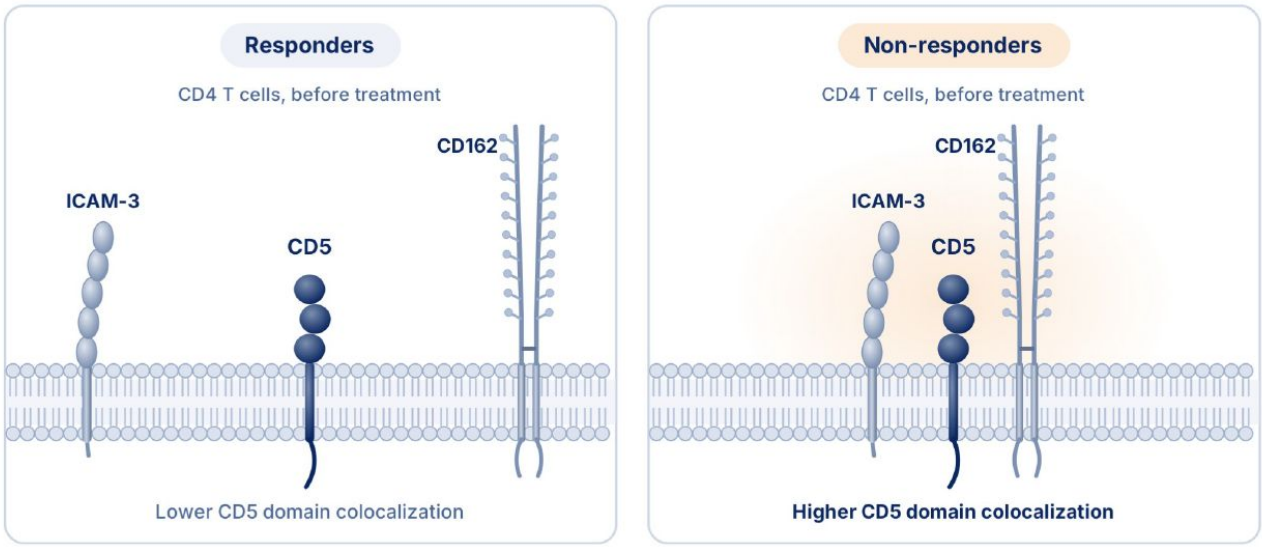
CD4 T cell surface organization predicts anti-PD-1 response in lung cancer

Andreas Lundqvist's group (Karolinska Institutet) profiled PBMCs taken before anti-PD-1 therapy from 62 patients with advanced non-small cell lung cancer (NSCLC), using the Proximity Network Assay (PNA), showing that protein organization predicts therapeutic response.



WHAT THE STUDY FOUND

1. **The importance of CD4 T cells.** Most immune cell populations were similar between the 29 responders and 33 non-responders. The clearest differences were found in CD4 T cells.
2. **A remodeled CD5 domain.** In non-responders, CD5 colocalized more with ICAM-3 and CD162, part of a wider domain of adhesion and activation proteins. Higher colocalization in this domain was linked to shorter survival.
3. **Organization predicts better than abundance.** In machine learning models, CD4 T cell colocalization predicted response better than protein levels.

WHY IT MATTERS

Few blood biomarkers predict who benefits from anti-PD-1 therapy. Protein organization represents a novel type of biomarker in immuno-oncology, with the potential to uncover mechanisms, improve patient stratification and pave the way for precision medicine.

Look beyond protein abundance

Pixelgen Proxiome Kits (PNA) measure abundance, clustering and colocalization of +150 surface proteins per cell, from standard PBMC samples.

Cinotti R, et al. CD4 T cell surface architecture is associated with response to anti-PD-1 therapy in non-small cell lung cancer. bioRxiv 2026. doi:10.64898/2026.10.26.761814. Preprint, not peer reviewed.

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