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TMB Harmonization Project

Jeff Allen, PhD President & CEO Friends of Cancer Research

November 9, 2019

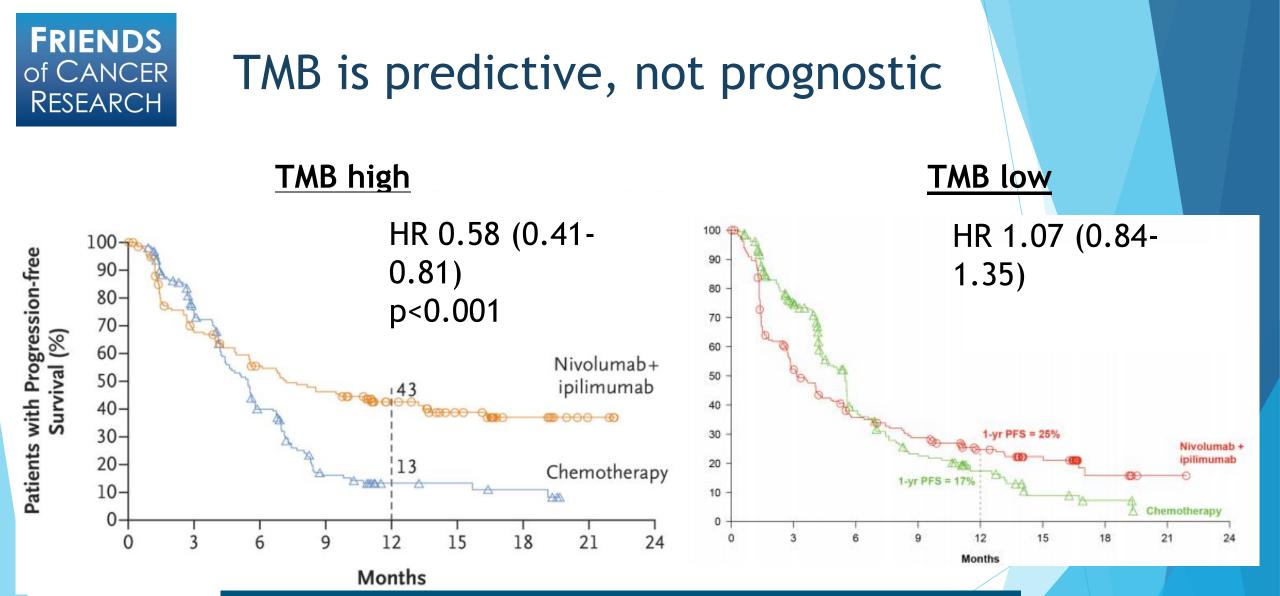


Financial Disclosures

- I have no disclosures to report.
- Funding for this project has been provided by the participants who have performed their individual TMB analyses.



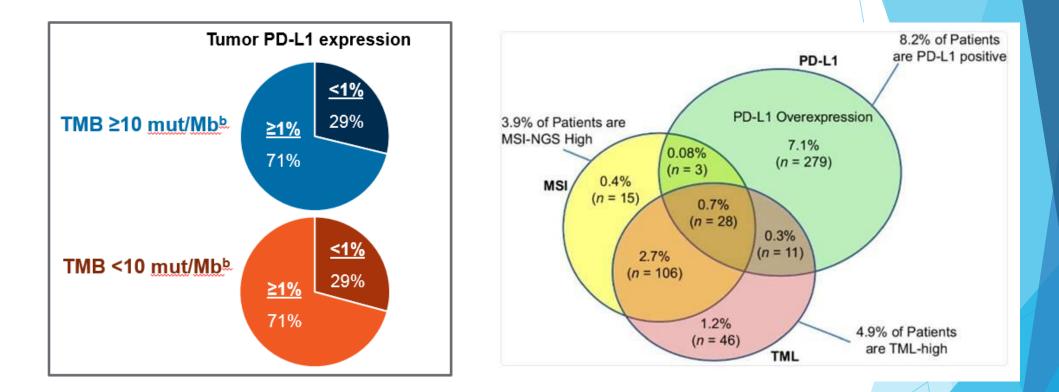




Predictive not prognostic: The positive association between TMB and outcome is limited to immunotherapy.

