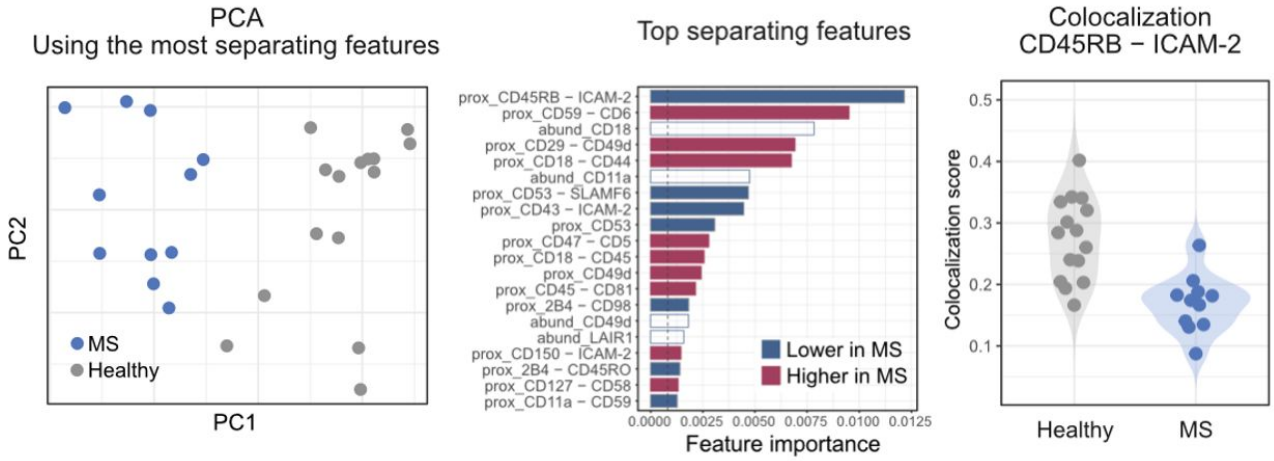
Protein colocalization separates multiple sclerosis from healthy samples

Blood immune cells (PBMC) from patients with multiple sclerosis (MS) and healthy donors, profiled with the Proximity Network Assay (PNA) to find biomarkers and drug effects.

Altered protein colocalization in NKT cells separates healthy and MS samples by machine learning



WHAT THE STUDY FOUND

1. **Altered colocalization in MS.** Several protein pairs on NKT cells, including CD45RB with ICAM-2, were organized differently in MS than in healthy samples.
2. **The top separating features - colocalization.** The majority of features important for MS separation was based on organization rather than abundance.
3. **Drug effects are visible.** Anti-CD49d treatment changed the organization of proteins such as ADAM10 and CD82 on CD4 memory T cells.

WHY IT MATTERS

MS is difficult to diagnose and treat. Protein organization can add a new biomarker layer to blood samples and unravels potential novel drug targets and mechanisms of action of treatments.

Find biomarkers beyond protein abundance

Pixelgen Proxiome kits measure abundance, clustering and colocalization of +150 proteins per cell in PBMC samples.

Source: Pixelgen application data, multiple sclerosis use case (unpublished).

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