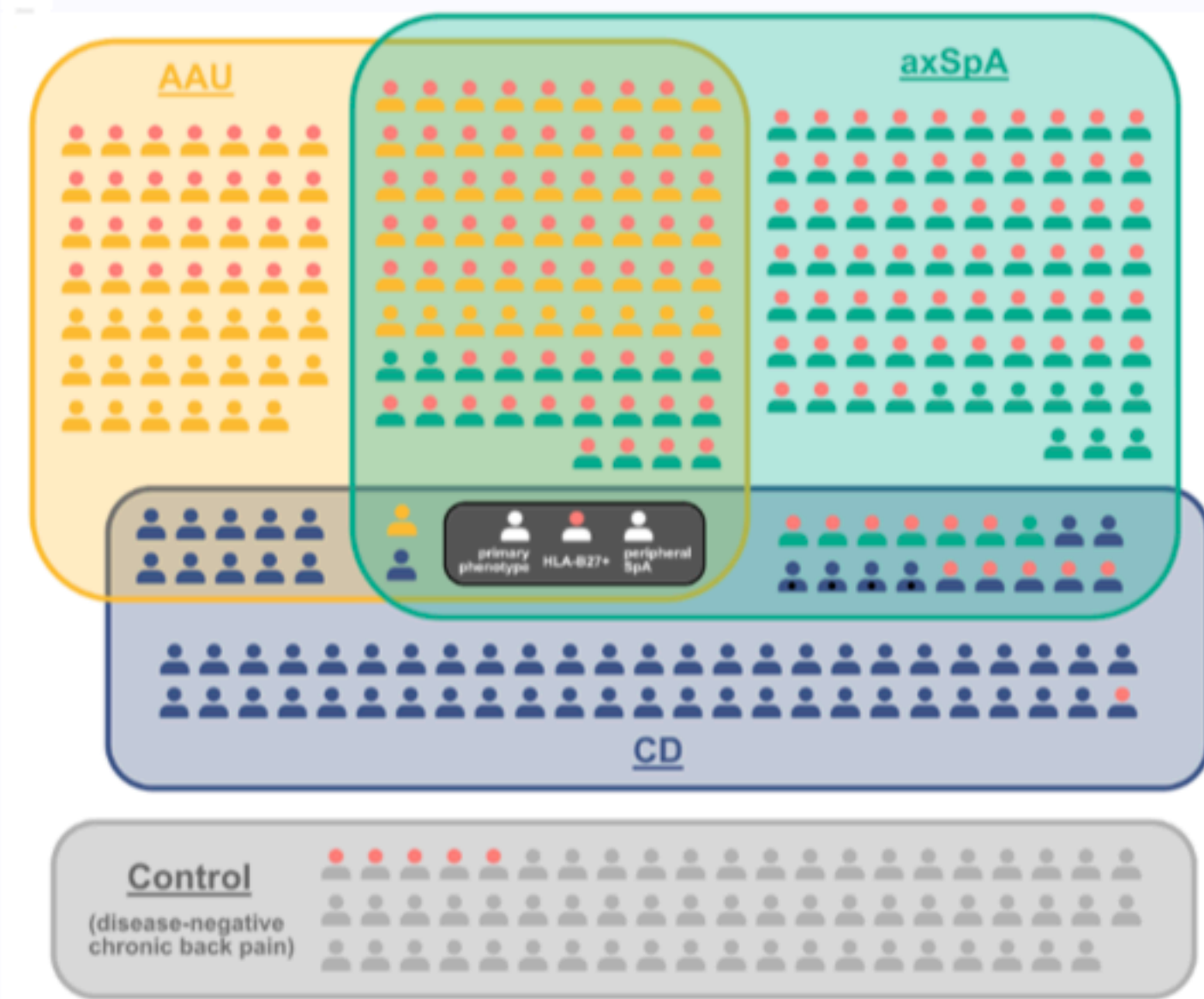
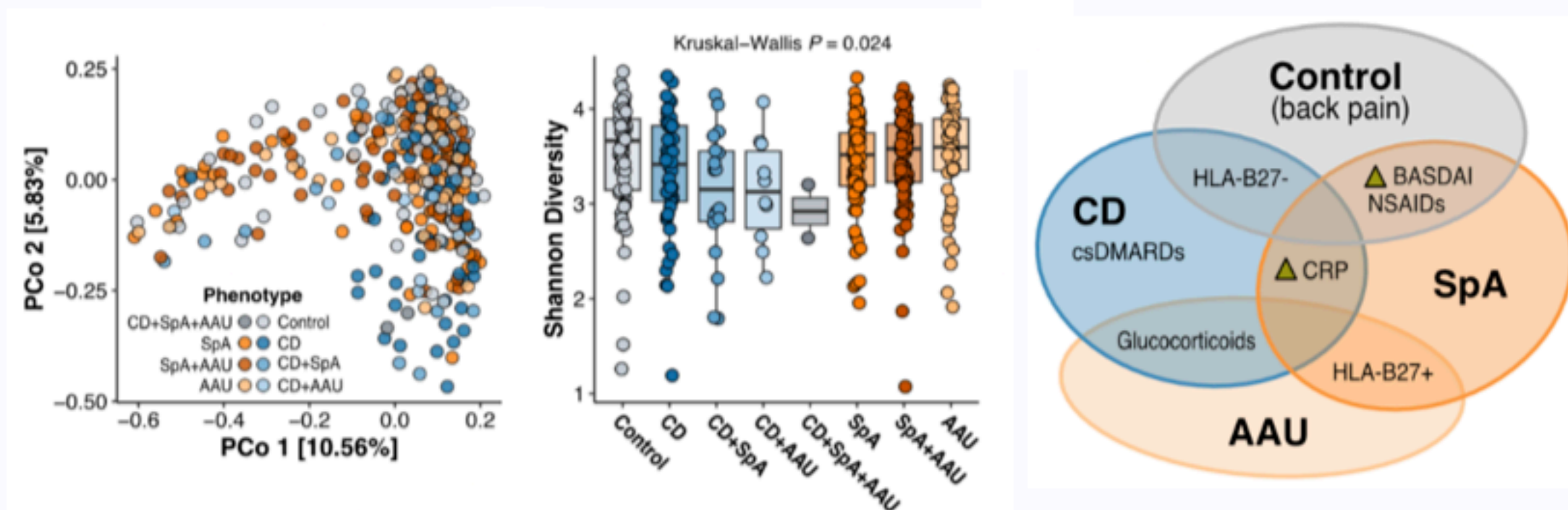