Hellmann, NEJM 2018

FRIENDS of CANCER RESEARCH TMB is an independent biomarker



Orthogonal, not overlapping: Mutation burden is independent of other predictive variables (PDL1, MSI, GEP)

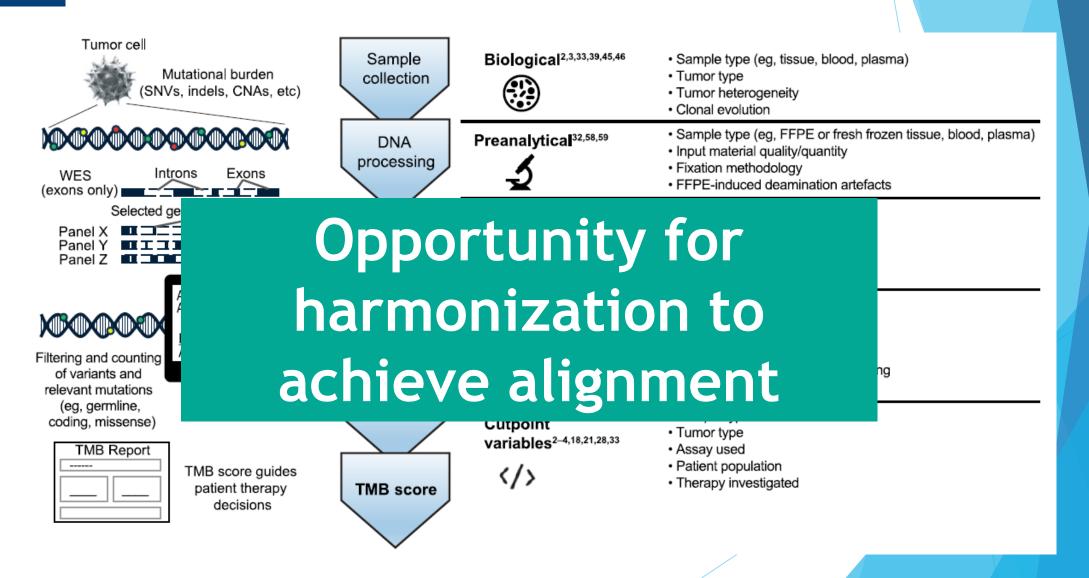
Hellmann, NEJM 2018 Salem, Mol Cancer Res 2018

of CANCER RESEARCH Need for Standardizing TMB Assessment

- Interest in TMB assessment as a biomarker for response to immune checkpoint inhibitors is increasing
 - The number of published studies and studies registered in the ClinicalTrials.gov database has increased over recent years¹
 - > 98 trials registered as of March 2019
- Methods of TMB estimation and reporting vary widely across clinical studies²⁻⁵
 - Assays: whole exome sequencing (WES) and various targeted gene panels
 - Parameters: sample type, genome coverage, genomic considerations, bioinformatics pipelines, cutoff values, and reporting methods
- Reliable TMB measurement is critical for consistent identification of patients who are likely to benefit from immune checkpoint inhibitors⁵⁻⁷

1. NIH. ClinicalTrials.gov. https://clinicaltrials.gov/ct2/home. Accessed March 2019. 2. Chalmers ZR, et al. *Genome Med* 2017;9:34. 3. Hellmann MD, et al. *N Engl J Med* 2018;378: 2093-2104. 4. Velcheti V, et al. *J Clin Oncol* 2018;36(suppl 15). Abstract 12001. 5. Chang H, et al. *Ann Oncol* 2018;29(suppl 8):viii14-viii57. 6. Chen H, et al. *Cancers (Basel)* 2015;7:1699-1715. 7. Deans ZC, et al. *Virchows Archiv* 2017;470:5-20.

