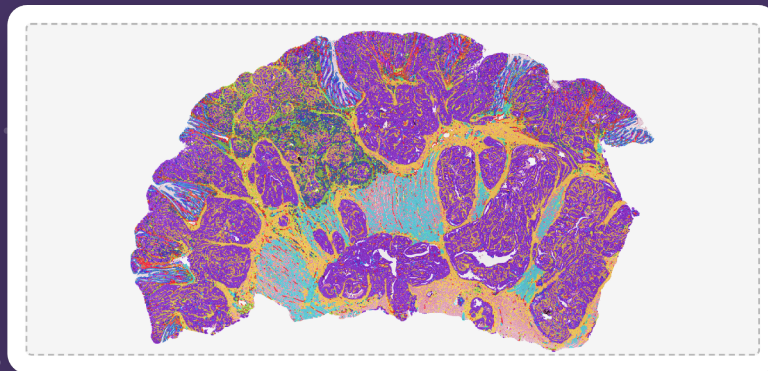


OPEN TME

Comprehensive spatial profiling of
H&E images from TCGA



CELL-CLASSIFICATION OVERLAY · TCGA WHOLE-SLIDE IMAGE

OpenTME provides **pre-computed readouts for thousands of TCGA slides**, generated with Aignostics' [Atlas H&E-TME](#). Paired with TCGA's molecular and clinical data, OpenTME gives life sciences teams a well-characterized external cohort to generate and validate hypotheses at scale.

4,691

WHOLE-SLIDE IMAGES

4.1B+

CELLS ANALYZED

30M+

SPATIAL FEATURES QUANTIFIED

8

TUMOR TYPES COVERED

WHAT'S INCLUDED



Spatial and quantitative readouts

Polygon outputs for 7 tissue segments and 9 cell classes, plus 4,500+ quantitative metrics for every slide. Includes spatial features such as TLS and WTR detection.



Intuitive viewer access

Every readout is viewable in Aignostics' digital pathology viewer, pre-configured for exploring OpenTME outputs.



Analysis tools via TME Studio

Marimo notebooks and detailed documentation for data loading, filtering, and downstream analysis.

COHORT COVERAGE

Tumor Type	No. of WSIs
Breast	1,125
Lung & Bronchus	1,041
Colorectum	600
Bladder	457
Prostate	448
Liver & Bile Ducts	411
Stomach	400
Pancreas	209
8 tumor types · total	4,691

WHY LIFE SCIENCES TEAMS USE OPENTME

Outperforms pathologists

Atlas H&E-TME was [validated](#) against an IHC-informed pathologist consensus, matching or exceeding expert pathologist performance.

Multimodal integration

Spatial features can be integrated with TCGA's genomic, transcriptomic, proteomic, and clinical data to support multimodal analyses.

Deep spatial readouts

Detailed readouts at the cell, tissue, and neighborhood level, for a comprehensive spatial picture of each slide.

GET STARTED

Request access to OpenTME

Reach out for a guided walkthrough, sample readouts, and details on licensing.

aignostics.com/products/atlas-he-tme/for-life-sciences

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