frontiers in Immunology

ORIGINAL RESEARCH
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subtle differences at baseline expression of innate immunity-related genes may be associated with an asymptomatic disease course in SARS-CoV-2 infection.

Blood Transcriptomes of Anti-SARS-CoV-2 Antibody-Positive Healthy Individuals Who Experienced Asymptomatic *Versus* Clinical Infection

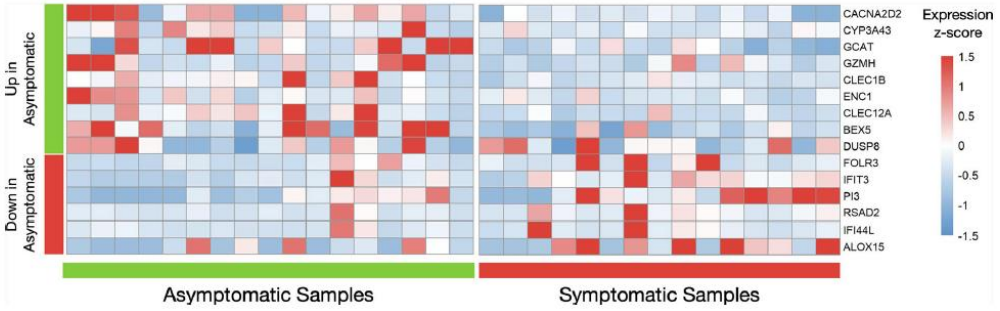
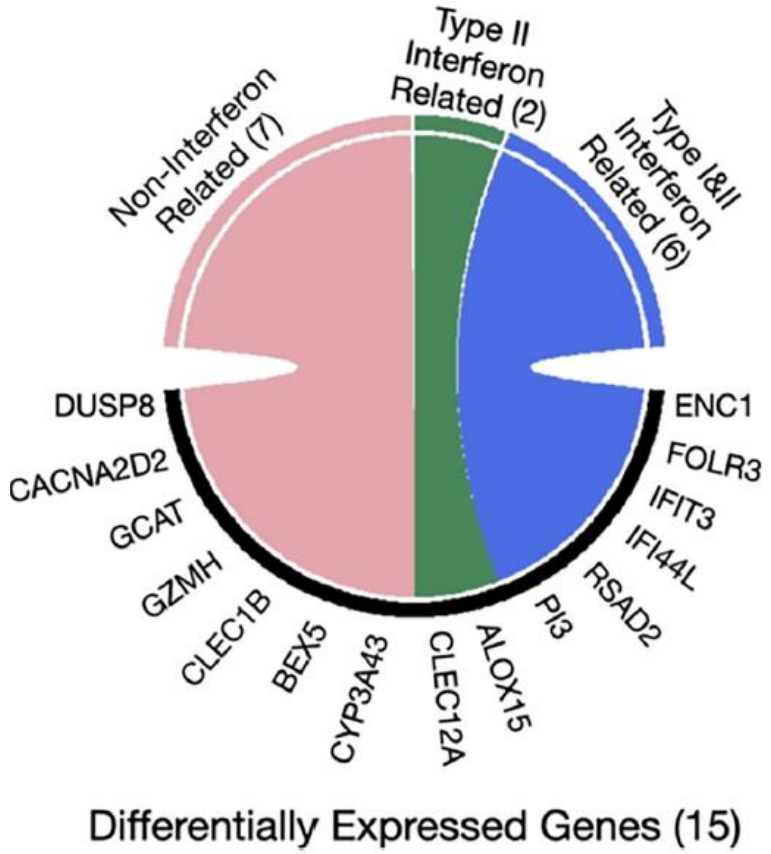


FIGURE 2 | Differential gene expression analysis in seropositive healthy individuals with prior asymptomatic or clinical SARS-CoV-2 infection. Heatmap of robustly differentially expressed genes (genes that were differentially expressed and highly expressed in three or more samples, logFC>|1|, meta p-value<0.05) in individuals with prior asymptomatic infection relatively to those with clinical ("symptomatic") SARS-CoV-2 infection, with raw expression values being scaled. The values for all samples (17 asymptomatic on the left and 15 clinical on the right) is plotted. The first nine genes are increased in the Asymptomatic group, while the next six are decreased.



