higher or lower concentrations in the PsA group compared to the control or the RA group. We selected two of these significant metabolites to build a classification model based on the linear support vector machine (SVM) method, and the area-under-the-curve (AUC) value of the resulting receiver operating characteristic (ROC) curve was 0.929 (95% confidence interval: 0.889-0.956). Similarly, 37 metabolites could differentiate AS samples from RAs and controls. A proposed diagnostic panel containing four metabolites demonstrated an AUC value of 0.890 (0.843-0.934). For the last step, distinguishing between PsA and AS, there were 15 significantly increased metabolites and 9 lowered ones. The biomarker panel consisting of the top three metabolites also achieved good discriminatory power with AUC = 0.827 (0.717-0.919).

**Conclusion:** Isotope-labeling-LC-MS-based metabolomics has revealed biomarker candidates that can specifically differentiate PsA or AS patients from control populations.

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### Table 1. Demographics of psoriatic arthritis (PsA) patients.

<table>
<thead>
<tr>
<th></th>
<th>IL-17Ai</th>
<th>TNFi</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of PsA patients</td>
<td>20</td>
<td>20</td>
</tr>
<tr>
<td>Gender (% female)</td>
<td>55%</td>
<td>75%</td>
</tr>
<tr>
<td>Mean Age (Years)</td>
<td>55.9 (9.5)</td>
<td>56.8 (7.9)</td>
</tr>
<tr>
<td>Mean Disease Duration (Years)</td>
<td>10.4 (6.9)</td>
<td>7.3 (7.9)</td>
</tr>
<tr>
<td>Mean DAPSA baseline</td>
<td>38.8 (17.5)</td>
<td>45.6 (28.9)</td>
</tr>
<tr>
<td>Responders (%) (DAPSA &lt;14)</td>
<td>35%</td>
<td>65%</td>
</tr>
<tr>
<td>Biologic naïve (%)</td>
<td>40%</td>
<td>60%</td>
</tr>
</tbody>
</table>

### Figure 1. PCA plots illustrating that DEGs of CD4+ cells can differentiate responders from non-responders when treated with: A. IL-17Ai; and B. TNFi.

**Conclusion:** Integration of cell-specific transcriptomic data with protein networks represents a very promising strategy for identifying biologic responders and pathways involved in predicting response that may have identified the Rho-GTP pathway as a potential marker to guide the choice of biologic agents for individual patients.

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### Figure 2. Over-represented terms in significantly enriched pathways considering DEGs between: A. IL-17i responders and non-responders (125 pathways); B. TNFi responders and non-responders (576 pathways).

**Conclusion:** Integration of cell-specific transcriptomic data with protein networks represents a very promising strategy for identifying biologic responders and pathways involved in predicting response that may have identified the Rho-GTP pathway as a potential marker to guide the choice of biologic agents for individual patients.

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