inōtiv
analyze. answer. advance.

Target Sufficiency® enables key decisions in immune checkpoint therapeutics

Imagine a protein assay equivalent to rtPCR—sensitive, precise, highly specific, and for *any* protein. Our Target Sufficiency platform employs high resolution mass spectrometry (MS) to simultaneously quantify multiple proteins in diverse specimen types, including cells, tissues, biofluids and archival FFPE sections.

CASE STUDY—ANALYSIS OF THE TIGIT AND PD-1 TARGET SYSTEMS IN LUNG ADENOCARCINOMA

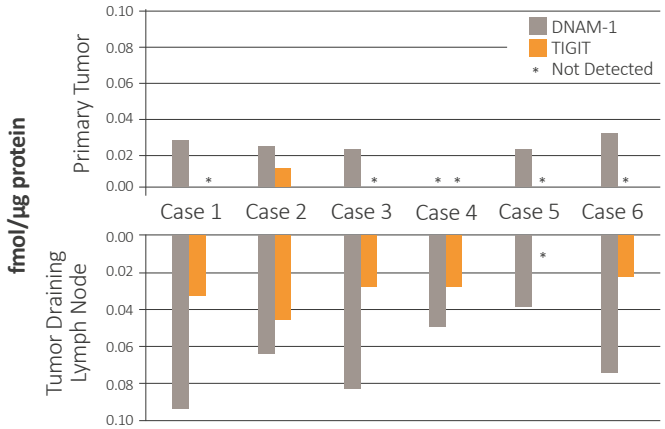
Target Sufficiency® provides precise quantitation of the immune checkpoint drug targets TIGIT and PD-1, which are the targets of combination immunotherapeutics. Our analyses of lung adenocarcinoma precisely quantify TIGIT and its regulatory system partner DNAM1 (CD226) (left) and of PD-1 and its ligands PD-L1 and PD-L2 (right). Primary lung tumors typically express no quantifiable TIGIT, whereas tumor draining lymph nodes (TDLN) co-express TIGIT and DNAM1 in varying abundance. In contrast, primary tumors all express PD-1, PD-L1, and PD-L2, but at lower levels than in TDLN.

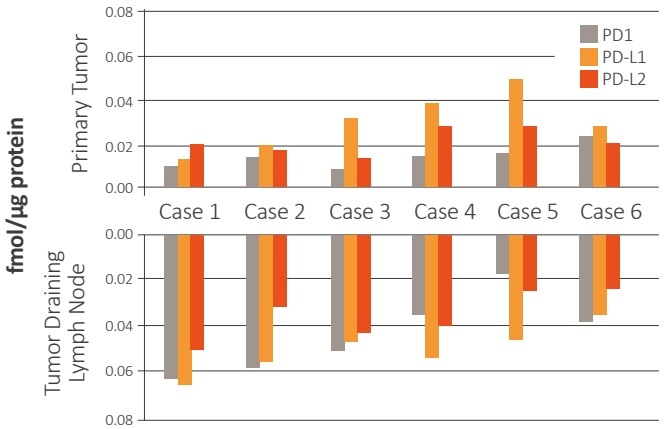
Target Sufficiency answers key questions:

Does this tumor type express the target protein and its functional partners?

Which preclinical models express the target system?

Can differences in target system expression explain efficacy in my clinical trial?





Target Sufficiency® can quantify immunotherapy targets in tumor tissues.
Co-expression of drug target systems may dictate efficacy of combination immunotherapies.
Retrospective analysis in tissue specimens can inform interpretation of trial outcomes.

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