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Original article

Distinct transcriptional profile of blood mononuclear cells in Behçet's disease: insights into the central role of neutrophil chemotaxis

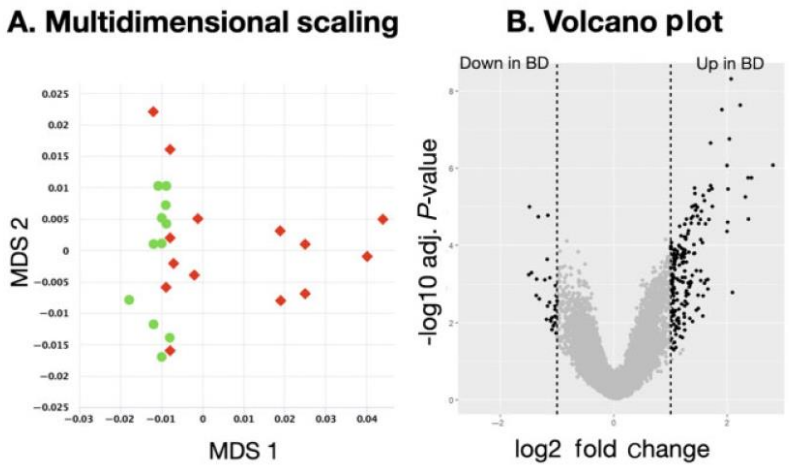
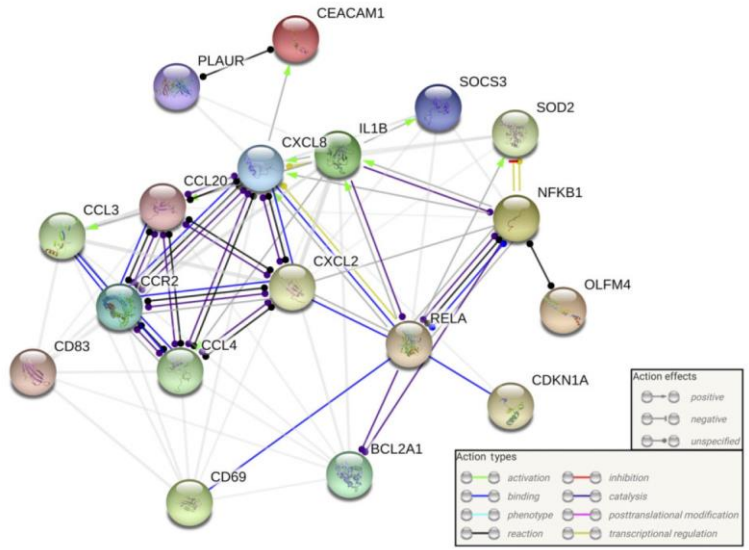


Fig. 3 Transcription factor enrichment analysis



- The most upregulated genes in Behçet's disease peripheral blood mononuclear cells comprised an abundance of CC- and CXC-chemokines.
- Of 10 top upregulated biological processes in Behçet's disease, 5 involved leucocyte recruitment to peripheral tissues, especially for neutrophils.
- The NF-kB p65/RELA subunit action was found to underlie the observed differences in the Behçet's disease transcriptome.

