

# Tumor Mutational Burden (TMB) Assay for Response to Immunotherapy

Tumor Mutational Burden (TMB) is a putative biomarker of response to checkpoint inhibitor therapy. IQVIA Laboratories offers a TMB assay that utilizes a whole exome sequencing (WES) of tumor specimens for reliable quantification of TMB across various tumor indications. The TMB assay is a component of our comprehensive immuno-oncology assay portfolio and is available for RUO or GCP applications.

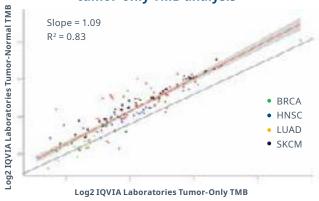
### **HIGHLIGHTS**

- TMB assay available in two formats: tumor-only specimens or matched tumor and germline control blood specimens
- Based on validated WES assay targeting ~60Mb of coding region of the human genome
- TMB tumor-only WES method modeled across multiple tumor indications
- High quantitative precision (CV%  $\leq$ 20%) for TMB >2, suitable for TMB analysis across a wide range of cancer indications including those with traditionally low TMB

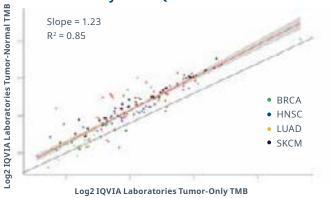
# IQVIA Laboratories TMB levels trend with published TMB levels across different cancer types

	LGG	CHOL	KIRC	COAD	BLCA	LUSC	SKCM
IQVIA Laboratories TMB (WES) <sup>1</sup>	1.5 (N=123)	2.4 (N=38)	2.4 (N=100)	4.6 (N=64)	8.7 (N=39)	10.1 (N=258)	13.2 (N=113)
Published TMB <sup>2</sup>	1.8 (N=220)	2.5 (N=1456)	2.7 (N=543)	4.5 (N=7758)	7.2 (N=80)	9 (N=2102)	14.4 (N=879)

# Correlation between paired tumor-normal and tumor-only TMB analysis



# Correlation between published TCGA TMB data<sup>3</sup> and TMB analysis at IQVIA Laboratories



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### TMB assay specifications

Sample types	Tumor tissue (FFPE, fresh frozen or DNA specimens) Normal tissue, optional (PBMC, whole blood or DNA)			
DNA requirements	250 ng DNA			
Assay method	Whole exome sequencing			
System compatibility	NovaSeq 6000			
Assay performance	>99.9% accuracy of variant calling for variants above 10% allelic frequency Quantitative precision ≤20% CV% across TMB range of 2-32			
Deliverables	TMB score, FASTQ, BAM, annotated VCF files			
Turnaround time	6 weeks for defined testing, faster TAT options upon request			

## IQVIA Laboratories global testing footprint



GENOMICS	FLOW CYTOMETRY / IMMUNOASSAYS	ANATOMICAL PATHOLOGY
<ul><li> TCR immune sequencing</li><li> Immune gene signature/</li></ul>	<ul><li>Immuno-phenotyping</li><li>CAR-T tracking</li></ul>	<ul><li> IHC (single and multiplex)</li><li> Tumor infiltrating lymphocytes (TILs)</li></ul>
epigenetic signatures	Receptor occupancy	Digital pathology
<ul> <li>Digital spatial profiling (AP-gene and</li> </ul>	(mono/bispecific mAbs)	• FISH
protein expression)	<ul> <li>Tumor infiltrating lymphocytes (TILs)</li> </ul>	
<ul> <li>Minimal residual disease (MRD)</li> </ul>	<ul> <li>Intracellular cytokine survey</li> </ul>	
<ul> <li>Tumor mutation burden (TMB)</li> </ul>	<ul> <li>Minimal residual disease (MRD)</li> </ul>	
<ul> <li>DNA-mismatch repair (MMR) deficiency/</li> </ul>	<ul> <li>Circulating soluble proteins</li> </ul>	
microsatellite instability (MSI)	<ul> <li>PBMC processing</li> </ul>	
<ul> <li>HLA and KIR typing</li> </ul>	• ELISpot	
<ul> <li>Whole exome sequencing</li> </ul>	<ul> <li>Pembrolizumab PK and</li> </ul>	
<ul> <li>Neoantigen discovery</li> </ul>	anti-pembrolizumab antibody	
<ul> <li>Microbiome 16S rRNA</li> </ul>		

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