Characterizing the gut microbiota in axial spondyloarthritis and related inflammatory diseases

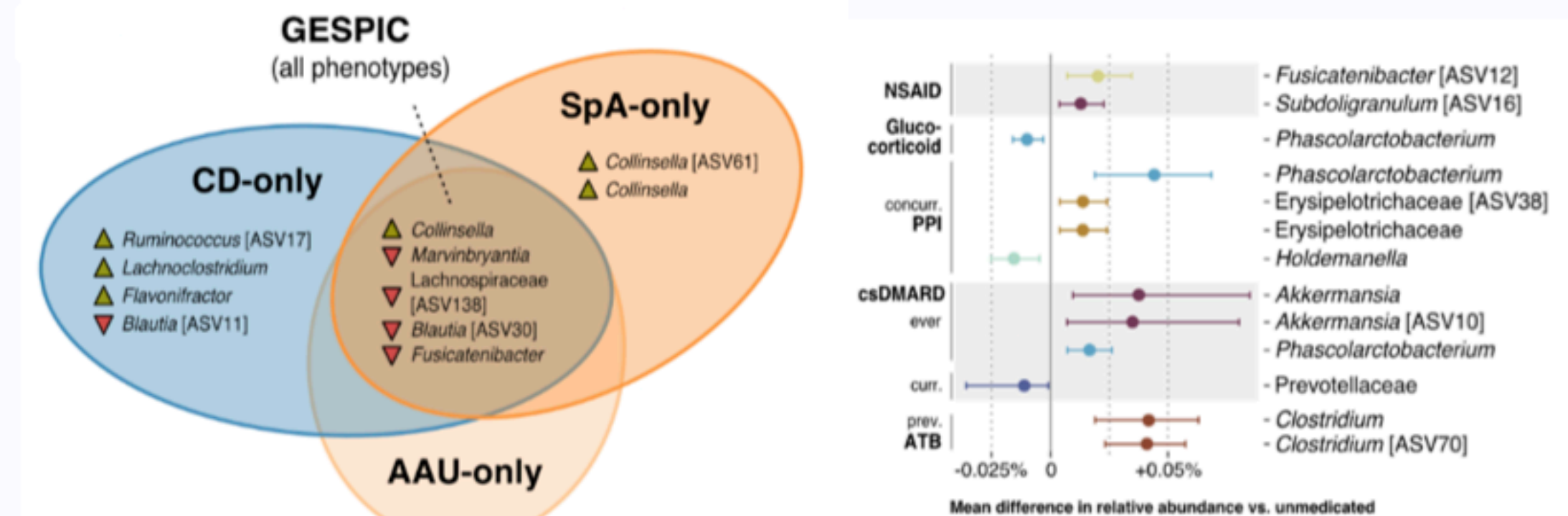
- 1 Sequenced **16S rRNA** genes in a **large mixed cohort** of 89% **bDMARD-naive** patients, allowing a better approximation of baseline disease signals



- 2 Considered **phenotypic heterogeneity** and a wide range of clinically-relevant factors in **case-control analyses**



- 3 Revealed associations between microbial taxa and **specific disease states**, considering **drug therapies** as potential confounders



Our data support a common gut dysbiosis among SpA and related diseases. Multiple findings suggest a potential keystone role of *Fusicatenibacter* in host inflammation and disease, but validation studies are still needed.