Pre-inflammatory mesenchymal (PRIME) cells were identified by mass cytometry in the peripheral blood of patients with active rheumatoid and psoriatic arthritis

Results

Table 1. Patients 'demographics (n=15) who enrolled in the study

Patients		N°	%
Median age (years)	Male	35	
	Female	53.6	
Sex	Male	1	6.67
	Female	14	93.33
Disease	Rheumatoid arthritis	10	66.67
	Psoriatic arthritis	5	33.33

Figure 1. Representative tSNE maps of **A.** Healthy donor, **B.** psoriatic arthritis patient, and **C.** rheumatoid arthritis patient

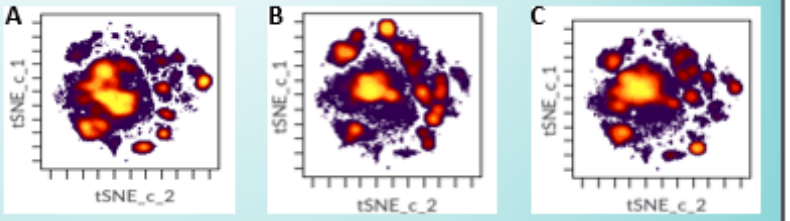
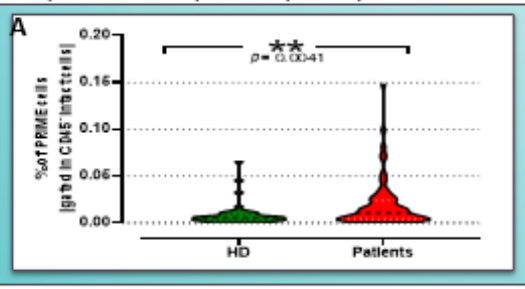


Figure 2. Percentages of circulating PRIME cells in patients and healthy donors. **A.** Circulating cells expressing cadherin-11 and/or podoplanin (both expressed on SFs), and/or CD90 (Thy-1, expressed on sublining SFs), and/or Notch-3 (expressed on endothelial cells and sublining SFs), and/or CD34 were detected in all patients. **B.** The increased PRIME cell levels were more pronounced in PsA than RA patients. Groups were compared by non-parametric Mann-Whitney



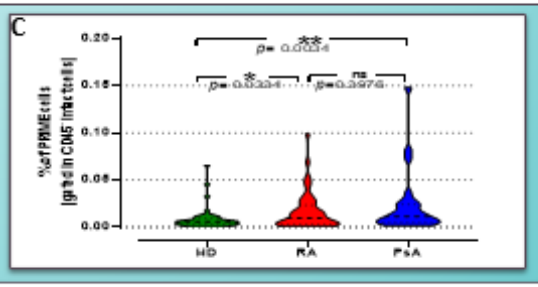


Figure 3. Detection of PRIME cells in the synovial fluid of RA samples. Increased percentages of PRIME cells in synovial fluid samples compared to the paired blood samples. Groups were compared by Wilcoxon matched-pairs signed rank test.

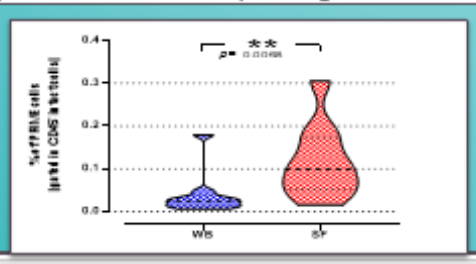
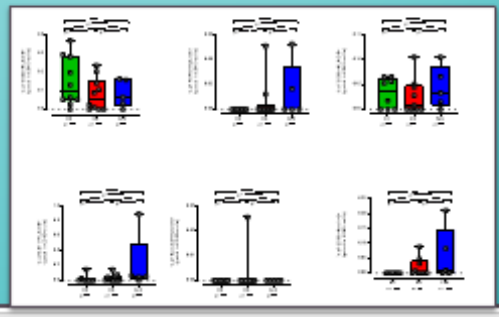


Figure 4. Detection of PRIME cells expressing HLA-DR in the peripheral blood of patients. Groups were compared non-parametric Mann-Whitney.



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Abstract n°:POS0427

On going projects

- Surgical specimen-derived synovial fibroblasts from patients with Rheumatoid Arthritis: Single cell Assay for Transposase-Accessible Chromatin (ATAC) sequencing to define aberrant molecular pathways

- Identification of inflammation-associated gene biomarkers expressed in human peripheral blood cells for the diagnosis of cancer *vs* infection *vs* autoimmunity: a machine – learning project based on publicly available RNA –seq data (first step)