FRIENDS
of CANCER
RESEARCHFactors That Impact TMB Estimation



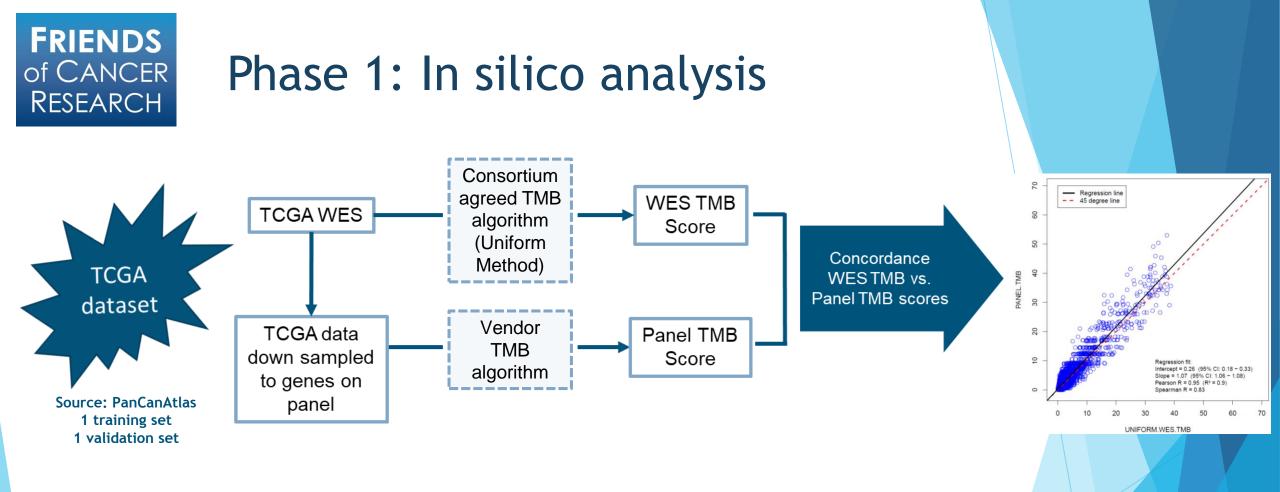
FRIENDS of CANCER RESEARCH

Friends of Cancer Research TMB Harmonization Effort

Multi-stakeholder working group to align on and publish universal best practices for defining TMB, and analytic validation approaches including alignment against reference standards.

Analytical Validation		────────────────────────────────────	
Workflow	Phase 1: In silico analysis	Phase 2: Empirical analysis	Phase 3: Clinical analysis
Samples	Publicly available TCGA data	Cells derived from human tumors	Clinical Samples
Goals	Identify sources of variability between TMB calculated using whole exome sequencing (WES) & various targeted panels used in the clinic	Agree upon creation of a universal reference standard using WES Identify sources of variability after alignment of TMB scores from targeted panels to the reference standard	Propose standards for defining clinical application of TMB and inform clinical use
Timeframe	May 2018	Spring 2019	Summer 2019

www.focr.org/tmb



Multi-stakeholder team: ACT Genomics, AstraZeneca, Bristol-Myers Squibb, Caris Life Sciences, Columbia University, EMD Serono, Foundation Medicine, Genentech, Guardant Health, Illumina, Johns Hopkins University, Memorial Sloan Kettering Cancer Center, Merck, National Cancer Institute, NeoGenomics Laboratories, OmniSeq, Pfizer, Personal Genome Diagnostics, precisionFDA, QIAGEN, Regeneron Pharmaceuticals, SeraCare, Thermo Fisher Scientific, U.S. FDA

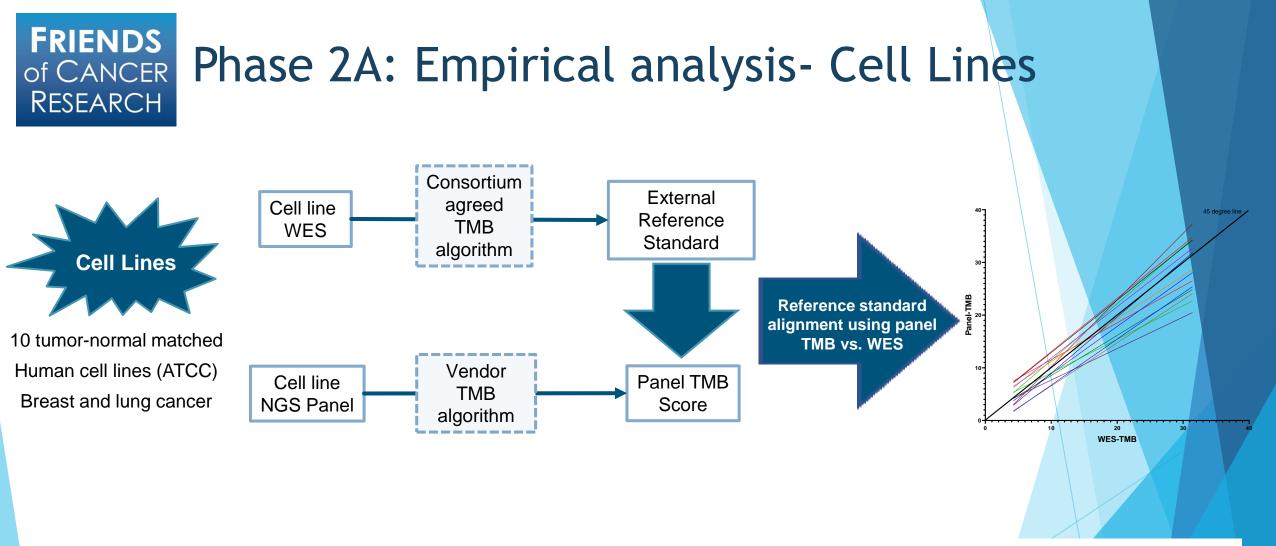
***bolded** = panel examined in the in silico analysis

