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Editorial note

Immuno-oncology Therapies

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These therapies are measured as to be promising anti-cancer treatments and treatments and generating excitement and hope among clinicians, patients and researchers. The torrent of ion portfolio of immune oncology next generation sequencing (NGS) enables multi-dimensional and ground-breaking approach to understanding the microenvironment tumor. Each assay about genomic uses the sensitivity of NGS to hidden biology within precious samples and can be independently implemented or combined more holistic view to improve positively impact study ouCDomes and clinical research study design. Few assays are given below

CDR Beta-SR assays of oncomine: This assay exactly cross-examines the CDR3 region of CDR beta chain, compatible with DNA and RNA enables detection of T cell minimal residual disease (MRD) in peripheral blood and characterization of immune status. For this assay requiring low sample input, this assay offers with superior informatics for accurate CDR3 CDR beta chain sequence and clonality.

BCR IGH LR assay of oncomine: This assay uses long sequencing capabilities ion torrent to cross-examine all determining regions to BCR of immunoglobulin heavy chain (IgH). The frequency hypermutation in biomarker research having a prognostic value for several cancers, are chronic lymphocyte leukemia, evaluating isotype abundance and clonal evaluation, it can be performed from both DNA and RNA samples.

Immune response research assay of oncomine: This assay was carefully selected for monitoring the tumor microenvironment (TME). It can identify biomarkers, study mechanism and other interactions. Help in combination therapy experiments. It can detect lower expressors these are associated with T-cell receptor signaling and check point inhibitors, to focus the correct CDR.

CDR Beta-LR assays of oncomine: This assay is designed to efficiently capture all three complimentary-determining regions of CDR beta chains those are CDR1, CDR2, and CDR3 with accuracy. It may approach for key applications those are T cell characterization, prognostic biomarker discovery and identification of gene polymorphism from samples those are RNA extracted from blood, frozen tissue, FACS sorted cells. Rare and abundant clones can achieve 10 ng RNA input.

Tumor mutation load assay of oncomine: Also called as tumor mutational burden is becoming an independent predictor for satisfaction of patient to immunotherapy response. This assay covers 409 cancer related genes relevant major cancer categories and it needs 20ng out of tumor DNA with streamlined analysis. This assay correlates with exome mutation counts need for exome sequencing, for higher percentage of samples conserving precious samples for additional biomarker.

Ion AmpliSeq mouse BCR IGH SR assay: This assay was designed to interrogate CDR3 region of BCR immunoglobulin heavy chain (IgH). The sequency accuracy ion torrent technology and attained with the panel. Clonal expansion assessed understanding of B cell response in immunotherapy and cancer research. Somatic hypermutations enable repertoire biomarker research analysis useful for vaccine research. A limit of detection improved monitoring disease state and respond within a model system.

Ion torrent immune sequencing was designed to help identify biomarkers relevant to research by using streamlined sequencing platform and integrated informatics solutions to analyze the result. This sample approach to result is a superior solution, sensitivity, bringing accuracy and ease to use immune-oncology research.

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