Predicting Cancer Immunotherapy Response with Tumor Mutational Burden (TMB)

Tumor Mutational Burden, or TMB, is a new, quantitative clinical marker that can help predict responses to certain cancer immunotherapies. Let's see how it works.

Cancer Immunotherapy

Cancer immunotherapies have the potential to treat cancer by harnessing the power of our **own immune systems**.

But right now, only about **20-40%** of people respond to this important new class of medicine.[1,2]

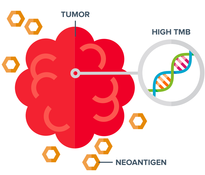
The ability to predict who is most likely to respond to cancer immunotherapies could save **significant cost and precious time**.

A New, Quantitative Clinical Marker

Tumor Mutational Burden (TMB) is the

TOTAL NUMBER OF MUTATIONS

per coding area of a tumor genome.



Higher TMB levels are correlated with

HIGHER LEVELS OF NEOANTIGENS

which help our immune system to recognize tumors.[3,4]

Measuring TMB

TMB can be measured by sequencing the genome of a tumor by **comprehensive genomic profiling**.[5]

Traditional "hotspot" genomic testing may give an **incomplete view** of the mutational landscape.

Predicting Better Responses

High TMB can help predict responses to FDA-approved cancer immunotherapies in **lung cancer, bladder cancer, and melanoma**.

High TMB was associated with

4X LONGER

progression-free survival (PFS) with anti-PD-1 immunotherapy in lung cancer compared to low TMB.[6]

In bladder cancer, high TMB predicted

BETTER RESPONSES

to anti-PD-L1 immunotherapy.[7]

High TMB was associated with

3.5 YEARS LONGER

overall survival (OS) in melanoma patients treated with anti-CTLA-4 immunotherapy compared to low TMB.[8]

All-In-One

Comprehensive genomic profiling simultaneously examines **>300** cancer-related genes, measuring TMB and other important clinical markers.

FOUNDATIONONE®

CLINICAL TRIALS | TARGETED THERAPIES | CANCER IMMUNOTHERAPIES

The comprehensive FoundationOne® test is designed to deliver

3X MORE

actionable insights than standard hotspot testing,[5] giving you the power to make more informed decisions.

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2. Wolchok et al. Nivolumab plus ipilimumab in advanced melanoma. N Engl J Med. 2013 July 11;369(2):122-33.
3. Brown et al. Neo-antigens predicted by tumor genome meta-analysis correlate with increased patient survival. Genome Res. 2014;24:743-750.
4. Schumacher & Schreiber. Neoantigens in cancer immunotherapy. Science. 2015;348(6230):69-74.
5. Frampton et al. Development and validation of a clinical cancer genomic profiling test based on massively parallel DNA sequencing. Nature Biotech. 2013;31:1023-1031.
6. Rizvi et al. Mutational landscape determines sensitivity to PD-1 blockade in non-small cell lung cancer. Science. 2015;348(6230):124-128.
7. Rosenberg et al. Atezolizumab in patients with locally advanced and metastatic urothelial carcinoma who have progressed following treatment with platinum-based chemotherapy: a single-arm, multicentre, phase 2 trial. Lancet. 2016;387(10031):1909-1920.
8. Snyder et al. Genetic basis for clinical response to CTLA-4 blockade in melanoma. NEJ Medi. 2014;371:2189-2199.