I declare that unless otherwise stated, all work presented in this thesis is my own. Some aspects of the thesis were a collaboration, with some of the work conducted with or by others.

All the healthy volunteers and psoriasis patients’ samples were collected by myself and processing was part of a collaborative effort with past and current lab members Dr Anna Sanniti, Dr Andrew Brown and Giuseppe Scozzafava. The psoriatic arthritis samples processed for ATAC, qPCR array and mass cytometry were part of the Immune Function in Inflammatory Arthritis (IFIA) study established in 2006 and sample collection was a collaborative effort with Dr Hussein Al-Mossawi and Dr Nicole Yager.

The fixation protocol for sorted primary cells using DSP was optimised by Moustafa Attar. RNA extraction, ATAC and ChIPm processing for the healthy controls and psoriasis cohorts was carried out together with the ankylosing spondylitis samples in collaboration with Dr Anna Sanniti and Dr Andrew Brown. Advice for ATAC and ChIPm library indexing and sequencing was provided by Amy Trebes. RNA-seq and 10X Genomics technology Chromium single cell 3' expression library preparations and sequencing together with ATAC and ChIPm sequencing were performed by Oxford Genomics Centre at the Wellcome Centre for Human Genetics. Processing of the qPCR array and mass cytometry samples was conducted by UCB and measurement of synovial fluid cytokine and chemokine abundance was carried out by collaborators in Basle.

Regarding analysis, mass cytometry data was analysed by Dr Nicole Yager. Advice for analysis of different datasets were provided by Dr Silvia Salatino, Dr Hai Fang, Dr Katie Burnham, Dr Gabriele Migliorini, Dr Adri \'{a}n Cort \'{e}s and Enrique V \'{a}quez de Luis. All the resources for fine-mapping analysis using genotyping or summary statistics data were provided by Dr Adri \'{a}n Cort \'{e}s. The script to calculate enrichment across TSS and a function for colour-coding KEGG pathways based on gene expression data were provided by Dr Silvia Salatino (part of the Oxford Genomics Centre resources) and Dr Hai Fang, respectively.