive and negative DNA controls are included in the kit.

Ordering Information

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<td>7-500-0007</td>
<td>LymphoTrack PGM Software*</td>
<td>1 CD</td>
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*only available with purchase of a LymphoTrack PGM Assay

This product is sold FOR RESEARCH USE ONLY, not for use in diagnostic procedures.
Reagents

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Figure 1: Simplified representation of the organization of the immunoglobulin heavy chain (IGH) gene on chromosome 14. Depicted are the variable region (VH) genes and downstream consensus joining region genes (JH) that are involved in rearrangements.

Figure 2: V-J Sequence Frequencies. The LymphoTrack PGM Software provides a stacked bar graph depicting the relative frequencies for the 200 most common V-J rearrangements sequenced and identified in the sample.

Figure 3: V-J Usage. In addition to the sequence frequency distribution, the LymphoTrack PGM Software also provides a 3D graph of relative usage frequencies of each of the V and J gene segments.

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