FRIENDS of CANCER RESEARCH Phase 1 Conclusions

- Panel-TMB was strongly correlated to WES-TMB in TCGA samples
- Associations between panel-TMB and WES-TMB were observed to differ by cancer type
- Theoretical variation in TMB quantification across panel-based diagnostic platforms exists and warrants empirical alignment with reference standard

Recommendations:

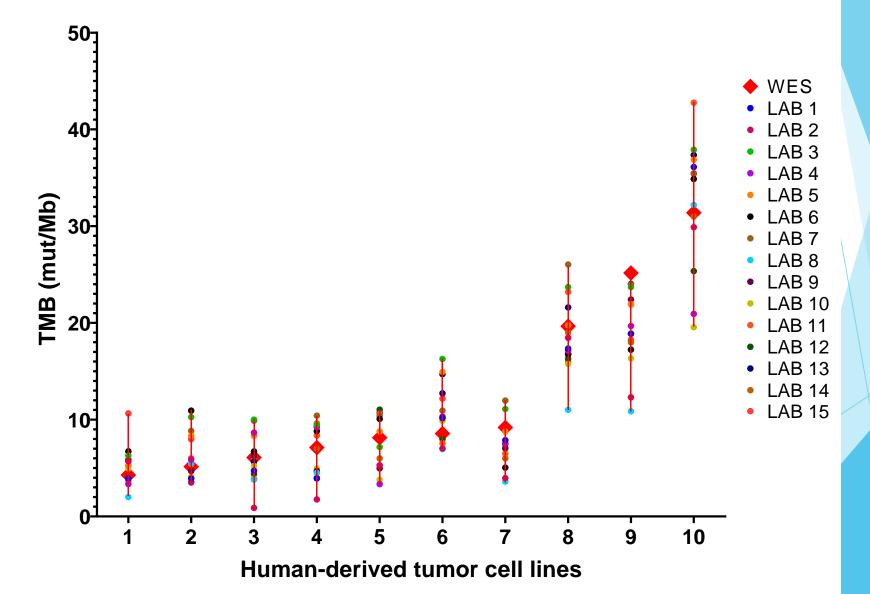
- Common definition of TMB to ensure reporting consistency
- Standardization of analytical validation studies
- Alignment against external reference standard

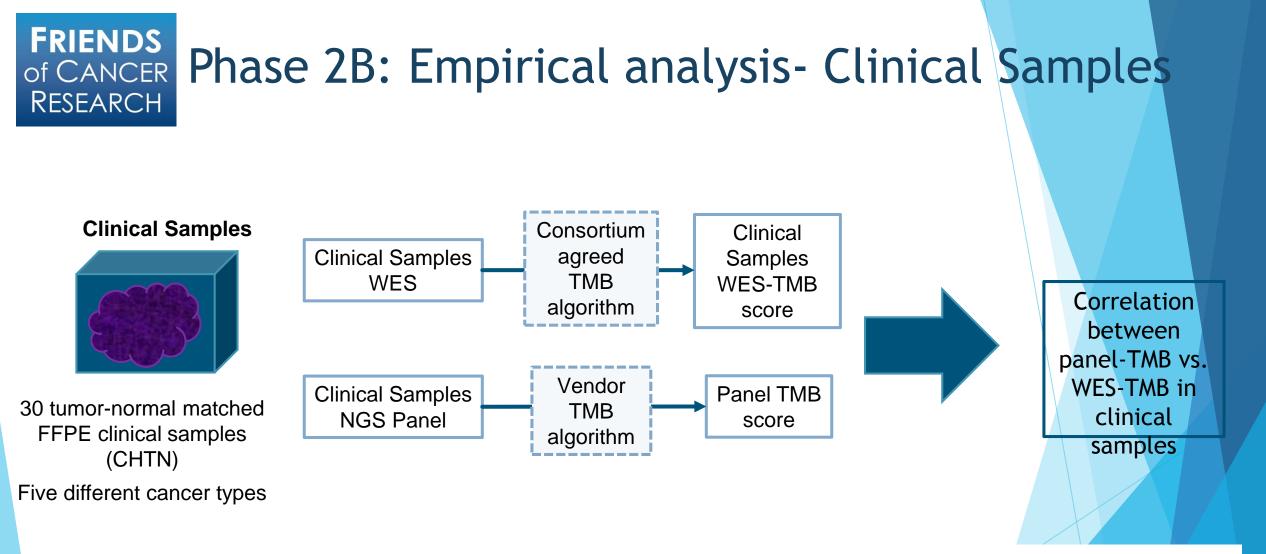


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*bolded = panel examined in the empirical analysis

FRIENDS
of CANCER
RESEARCHVariability in TMB estimates for each tumor cell line
across all 15 participating laboratories





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*bolded = panel examined in the empirical analysis

FRIENDS of CANCER RESEARCH Multistakeholder International Collaboration

Partners:

Diagnostic

- ACT Genomics Company, Ltd
- Caris Life Sciences, Inc
- Foundation Medicine, Inc
- Guardant Health, Inc
- Illumina, Inc
- Navican
- NeoGenomics Laboratories, Inc
- OmniSeq, Inc
- Personal Genome Diagnostics, Inc
- Q² | EA Genomics
- QIAGEN, NV
- Thermo Fisher Scientific, Inc Academic
 - Brigham & Women's Hospital, MA
 - Columbia University, NY
 - Memorial Sloan Kettering Cancer Center, NY
 - Johns Hopkins University, MD
- Pharmaceutical
- AstraZeneca, LP
- Bristol-Myers Squibb Company, Inc
- EMD Serono, Inc
- Genentech, Inc
- Merck & Company, Inc
- Pfizer, Inc
- Regeneron Pharmaceuticals, Inc Other
 - EORTC
 - NIH National Cancer Institute
 - precisionFDA
 - SeraCare Life Sciences, Inc
 - US Food and Drug Administration

Partners:

- Diagnostic
 - Foundation Medicine, Inc
 - Illumina, Inc
- NEO New Oncology, AG
- QIAGEN, NV
- Thermo Fisher Scientific, Inc Academic
 - Charité Berlin
- LMU Munich
- Technical University Munich
- University Hospital Cologne
- University Hospital Dresden
- University Hospital Erlangen
- University Hospital Halle (Saale)
- University Hospital Heidelberg
- University Hospital Regensburg
- University Hospital Zurich Pharmaceutical
- Bristol-Myers Squibb Company, Inc
- Merck Sharp & Dohme, Ltd
- F. Hoffmann-La Roche, AG Other
 - German Cancer Consortium (DKTK)
- Institute for Hematopathology, Hamburg

Stenzinger A, Allen JD, et al. Genes Chromosomes Cancer



Policy Opportunities Beyond TMB

- Demonstrate opportunities for the use of *in silico* and human-derived cell line reference material to optimize diagnostic development
- Inform policy discussions on optimal trial strategies for quantitative biomarkers, diagnostic and drug labeling considerations, and regulatory pathways
- Consortium effort as a model for future harmonization efforts



TMB Harmonization Consortium

- ACT Genomics
- AstraZeneca
- Brigham & Women's Hospital
- Bristol-Myers Squibb
- Caris Life Sciences
- Columbia University
- EMD Serono
- European Organisation for Research and Treatment of Cancer (EORTC)
- Foundation Medicine

- Guardant Health
- Illumina
- Johns Hopkins University
- Navican
- Memorial Sloan Kettering Cancer Center
- Merck
- National Cancer Institute (NCI)
- National Institutes of Health (NIH)
- NeoGenomics Laboratories

- OmniSeq
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